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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 15:25:45

Residue	ddGcalc [kcal/mol]	Degree Of Buriedness	Possible Saltbridges
LEU3A	0.45	5.45	-
PHE28A	0.15	5.00	-
GLN47A	0.08	2.96	-
ASN49A	0.22	7.17	-
LEU51A	1.08	5.45	-
LYS53A	0.34	3.32	-
ASP59A	1.86	9.43	-
ASP61A	1.46	3.71	-
PHE62A	0.94	5.54	-
THR63A	0.15	4.82	-
LEU64A	0.61	3.67	-
THR65A	0.38	8.45	-
GLU66A	0.12	3.10	-
SER67A	0.10	1.60	-
VAL68A	1.52	4.27	-
ILE70A	0.11	3.61	-
LEU72A	0.12	2.78	-
TYR73A	2.85	8.80	-
LEU74A	0.05	1.83	-
THR75A	0.11	3.63	-
ARG76A	1.73	5.35	X
LYS77A	1.67	8.22	-
TYR78A	1.01	4.01	-
LYS79A	0.05	1.68	-
GLN87A	0.17	5.98	-
ARG92A	0.26	6.10	X
ASP96A	0.05	5.00	-
GLU97A	-0.16	5.24	-
TYR98A	0.12	4.01	-
LEU99A	0.24	3.61	-
TRP101A	0.12	4.14	-
HIS103A	0.06	5.78	-
THR104A	0.38	3.70	-
ARG107A	-0.17	6.10	-
ARG108A	0.73	6.14	X
ARG112A	0.25	6.10	X
TRP234A	0.09	2.07	-
LEU236A	0.05	1.83	-
MET238A	0.45	5.50	-
ILE239A	0.08	2.78	-
ARG240A	1.44	7.29	X

