

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

In silico alanine scanning on chain A for PDB-ID cluster7_1.
(file uploaded by user)

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| Residue | ddGcalc [kcal/mol] | Degree Of Buriedness | Possible Saltbridges |
|---------|-----------------------|-------------------------|-------------------------|
| TYR9A | 0.12 | 4.01 | - |
| PHE10A | 0.72 | 6.74 | - |
| ASN11A | 0.04 | 1.22 | - |
| ARG15A | 0.56 | 3.03 | - |
| ILE35A | 0.19 | 6.44 | - |
| LYS36A | 0.05 | 1.68 | - |
| SER37A | 0.27 | 9.16 | - |
| GLU39A | 0.23 | 4.23 | - |
| ASP40A | 0.18 | 6.28 | - |
| LEU41A | 0.48 | 3.67 | - |
| ASP42A | 0.50 | 3.78 | - |
| ARG45A | -0.23 | 3.77 | - |
| LEU50A | 0.11 | 3.61 | - |
| MET51A | 0.20 | 1.89 | - |
| PHE52A | 1.00 | 4.72 | - |
| GLN53A | 1.40 | 6.89 | - |
| GLN54A | 0.75 | 4.96 | - |
| VAL55A | 0.10 | 2.16 | - |
| MET63A | 0.13 | 3.61 | - |
| LEU65A | 0.49 | 2.72 | - |
| VAL66A | 0.12 | 4.27 | - |
| GLN67A | 1.17 | 5.98 | - |
| THR68A | 0.27 | 4.82 | - |
| ARG69A | 3.27 | 6.05 | X |
| ILE71A | 0.13 | 4.50 | - |
| ASN73A | 1.41 | 9.33 | - |
| TYR74A | 0.18 | 3.96 | - |
| SER77A | 0.09 | 3.11 | - |
| TYR82A | 0.55 | 8.11 | - |
| ILE86A | 1.04 | 2.72 | - |
| LYS87A | 0.10 | 1.68 | - |
| ARG89A | 0.68 | 5.31 | - |
| LEU91A | 0.08 | 2.72 | - |
| ASP93A | 1.02 | 8.78 | - |
| MET94A | 0.32 | 5.50 | - |
| ILE96A | 0.23 | 3.67 | - |
| GLU97A | 0.50 | 5.18 | - |
| ASP101A | 1.38 | 4.92 | - |
| LEU102A | 0.08 | 2.72 | - |
| GLU104A | 0.58 | 7.33 | - |
| MET105A | 0.38 | 5.39 | - |
| ILE106A | 0.08 | 2.72 | - |
| LEU107A | 0.11 | 3.67 | - |
| LEU108A | 0.92 | 5.50 | - |
| VAL111A | 0.62 | 4.27 | - |
| CYS112A | 0.19 | 6.57 | - |
| GLU115A | 0.97 | 6.32 | X |
| GLU116A | 0.37 | 6.86 | - |
| LYS117A | 0.15 | 5.00 | - |
| ASP118A | 0.04 | 1.29 | - |
| LYS120A | 0.48 | 5.49 | - |
| LEU123A | 0.11 | 3.67 | - |
| ARG131A | 0.09 | 3.03 | - |

| | | | |
|---------|------|------|---|
| TYR132A | 0.09 | 3.22 | - |
| MET208A | 0.18 | 2.78 | - |

