**Table S3. Similar structures of VosA velvet domain in the 3D macromolecular structures database of NCBI by VAST+**

| | PDB ID | Description | Taxonomy | RMSD | Aligned residues | Sequence identity |
|---|---|---|---|---|---|---|
| 1 | 3QRF | Structure of a domain-swapped FOXP3 dimer | Homo sapiens | 3.20Å | 120 | 18% |
| 2 | 1A02 | STRUCTURE OF THE DNA BINDING DOMAINS OF NFAT, FOS AND JUN BOUND TO DNA | Others | 3.24Å | 117 | 18% |
| 3 | 1PZU | An Asymmetric Nfat1-Rhr Homodimer On A Pseudo-Palindromic, Kappa-B Site | Others | 2.42Å | 110 | 19% |
| 4 | 2V2T | X-Ray Structure Of A Nf-Kb P50-Relb-Dna Complex | Others | 3.21Å | 106 | 14% |
| 5 | 1S9K | Crystal Structure Of Human Nfat1 And Fos-Jun On The Il-2 Arre1 Site | Others | 2.38Å | 103 | 19% |
| 6 | 1LE9 | Crystal structure of a NF-kB heterodimer bound to the Ig/HIV-kB siti | Others | 2.53Å | 100 | 18% |
| 7 | 1GJI | Crystal Structure Of C-Rel Bound To Dna | Others | 2.69Å | 99 | 16% |
| 8 | 2I9T | Structure of NF-kB p65-p50 heterodimer bound to PRDII element of B-interferon promoter | Mus musculus | 2.73Å | 98 | 19% |
| 9 | 1LE5 | Crystal structure of a NF-kB heterodimer bound to an IFNb-kB | Others | 2.15Å | 97 | 19% |
| 10 | 2O6D | Structure of native rTp34 from Treponema pallidum | Treponema pallidum | 3.42Å | 97 | 10% |
| 11 | 6MBZ | Structure of Transcription Factor | Homo sapiens | 2.40Å | 96 | 14% |
| 12 | 3PJL | The Crystal Structure Of Tp34 Bound To Co (Ii) Ion At Ph 7.5 | Treponema pallidum | 3.39Å | 96 | 10% |
| 13 | 1LEI | The kB DNA sequence from the HLV-LTR functions as an allosteric regulator of HIV transcription | Others | 1.99Å | 95 | 19% |
| 14 | 3DO7 | X-Ray Structure Of A Nf-Kb P52RELBDNA COMPLEX | Others | 2.00Å | 95 | 21% |
| 15 | 1VKX | Crystal Structure Of The Nfkb P50P65 HETERODIMER COMPLEXED To The Immunoglobulin Kb Dna | Others | 2.26Å | 95 | 20% |
| 16 | 1IKN | IkappabalphaNF-Kappab Complex | Homo sapiens/Mus musculus | 2.70Å | 94 | 16% |
| 17 | 6MBW | Structure of Transcription Factor | Homo sapiens | 2.21Å | 93 | 13% |
| 18 | 5ZHU | Crystal structure of the DNA-binding domain of human myelin-gene regulatory factor | Homo sapiens | 2.57Å | 93 | 15% |
| 19 | 2O6F | Structure of metal- free rTp34 from Treponema pallidum | Treponema pallidum | 3.29Å | 93 | 11% |
| 20 | 1BVO | DORSAL HOMOLOGUE GAMBIF1 BOUND TO DNA | Anopheles gambiae | 2.03Å | 92 | 16% |
| 21 | 1NFK | STRUCTURE OF THE NUCLEAR FACTOR KAPPA-B (NF-KB) P50 HOMODIMER | Mus musculus | 2.10Å | 92 | 20% |
| 22 | 4Y5W | Transcription Factor-dna Complex | Homo sapiens | 2.11Å | 92 | 11% |
| 23 | 1EAO | The Runx1 Runt Domain At 1.4a Resolution: A Structural Switch And Specifically Bound Chloride Ions Modulate Dna Binding | Mus musculus | 2.19Å | 92 | 11% |
