

Additional file 7: Overview of the significance of the found amino acid-base FreSCOs in the protein-DNA complex structure dataset. Frequency and cohesion radius of the significant amino acid-base patterns. P-value based on the cohesion radius of the same FreSCOs in permuted DNA-protein structures.

| FreSCO | Frequency | Cohesion radius | P-value |
|--------------|-----------|-----------------|-----------|
| DT GLY ARG | 0.939676 | 6.127467 | 2.97E-283 |
| DT GLY | 0.939676 | 4.530339 | 4.51E-266 |
| DT GLY SER | 0.935195 | 6.155224 | 1.95E-209 |
| DT THR GLY | 0.935195 | 6.386277 | 2.00E-158 |
| DT GLY ALA | 0.936574 | 6.389396 | 1.46E-108 |
| DT SER | 0.943123 | 4.683291 | 9.63E-100 |
| DA DT DG SER | 0.89314 | 6.752896 | 4.90E-97 |
| DT LYS ASN | 0.940021 | 6.627604 | 1.00E-92 |
| DC DA DG SER | 0.892106 | 6.796654 | 3.98E-86 |
| DT LYS SER | 0.942778 | 6.13308 | 8.37E-82 |
| DA DT DG ARG | 0.896932 | 6.617025 | 4.68E-79 |
| DT ARG SER | 0.943123 | 6.229689 | 2.21E-78 |
| DC GLY ARG | 0.922096 | 6.308396 | 7.48E-78 |
| DC GLY | 0.922096 | 4.890112 | 9.94E-75 |
| DT THR SER | 0.939676 | 6.496252 | 1.35E-71 |
| DT SER ASN | 0.937608 | 6.809997 | 2.21E-61 |
| DT LYS THR | 0.942778 | 6.349891 | 4.12E-58 |
| DA DT DG GLY | 0.889004 | 6.7881 | 1.08E-57 |
| DC THR GLY | 0.916925 | 6.672068 | 6.23E-54 |
| DC DT GLY | 0.895209 | 6.047739 | 9.24E-54 |
| DC LYS GLY | 0.921751 | 6.251711 | 2.82E-53 |
| DC LYS THR | 0.924509 | 6.524064 | 2.54E-51 |
| DA DT GLY | 0.896932 | 6.10275 | 4.48E-50 |
| DT LYS GLY | 0.939331 | 6.169234 | 3.84E-49 |
| DT ASN | 0.940021 | 5.325566 | 1.60E-48 |
| DT GLY PRO | 0.927956 | 6.920673 | 3.68E-47 |
| DT LYS ARG | 0.94726 | 6.160239 | 8.12E-46 |
| DC LYS ARG | 0.929679 | 6.166498 | 5.97E-43 |
| DC THR ARG | 0.924853 | 6.571643 | 1.42E-41 |
| DT GLY ASN | 0.932092 | 6.922134 | 8.47E-40 |
| DT GLN SER | 0.932092 | 6.923004 | 3.25E-39 |
| DC SER | 0.924509 | 4.8843 | 5.42E-38 |
| DC GLY SER | 0.91658 | 6.414189 | 6.40E-37 |
| DC DA DG GLY | 0.889004 | 6.89531 | 1.27E-36 |
| DT ILE GLY | 0.930024 | 6.582475 | 1.31E-36 |
| DA DT ASN | 0.897277 | 6.770477 | 2.05E-35 |
| DA DT DG | 0.905895 | 2.950319 | 3.32E-35 |
| DC LYS SER | 0.924164 | 6.348909 | 6.06E-35 |
| DA DG SER | 0.903137 | 6.234865 | 7.44E-35 |

