**DIRseq: a method for predicting drug-interacting residues of intrinsically disordered proteins from sequences**

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Supplementary File 1

Supplementary File 1A. List of IDPs and drugs that bind to them

|  |  |  |  |
| --- | --- | --- | --- |
| IDP name | IDP sequence | Drug name (MW in Da) | Drug structurea |
| p27(UniProt P46527; residues 22-105) | EHPKPSACRNLFGPVDHEELTRDLEKHCRDMEEASQRKWNFDFQNHKPLEGKYEWQEVEKGSLPEFYYRPPRPPKGACKVPAQE | SJ403(275.3) | A green blue and red molecule  AI-generated content may be incorrect. |
| p21(UniProt P38936; residues 10-82) | QNPCGSKACRRLFGPVDSEQLSRDCDALMAGCIQEARERWNFDFVTETPLEGDFAWERVRGLGLPKLYLPTGP |
| p53(UniProt P04637; residues 1-91) | MEEPQSDPSVEPPLSQETFSDLWKLLPENNVLSPLPSQAMDDLMLSPDDIEQWFTEDPGPDEAPRMPEAAPPVAPAPAAPTPAAPAPAPSW | EGCG(458.4) | A green and red molecule  AI-generated content may be incorrect. |
| α-synuclein (UniProt P37840; residues 1-140) | MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEKTKEQVTNVGGAVVTGVTAVAQKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMPVDPDNEAYEMPSEEGYQDYEPEA | Fasudil(291.4) | A colorful hexagons connected to each other  AI-generated content may be incorrect. |
| Ligand-47 (323.4) | A colorful molecule structure on a black background  AI-generated content may be incorrect. |
| Tau-5\* (BMRB 51480; residues 330-448) | AAGSSGTLELPSTLSLYKSGALDEAAAYQSRDYYNFPLALAGPPPPPPPPHPHARIKLENPLDYGSAWAAAAAQCRYGDLASLHGAGAAGPGSGSPSAAASSSWHTLFTAEEGQLYGPC | 1aa(376.8) | A green and red hexagons on a black background  AI-generated content may be incorrect. |
| EPI-001(394.9) | A green and red molecule  AI-generated content may be incorrect. |
| NS5A-D2D3(residues 247-466, corresponding to UniProt Q99IB8 residues 2223-2442) | SNTYDVDMVDANLLMEGGVAQTEPESRVPVLDFLEPMAEEESDLEPSIPSECMLPRSGFPRALPAWARPDYNPPLVESWRRPDYQPPTVAGCALPPPKKAPTPPPRRRRTVGLSESTISEALQQLAIKTFGQPPSSGDAGSSTGAGAAESGGPTSPGEPAPSETGSASSMPPLEGEPGDPDLESDQVELQPPPQGGGVAPGSGSGSWSTCSEEDDTTVCC | 5-Fluoroindole (135.1) | A green and blue molecule  AI-generated content may be incorrect. |
| β2 microglobulin(UniParc UPI0000110347; residues 1-99) | IQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSQPKIVKWDRDM | Rifamycin SV (697.8) | A green and red molecule  AI-generated content may be incorrect. |
| hIAPP(UniParc UPI000002B886; residues 1-37) | KCNTATCATQRLANFLVHSSNNFGAILSSTNVGSNTY | YX-I-1(435.5) | A green and blue molecule  AI-generated content may be incorrect. |
| Aβ42(UniParc UPI00000315E8; residues 1-42) | DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA | Myricetin (320.3) | A green and red molecule  AI-generated content may be incorrect. |
| c-Myc(UniProt P01106-1; residues 363-412) | ERQRRNELKRSFFALRDQIPELENNEKAPKVVILKKATAYILSVQAEEQK | 10074-G5 (332.3) | A green and blue molecule  AI-generated content may be incorrect.  |
| 10074-A4 (409.3) | A green and blue molecule  AI-generated content may be incorrect. |
| 10058-F4 (249.4) | A green molecule with blue and green sticks  AI-generated content may be incorrect. |

aAtom color scheme: carbon, green; nitrogen, blue; oxygen, red; sulfur, yellow, fluorine, sky blue; and chlorine, dark green.

Supplementary File 1B. Dependences of prediction accuracies on model parameters

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | *r* | *r* sum | FP | FN | TP | TP-FP |
|  | p27 | p21 | p53 | α-syn |
| *q* parameters |
| seqDYN orig | 0.79 | 0.57 | 0.61 | 0.46 | 2.43 | 12 | 12 | 19 |  7 |
| DIRseq L only | 0.82 | 0.55 | 0.67 | 0.49 | 2.53 |  8 |  7 | 24 |  16 |
| DIRseq I only | 0.79 | 0.62 | 0.56 | 0.46 | 2.43 | 10 | 11 | 20 |  10 |
| DIRseq M only | 0.80 | 0.58 | 0.60 | 0.39 | 2.37 | 11 | 14 | 17 |  6 |
| DIRseq D only | 0.73 | 0.63 | 0.62 | 0.54 | 2.52 | 12 | 11 | 20 |  8 |
| DIRseq | 0.82 | 0.66 | 0.67 | 0.51 | 2.66 | 10 |  6 | 25 |  15 |
| Aromatic | 0.74 | 0.74 | 0.56 | 0.62 | 2.66 | 22 | 10 | 21 |  -1 |
| CALDAVOS2 | 0.52 | 0.23 | 0.33 | 0.13 | 1.21 | 27 | 25 |  6 | -21 |
| Avg HPS scale | 0.13 | 0.01 | 0.16 | 0.14 | 0.44 | 23 | 28 |  3 | -20 |
| *b* value |
| 0.0316 | 0.32 | 0.58 | 0.57 | 0.63 | 2.10 | 15 | 11 | 20 |  5 |
| 0.1 | 0.77 | 0.66 | 0.64 | 0.59 | 2.66 | 14 | 11 | 20 |  6 |
| 0.3 | 0.82 | 0.66 | 0.67 | 0.51 | 2.66 | 10 |  6 | 25 |  15 |
| 0.5 | 0.81 | 0.65 | 0.66 | 0.48 | 2.60 |  9 |  7 | 24 |  15 |
| 1 | 0.77 | 0.61 | 0.65 | 0.42 | 2.45 |  7 | 12 | 19 |  12 |
| 3 | 0.68 | 0.51 | 0.58 | 0.32 | 2.09 |  4 | 21 | 10 |  6 |
| *s*1 value |
| 0.5 | 0.71 | 0.60 | 0.55 | 0.42 | 2.28 | 71 |  2 | 29 | -42 |
| 1 | 0.79 | 0.65 | 0.61 | 0.47 | 2.52 | 35 |  4 | 27 |  -8 |
| 1.5 | 0.82 | 0.66 | 0.67 | 0.51 | 2.66 | 10 |  6 | 25 |  15 |
| 2 | 0.82 | 0.63 | 0.71 | 0.55 | 2.71 |  5 | 19 | 12 |  7 |
| 2.5 | 0.80 | 0.58 | 0.72 | 0.58 | 2.68 |  1 | 25 |  6 |  5 |
| *s*2 value |
| 5 | 0.74 | 0.62 | 0.63 | 0.43 | 2.42 | 10 |  6 | 25 |  15 |
| 10 | 0.79 | 0.65 | 0.65 | 0.48 | 2.57 | 10 |  6 | 25 |  15 |
| 14 | 0.82 | 0.66 | 0.67 | 0.51 | 2.66 | 10 |  6 | 25 |  15 |
| 20 | 0.84 | 0.66 | 0.67 | 0.56 | 2.73 | 10 |  6 | 25 |  15 |