| 24 | 3LZR | Crystal Structure Analysis Of Manganese Treated P19 Protein From Campylobacter Jejuni At 2.73 A At Ph 9 And Manganese Peak Wavelength (1.893 A) | Campylobacter jejuni subsp. jejuni 81-176 | 3.75Å | 92 | 12% |
| 25 | 5D39 | Transcription Factor-dna Complex | Homo sapiens | 2.12Å | 91 | 11% |
| 26 | 5U01 | Cooperative DNA binding by two RelA dimers | Mus musculus/Synthesium | 2.25Å | 91 | 16% |
| 27 | 1E50 | AML1/CBFbeta complex | Homo sapiens | 2.31Å | 91 | 10% |
| 28 | 6HQC | Structural investigation of the TasA anchoring protein TapA from Bacillus subtilis | Bacillus subtilis | 2.94Å | 91 | 3% |
| 29 | 2XTJ | The crystal structure of PCSK9 in complex with 1D05 Fab | Homo sapiens | 3.11Å | 91 | 8% |
| 30 | 5TVZ | Solution NMR structure of Saccharomyces cerevisiae Pom152 Ig-like repeat, residues 718-820 | Saccharomyces cerevisiae | 3.90Å | 91 | 10% |
| 31 | 1A3Q | Human Nf-Kappa-B P52 Bound To Dna | Others | 1.77Å | 90 | 22% |
| 32 | 3GUT | Crystal structure of a higher-order complex of p50:RelA bound to the HIV-1 LTR | Others | 2.20Å | 90 | 17% |
| 33 | 6GGR | Crystal structure of Salmonella zinc metalloprotease effector GtgA in complex with p65 | Others | 2.26Å | 90 | 17% |
| 34 | 1HJC | CRYSTAL STRUCTURE OF RUNX-1/AML1/CBFALPHA RUNT DOMAIN BOUND TO A DNA FRAGMENT FROM THE CSF-1R PROMOTER | Homo sapiens/Mus musculus | 2.29Å | 90 | 10% |
| 35 | 1IO4 | Crystal Structure Of Runx-1AML1CBFALPHA RUNT DOMAIN- Cbfbeta Core Domain Heterodimer And CEBPBETA BZIP Homodimer Bound To A Dna Fragment From The Csf-1r Promoter | Others | 2.31Å | 90 | 10% |
| 36 | 1HJB | CRYSTAL STRUCTURE OF RUNX-1/AML1/CBFALPHA RUNT DOMAIN AND C/EBPBETA BZIP HOMODIMER BOUND TO A DNA FRAGMENT FROM THE CSF-1R PROMOTER | Homo sapiens/Mus musculus | 2.33Å | 90 | 10% |

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| 37 | 1LJM | Dna Recognition Is Mediated By Conformational Transition And By Dna Bending | Homo sapiens | 2.36Å | 90 | 9% |
| 38 | 3WTT | Crystal structure of the complex comprised of phosphorylated ETS1, RUNX1, CBFBETA, and the tcralpha gene enhancer DNA | Others | 2.36Å | 90 | 10% |
| 39 | 3WTY | Crystal structure of the complex comprised of ETS1(G333P), RUNX1, CBFBETA, and the tcralpha gene enhancer DNA | Others | 2.37Å | 90 | 10% |
| 40 | 3WTS | Crystal structure of the complex comprised of ETS1, RUNX1, CBFBETA, and the tcralpha gene enhancer DNA | Others | 2.38Å | 90 | 10% |
| 41 | 6F58 | Crystal structure of human Brachyury (T) in complex with DNA | Homo sapiens | 2.57Å | 90 | 6% |
| 42 | 2RAM | A Novel Dna Recognition Mode By Nf-Kb P65 Homodimer | Others | 2.04Å | 89 | 17% |
| 43 | 1EAQ | The Runx1 Runt Domain At 1.25a Resolution: A Structural Switch And Specifically Bound Chloride Ions Modulate Dna Binding | Mus musculus | 2.07Å | 89 | 10% |
| 44 | 2J6W | R164n Mutant Of The Runx1 Runt Domain | Mus musculus | 2.14Å | 89 | 10% |