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| DC DA DG ARG | 0.896932 | 6.716098 | 1.80E-34 |
| DT THR ARG | 0.943123 | 6.482018 | 1.86E-33 |
| DC ARG ASN | 0.921751 | 6.755637 | 4.72E-33 |
| DA DG ARG | 0.907963 | 6.089308 | 1.35E-32 |
| DT ARG ASN | 0.940021 | 6.777521 | 8.04E-32 |
| DC ARG SER | 0.924509 | 6.374127 | 8.82E-32 |
| DC THR SER | 0.921062 | 6.683413 | 5.35E-31 |
| DT THR ASN | 0.936574 | 6.987177 | 6.83E-31 |
| DA DT SER | 0.901413 | 6.211182 | 2.70E-30 |
| DC DA DT GLY | 0.882799 | 6.885953 | 1.73E-29 |
| DT ILE ASN | 0.932437 | 6.976099 | 2.03E-29 |
| DA DT ARG | 0.905205 | 6.074988 | 5.85E-28 |
| DT THR | 0.947949 | 5.079601 | 8.54E-28 |
| DC DT DG SER | 0.890038 | 6.941497 | 1.41E-24 |
| DT GLY VAL | 0.931058 | 6.621836 | 5.37E-24 |
| DC LYS ASN | 0.921751 | 6.834252 | 9.23E-24 |
| DT ILE SER | 0.935884 | 6.674606 | 2.59E-22 |
| DC DT DG GLY | 0.886936 | 6.9326 | 1.28E-21 |
| DT ILE THR | 0.934161 | 6.804892 | 6.87E-20 |
| DA DG GLY | 0.900034 | 6.276371 | 1.78E-19 |
| DC DG SER | 0.906929 | 6.245179 | 2.35E-19 |
| DC DG GLY | 0.904516 | 6.2695 | 3.78E-19 |
| DC DT SER | 0.898311 | 6.175282 | 4.97E-19 |
| DC DA DG LYS | 0.896932 | 6.751376 | 1.31E-18 |
| DC DA DT SER | 0.886936 | 6.945109 | 1.34E-18 |
| DC DT LYS | 0.903137 | 6.000176 | 3.24E-18 |
| DC DA DT ARG | 0.890727 | 6.794205 | 1.55E-17 |
| DC ASN | 0.921751 | 5.436475 | 2.21E-17 |
| DC DT ASN | 0.895209 | 6.70148 | 2.88E-17 |
| DT ARG | 0.947949 | 4.800107 | 5.10E-17 |
| DC ALA SER | 0.923819 | 6.537923 | 6.55E-16 |
| DA DT DG LYS | 0.896932 | 6.803256 | 1.21E-15 |
| DT ALA SER | 0.941744 | 6.558472 | 8.41E-15 |
| DA DG ASN | 0.89969 | 6.87482 | 1.37E-14 |
| DC DT ARG | 0.903137 | 6.04922 | 6.88E-14 |
| DC ARG | 0.930369 | 4.857176 | 3.00E-13 |
| DT LYS | 0.947949 | 4.771483 | 1.69E-12 |
| DA DT THR | 0.905205 | 6.563358 | 2.11E-11 |
| DC DT DG ARG | 0.894864 | 6.807256 | 6.53E-11 |
| DT THR ALA | 0.941055 | 6.664431 | 2.02E-10 |
| DT DG GLY | 0.90555 | 6.277393 | 1.32E-09 |
| DT SER VAL | 0.935884 | 6.714867 | 2.04E-09 |
| DC DG ASN | 0.904516 | 6.776123 | 3.55E-09 |
| DA GLY ARG | 0.918649 | 6.703545 | 6.01E-09 |
| DC DA DT LYS | 0.890727 | 6.8367 | 1.32E-08 |

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| DT DG ARG | 0.913478 | 6.159504 | 1.71E-08 |
| DT DG SER | 0.908652 | 6.307371 | 4.62E-08 |
| DT THR VAL | 0.935195 | 6.820829 | 1.95E-07 |
| DA DT LYS | 0.905205 | 6.185748 | 1.12E-06 |
| DC ILE GLY | 0.911755 | 6.794858 | 1.49E-06 |
| DC GLY ALA | 0.919683 | 6.691878 | 1.54E-06 |
| DC DT DG LYS | 0.894864 | 6.827585 | 1.73E-06 |
| DC DT THR | 0.902792 | 6.529231 | 3.52E-06 |
| DT ILE ARG | 0.937608 | 6.724475 | 3.98E-06 |
| DC DG ARG | 0.912789 | 6.13217 | 7.76E-06 |