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*** DrugScore-PPI 1.0 ***
Knowledge-based Scoring Function to
Predict Protein-Protein Interactions
D. M. Krüger, H. Gohlke
2009

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In silico alanine scanning on chain A for PDB-ID 1Z92.
(original file, uploaded from PDB)

Date: 2010-01-27 16:34:56

Residue	ddGcalc [kcal/mol]	Degree Of Buriedness	Possible Saltbridges
TYR31A	0.02	0.83	-
ASN33A	0.24	8.25	-
LYS35A	0.93	4.95	-
THR37A	0.14	3.63	-
ARG38A	1.60	6.05	X
MET39A	0.16	5.50	-
THR41A	0.45	7.33	-
PHE42A	1.13	4.19	-
LYS43A	0.45	4.14	-
PHE44A	0.32	5.00	-
TYR45A	4.05	5.71	-
GLU60A	0.18	6.26	-
GLU61A	0.11	7.88	-
GLU62A	0.59	8.34	X
LYS64A	0.05	1.68	-
LEU66A	0.08	2.72	-
GLU67A	0.12	4.17	-
GLU68A	0.27	5.18	-
VAL69A	0.30	4.96	-
ASN71A	0.13	3.52	-
LEU72A	0.60	5.09	-
MET104A	0.03	0.94	-
CYS105A	0.22	7.42	-
GLU106A	-0.24	4.17	-
TYR107A	1.19	9.58	-
ASP109A	0.24	3.71	-
GLU110A	0.09	3.10	-
THR111A	0.07	2.44	-