| 45 | 4L18 | Crystal Structure Of Runx1 And Ets1 Bound To Tcr Alpha Promoter (crystal Form 3) | Homo sapiens/Mus musculus | 2.19Å | 89 | 9% |
| 46 | 4L0Y | Crystal Structure Of Runx1 And Ets1 Bound To Tcr Alpha Promoter (crystal Form 1) | Homo sapiens/Mus musculus | 2.20Å | 89 | 10% |
| 47 | 3WTU | Crystal structure of the complex comprised of ETS1 (V170A), RUNX1, CBFBETA, and the tcralpha gene enhancer DNA | Others | 2.23Å | 89 | 10% |
| 48 | 3WTX | Crystal structure of the complex comprised of ETS1(Y329A), RUNX1, CBFBETA, and the tcralpha gene enhancer DNA | Others | 2.25Å | 89 | 10% |
| 49 | 4L0Z | Crystal Structure Of Runx1 And Ets1 Bound To Tcr Alpha Promoter (crystal Form 2) | Homo sapiens/Mus musculus | 2.31Å | 89 | 10% |
| 50 | 1H9D | Aml1/cbf-beta/dna complex | Homo sapiens | 2.32Å | 89 | 10% |
| 51 | 6F59 | Crystal structure of human Brachyury (T) G177D variant in complex with DNA | Homo sapiens | 2.42Å | 89 | 7% |
| 52 | 3WU1 | Crystal structure of the ETS1-RUNX1-DNA ternary complex | Others | 2.17Å | 88 | 10% |
| 53 | 3WTV | Crystal structure of the complex comprised of ETS1(V170G), RUNX1, CBFBETA, and the tcralpha gene enhancer DNA | Others | 2.35Å | 88 | 10% |
| 54 | 3E9U | Crystal Structure Of Calx Cbd2 Domain | Drosophila melanogaster | 4.30Å | 88 | 2% |
| 55 | 1YVL | Structure Of Unphosphorylated Stat1 | Others | 1.56Å | 87 | 13% |
| 56 | 4Y5U | Transcription Factor | Homo sapiens | 1.92Å | 87 | 11% |
| 57 | 1EAN | The Runx1 Runt Domain At 1.70a Resolution: A Structural Switch And Specifically Bound Chloride Ions Modulate Dna Binding | Mus musculus | 2.17Å | 86 | 9% |
| 58 | 5QSA | PanDDA analysis group deposition -- Crystal Structure of human Brachyury G177D variant in complex with Z2856434778 | Homo sapiens | 2.22Å | 86 | 7% |
| 59 | 3WTW | Crystal structure of the complex comprised of ETS1(K167A), RUNX1, CBFBETA, and the tcralpha gene enhancer DNA | Others | 2.22Å | 86 | 10% |
| 60 | 2JHS | Crystal Structure Of Rhogdi K135h,K138h,K141h Mutant | Homo sapiens | 3.26Å | 86 | 9% |
| 61 | 2X6V | Crystal Structure Of Human Tbx5 In The Dna-Bound And Dna- Free Form | Others | 2.07Å | 85 | 9% |
| 62 | 3PJN | The Crystal Structure Of Tp34 Bound To Zn(Ii) Ion At Ph 7.5 | Treponema pallidum | 2.80Å | 85 | 12% |
| 63 | 2O6E | Structure of native rTp34 from Treponema pallidum from zinc-soaked crystals | Treponema pallidum | 2.82Å | 85 | 12% |
| 64 | 2OZN | The Cohesin-Dockerin Complex Of Nagj And Nagh From Clostridium Perfringens | Clostridium perfringens/Clostridium perfringens ATCC 13124 | 3.04Å | 85 | 12% |
| 65 | 1Z8Y | Mapping the E2 Glycoprotein of Alphaviruses | Sindbis virus | 3.45Å | 84 | 8% |
| 66 | 5FLV | Crystal Structure Of Nkx2-5 And Tbx5 Bound To The Nppa Promoter Region | Mus musculus | 2.16Å | 81 | 9% |
| 67 | 6D4A | Cell Surface Receptor with Bound Ligand at 1.75-A Resolution | Homo sapiens | 3.10Å | 81 | 6% |
