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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 cluster2_1.
(file uploaded by user)

Date: 2018-05-08 15:09:51

Residue	ddGcalc [kcal/mol]	Degree Of Buriedness	Possible Saltbridges
TYR9A	0.12	4.01	-
PHE10A	0.36	2.50	-
ASN11A	0.02	2.44	-
ARG15A	0.07	2.28	-
ILE35A	0.08	2.72	-
LYS36A	0.11	3.37	-
SER37A	0.18	6.14	-
GLU39A	0.07	2.15	-
LEU41A	0.24	2.72	-
ASP42A	2.51	8.85	-
LYS43A	0.10	3.32	-
ARG45A	0.89	5.01	-
ASN46A	1.24	4.67	-
MET51A	0.27	2.72	-
PHE52A	0.97	5.54	-
GLN53A	1.04	8.94	-
GLN54A	0.24	3.93	-
VAL55A	0.06	2.16	-
GLN67A	0.82	3.99	-
ARG69A	-0.19	3.03	-
ASN73A	0.33	7.03	-
TYR82A	0.26	8.89	-
ARG89A	-0.10	3.77	X
GLU97A	0.25	6.32	-
ASP101A	4.35	7.49	-
GLU104A	0.13	6.32	-
MET105A	0.11	2.72	-
LEU108A	0.08	2.72	-
LEU109A	0.11	3.67	-
VAL111A	0.63	5.38	-
CYS112A	0.11	3.93	-
GLU115A	0.57	6.32	-
GLU116A	0.09	3.10	-
LYS120A	0.14	4.68	-
LYS127A	0.17	5.87	-
ARG131A	-0.09	4.56	-
TYR132A	0.18	4.01	-
MET208A	0.06	1.89	-
ASP209A	-3.19	1.21	-

