Figure S1

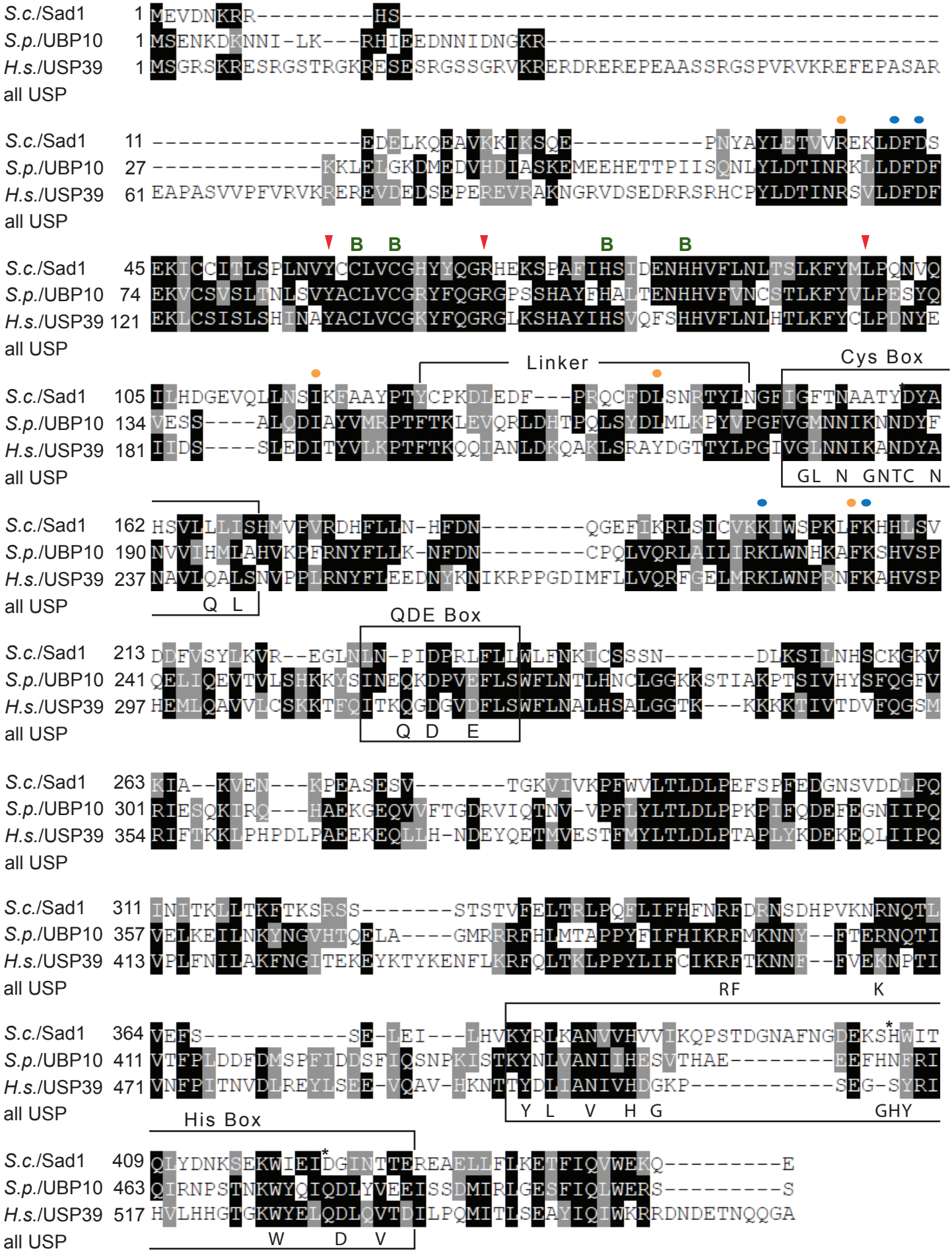
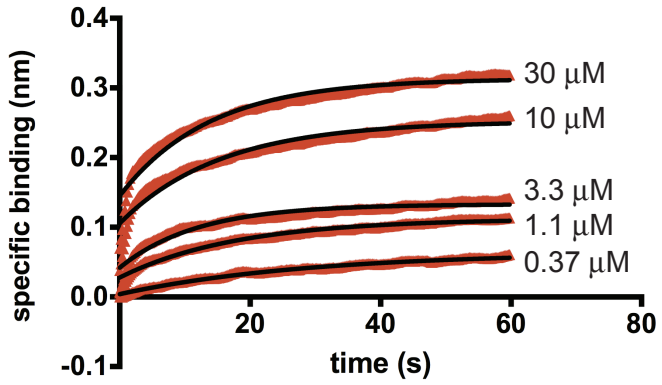
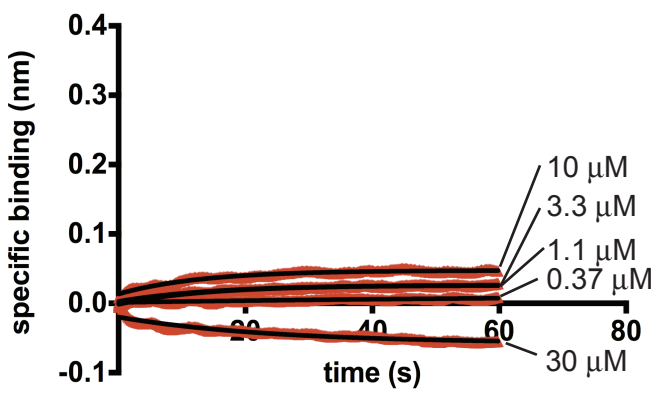