| 68 | 6TLC | Unphosphorylated human STAT3 in complex with MS3-6 monobody | Homo sapiens | 1.36Å | 80 | 13% |

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| 69 | 2LT9 | The solution structure of Ca2+ binding domain 2B of the third isoform of the Na+/Ca2+ exchanger | Mus musculus | 3.92Å | 80 | 4% |
| 70 | 3MQI | Human Early B-Cell Factor 1 (Ebf1) IptTIG DOMAIN | Homo sapiens | 3.08Å | 79 | 9% |
| 71 | 6D48 | Cell Surface Receptor | Homo sapiens | 3.19Å | 79 | 6% |
| 72 | 4NLH | Skich Domain Of Human Tax1bp1 | Homo sapiens | 2.54Å | 78 | 9% |
| 73 | 4HUM | Mate Transporter Norm-ng In Complex With Ethidium And Monobody | Escherichia coli/Neisseria gonorrhoeae TCDC-NG08107 | 2.96Å | 78 | 5% |
| 74 | 6P1E | Cu-bound PmoF1 PCuAC domain (dimer) | Methylocystis sp. ATCC 49242 | 3.01Å | 78 | 8% |
| 75 | 5Z7G | Crystal structure of TAX1BP1 SKICH region in complex with NAP1 | Homo sapiens | 2.53Å | 77 | 9% |
| 76 | 5Z7A | Crystal structure of NDP52 SKICH region | Homo sapiens | 2.58Å | 77 | 5% |
| 77 | 3LZN | Crystal Structure Analysis Of The Apo P19 Protein From Campylobacter Jejuni At 1.59 A At Ph 9 | Campylobacter jejuni subsp. jejuni 81-176 | 3.07Å | 77 | 5% |
| 78 | 3K2M | Crystal Structure of Monobody HA4/Abl1 SH2 Domain Complex | Homo sapiens | 3.13Å | 76 | 3% |
| 79 | 2NMS | The Crystal Structure Of The Extracellular Domain Of The Inhibitor Receptor Expressed On Myeloid Cells Irem-1 | Homo sapiens | 2.60Å | 75 | 4% |
| 80 | 3IDU | Crystal Structure of the CARDB domain of the PF1109 protein in complex with di-metal ions from Pyrococcus furiosus, Northeast Structural Genomics Consortium Target PfR193A | Pyrococcus furiosus | 2.68Å | 73 | 11% |
| 81 | 5I0V | Iron And Copper-bound P19 From Campylobacter Jejuni Under Oxidizing Conditions | Campylobacter jejuni subsp. jejuni 81-176 | 2.79Å | 72 | 4% |
| 82 | 4U6T | Crystal structure of the Clostridium histolyticum colH collagenase polycystic kidney disease-like domain 2a at 1.76 Angstrom resolution | Hathewaya histolytica | 2.60Å | 71 | 3% |
| 83 | 4HUN | MATE transporter NorM-NG in complex with R6G and monobody | Escherichia coli/Neisseria gonorrhoeae TCDC-NG08107 | 2.75Å | 71 | 6% |
| 84 | 2AW2 | Crystal Structure Of The Human Btla-hvem Complex | Homo sapiens | 2.79Å | 70 | 14% |
| 85 | 3VVV | Skich Domain Of Ndp52 | Homo sapiens | 2.35Å | 69 | 4% |
| 86 | 6VHI | Crystal structure of the human ILRUN Fw domain | Homo sapiens | 2.52Å | 69 | 6% |
| 87 | 1U36 | Crystal structure of WLAC mutant of dimerisation domain of NF-kB p50 transcription factor | Mus musculus | 2.53Å | 69 | 14% |
| 88 | 3TEU | Crystal structure of fibcon | Others | 2.53Å | 69 | 7% |
| 89 | 1U3Y | Crystal structure of ILAC mutant of dimerisation domain of NF-kB p50 transcription factor | Mus musculus | 2.57Å | 69 | 14% |
| 90 | 1U41 | Crystal structure of YLGV mutant of dimerisation domain of NF-kB p50 transcription factor | Mus musculus | 2.58Å | 69 | 14% |
