

*** DrugScore-PPI 1.0 ***
Knowledge-based Scoring Function to
Predict Protein-Protein Interactions
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2009

In silico alanine scanning on chain B for PDB-ID cluster7_1.
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Residue	ddGcalc [kcal/mol]	Degree Of Buriedness	Possible Saltbridges
ASP279B	0.18	6.28	-
LYS282B	0.37	3.32	-
LEU286B	0.43	2.72	-
TYR287B	3.08	6.40	-
LYS290B	0.37	2.22	-
GLU291B	0.16	2.09	-
GLU295B	0.39	6.32	-
ARG298B	0.73	5.31	-
ILE324B	0.11	3.61	-
GLN325B	0.01	4.96	-
ASP326B	-0.08	6.28	-
TYR327B	0.45	3.96	-
ASP328B	0.75	5.07	-
PHE357B	0.12	4.19	-
ARG361B	1.65	8.38	X
ARG362B	0.91	4.52	-
ASN363B	0.17	5.89	-
LEU364B	0.13	4.61	-
ARG395B	0.27	9.17	-
LYS512B	0.62	5.00	-
GLU516B	0.28	9.48	-
THR550B	0.18	6.08	-
THR552B	0.28	6.08	-
ASP553B	3.24	7.49	-
VAL554B	0.17	4.39	-
THR555B	0.40	4.82	-
VAL556B	0.14	4.27	-
ILE577B	0.03	0.94	-
ASN579B	0.46	5.49	-
GLU582B	-0.16	2.09	-
GLU583B	0.15	5.24	-
LYS584B	0.89	4.95	-
VAL612B	0.18	6.01	-
SER613B	0.26	6.14	-
ILE614B	1.36	3.61	-
SER615B	0.23	7.83	-
LYS616B	0.46	3.04	-
PHE617B	0.05	1.68	-
GLU618B	-0.22	4.17	-
GLU619B	0.04	4.17	-
GLU640B	0.03	3.16	-
LEU641B	0.58	3.67	-
CYS643B	0.19	6.57	-
LYS644B	1.29	6.69	-
LYS645B	0.70	4.14	-
PHE646B	0.11	3.86	-
PHE647B	0.76	8.14	-
GLU648B	-0.23	7.33	X
MET649B	0.23	4.50	-
ASN651B	-0.06	3.52	-
THR652B	0.75	8.52	-
ILE653B	0.49	2.78	-
THR654B	0.18	6.08	-

GLU655B -0.21 3.10 -