S.c./Sad1
S.p./UBP10
H.s./USP39
all USP
Linker
Cys Box
GL N GNTC N
Q L
QDE Box
Q D E
RF
K
Y L V H G
GHY
His Box
W D V

Figure S2

A



B



C

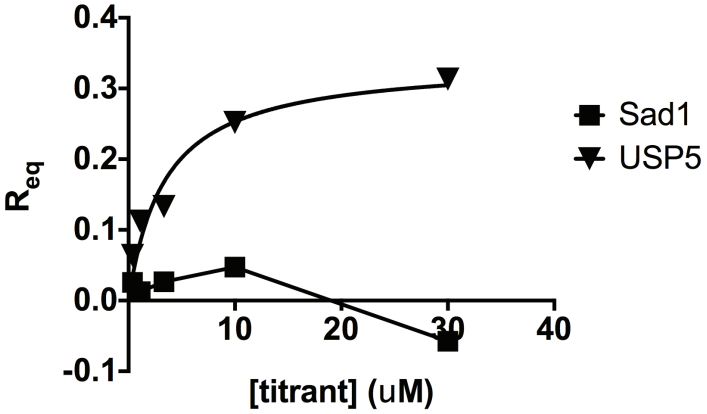
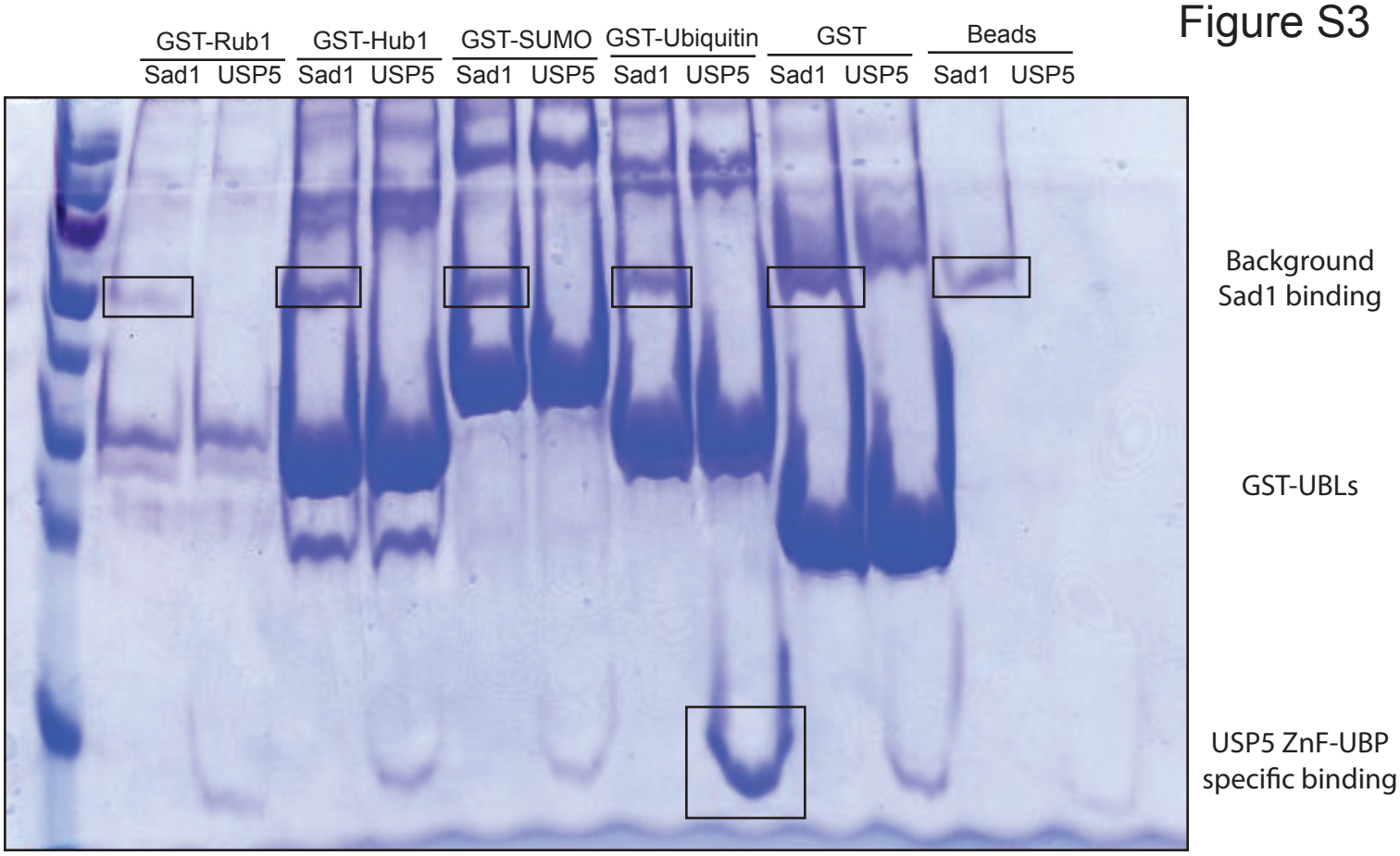