| 91 | 2Y72 | Crystal Structure Of The Pkd Domain Of Collagenase G From Clostridium Histolyticum At 1.18 Angstrom Resolution | Hathewaya histolytica | 2.91Å | 69 | 10% |
| 92 | 2R39 | Crystal Structure Of Fixg-Related Protein From Vibrio Parahaemolyticus | Vibrio parahaemolyticus RIMD 2210633 | 2.37Å | 68 | 9% |
| 93 | 4JRW | Crystal structure of Clostridium histolyticum colg collagenase PKD domain 2 at 1.6 Angstrom resolution | Hathewaya histolytica | 2.71Å | 68 | 9% |
| 94 | 4AQO | Crystal Structure Of The Calcium Bound Pkd-like Domain Of Collagenase G From Clostridium Histolyticum At 0.99 Angstrom Resolution | Hathewaya histolytica | 2.87Å | 68 | 9% |
| 95 | 4MMX | Integrin AlphaVBeta3 ectodomain bound to the tenth domain of Fibronectin | Homo sapiens | 2.87Å | 68 | 6% |
| 96 | 3LZQ | Crystal Structure Analysis Of Manganese Treated P19 Protein From Campylobacter Jejuni At 1.41 A At Ph 9 | Campylobacter jejuni subsp. jejuni 81-176 | 2.50Å | 67 | 12% |
| 97 | 5L74 | Plexin A2 extracellular segment domains 4-5 (PSI2-IPT2), resolution 1.36 Angstrom | Mus musculus | 2.63Å | 67 | 7% |
| 98 | 1U3J | Crystal structure of MLAV mutant of dimerisation domain of NF-kB p50 transcription factor | Mus musculus | 2.65Å | 67 | 12% |
| 99 | 6NYP | Crystal structure of UL144/BTLA complex | Others | 2.73Å | 67 | 13% |
| 100 | 4U7K | Crystal structure of the Clostridium histolyticum colH collagenase polycystic kidney disease-like domain 2a in the presence of calcium at 1.9 Angstrom resolution | Hathewaya histolytica | 2.90Å | 67 | 3% |

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| 101 | 2LFE | Solution NMR structure of N-terminal domain of human E3 ubiquitin-protein ligase HECW2, Northeast structural genomics consortium (NESG) target ht6306A | Homo sapiens | 2.59Å | 66 | 8% |
| 102 | 4TN9 | Crystal structure of Clostridium histolyticum ColG collagenase polycystic kidney disease-like domain at 1.4 Angstrom resolution | Hathewaya histolytica | 2.71Å | 66 | 9% |
| 103 | 4HJI | Structure Of The Cooa Pilin Subunit From Enterotoxigenic Escherichia Coli | Escherichia coli | 3.19Å | 66 | 8% |
| 104 | 5FM8 | Structure of the C-terminally extended domain My4 of human myomesin (space group P65) | Homo sapiens | 2.27Å | 65 | 11% |
| 105 | 4N68 | Crystal Structure Of An Internal Fn3 Domain From Human Contactin-5 [psi-nysgrc-005804] | Homo sapiens | 2.50Å | 65 | 6% |
| 106 | 5Z7L | Crystal structure of NDP52 SKICH region in complex with NAP1 | Homo sapiens | 2.58Å | 65 | 8% |
| 107 | 2W0P | Crystal Structure Of The Filamin A Repeat 21 Complexed With The Migfilin Peptide | Homo sapiens | 2.67Å | 64 | 13% |
| 108 | 2JJT | Structure of human CD47 in complex with human signal regulatory protein (SIRP) alpha | Homo sapiens | 2.97Å | 64 | 11% |
| 109 | 6W8X | Cryo-EM of the S. solfataricus pilus | Saccharolobus solfataricus | 4.08Å | 64 | 11% |
| 110 | 5IUS | Crystal Structure Of Human Pd-l1 In Complex With High Affinity Pd-1 Mutant | Homo sapiens | 2.74Å | 63 | 5% |
| 111 | 1I8L | Human B7-1CTLA-4 Co-Stimulatory Complex | Homo sapiens | 2.42Å | 62 | 8% |
| 112 | 2CD0 | Structure Of Human Lambda-6 Light Chain Dimer Wil | Homo sapiens | 2.93Å | 62 | 6% |
| 113 | 6C6Q | Crystal Structure of the Murine Norovirus VP1 P Domain in complex with the CD300lf Receptor | Others | 2.45Å | 61 | 2% |
| 114 | 5OC7 | Crystal structure of the pleckstrin-homology domain of Bcr-Abl in complex with monobody Mb(Bcr-PH_4) | Others | 2.15Å | 60 | 7% |
| 115 | 2MOG | Solution structure of the terminal Ig-like domain from Leptospira interrogans LigB | Leptospira interrogans | 2.41Å | 60 | 8% |
| 116 | 2HAZ | Crystal Structure Of The First Fibronectin Domain Of Human Ncam1 | Homo sapiens | 2.47Å | 60 | 3% |
| 117 | 3RNK | Crystal structure of the complex between mouse PD-1 mutant and PD-L2 IgV domain | Mus musculus | 2.48Å | 58 | 9% |
| 118 | 6HIG | hPD-1/NBO1a Fab complex | Homo sapiens/Mus musculus | 3.03Å | 58 | 10% |
| 119 | 2N1K | Structure of the Third Type III Domain from Human Fibronectin | Homo sapiens | 1.92Å | 56 | 13% |
| 120 | 6C74 | Crystal Structure of Murine CD300lf in complex with phosphocholine | Mus musculus | 2.20Å | 56 | 2% |
| 121 | 7BYR | BD23-Fab in complex with the S ectodomain trimer | Others | 2.27Å | 55 | 4% |
| 122 | 1AC6 | Crystal Structure Of A Variable Domain Mutant Of A T-cell Receptor Alpha Chain | Mus musculus | 2.41Å | 55 | 11% |
| 123 | 3B83 | Computer-based Redesign Of A Beta Sandwich Protein Suggests That Extensive Negative Design Is Not Required For De Novo Beta Sheet Design | Homo sapiens | 3.10Å | 55 | 7% |
| 124 | 4U3H | Crystal Structure Of Fn3con | Others | 2.05Å | 54 | 7% |
| 125 | 5ECJ | Crystal structure of monobody Mb(S4) bound to Prdm14 in complex with Mtgr1 | Homo sapiens/Mus musculus | 1.73Å | 53 | 11% |
| 126 | 1CD0 | Structure Of Human Lamda-6 Light Chain Dimer Jto | Homo sapiens | 2.65Å | 53 | 9% |
| 127 | 6BYN | Crystal structure of WDR5-Mb(S4) monobody complex | Homo sapiens | 1.88Å | 52 | 8% |
| 128 | 4JE4 | Crystal Structure Of Monobody Nsa1/shp2 N-sh2 Domain Complex | Homo sapiens | 2.11Å | 51 | 12% |
| 129 | 3SO5 | Crystal structure of an Immunoglobulin I-set domain of Lrig3 protein (Lrig3) from MUS MUSCULUS at 1.70 A resolution | Mus musculus | 1.97Å | 50 | 12% |
| 130 | 5FQ7 | Crystal Structure Of The Suscd Complex Bt2261-2264 From Bacteroides Thetaiotaomicron | Bacteroides thetaiotaomicron | 2.25Å | 50 | 12% |
| 131 | 3RZW | Crystal Structure of the Monobody ySMB-9 bound to human SUMO1 | Homo sapiens | 1.92Å | 49 | 10% |
| 132 | 2MTP | The structure of Filamin repeat 21 bound to integrin | Homo sapiens | 2.69Å | 44 | 9% |