Figure S3

A


GST-Rub1
GST-Hub1
GST-SUMO
GST-Ubiquitin
GST
Beads
Sad1 USP5 Sad1 USP5 Sad1 USP5 Sad1 USP5 Sad1 USP5 Sad1 USP5
Background Sad1 binding
GST-UBLs
USP5 ZnF-UBP specific binding

B

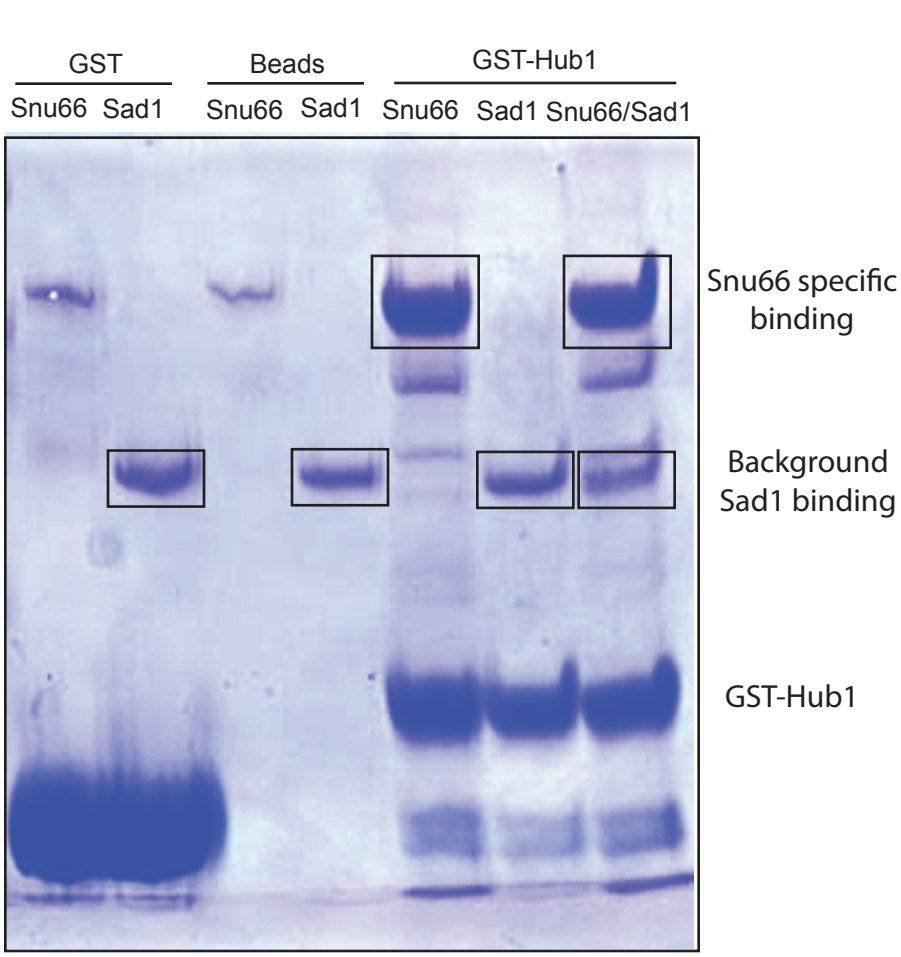

GST
Beads
GST-Hub1
Snu66 Sad1 Snu66 Sad1 Snu66 Sad1 Snu66/Sad1
Snu66 specific binding
Background Sad1 binding
GST-Hub1

Figure S4

A

Sad1 Molprobity

Summary statistics

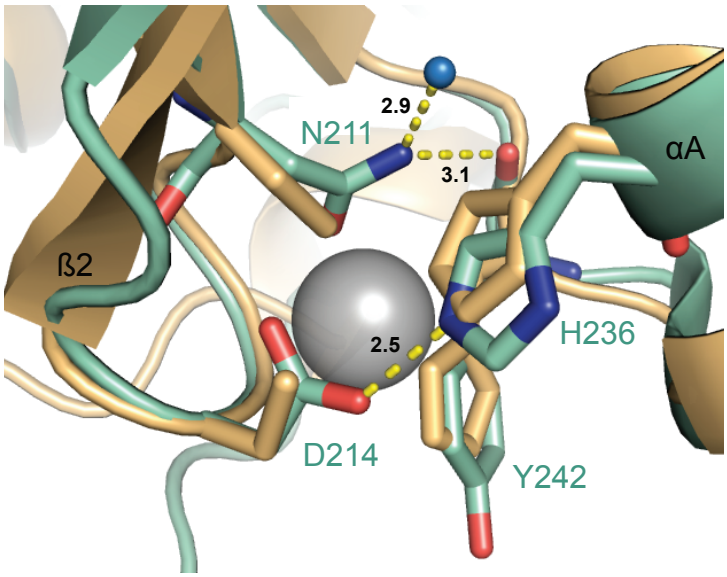
All-Atom Contacts	Clashscore, all atoms:	1.91		100th percentile* (N=778, 1.870Å ± 0.25Å)
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	3	0.81%	Goal: <1%
	Ramachandran outliers	0	0.00%	Goal: <0.05%
	Ramachandran favored	378	97.67%	Goal: >98%
	MolProbity score^	1.03		100th percentile* (N=11964, 1.870Å ± 0.25Å)
	Cβ deviations >0.25Å	0	0.00%	Goal: 0
	Bad backbone bonds:	0 / 1576	0.00%	Goal: 0%
	Bad backbone angles:	0 / 1963	0.00%	Goal: <0.1%

In the two column results, the left column gives the raw count, right column gives the percentage.
* 100th percentile is the best among structures of comparable resolution; 0th percentile is the worst. For clashscore the comparative set of structures was selected in 2004, for MolProbity score in 2006.
^ MolProbity score combines the clashscore, rotamer, and Ramachandran evaluations into a single score, normalized to be on the same scale as X-ray resolution.

Figure S5

A

Sad1 ZnF-UBP
USP5 ZnF-UBP



B