Additional file 3: Structure-based sequence alignment of CSA-binding DBL domains from A4 and 3D7 *var2CSA*. The disulfide linkages are colored in pairs. 'S' and 'H' denote sheet and helix region respectively for the A4 DBL 3X crystal structure (PDB code: 3BQK). The regions underlined in the N- and C- terminal regions could not be completely aligned. Residues underlined and in italics are disordered in A4 DBL 3X. Residues forming secondary structure are shown in bold. Surface identical/conserved residues constituting regions CR1, CR2 and CR3 are colored green, cyan and red respectively

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3D7-DBL5ε 1983
                 DRCFDDKSKMKVCDLIGDAIGCKHKTKLDEL----DEWNDVDMRDPYN-K---- 2027
A4-DBL6 2320 HHEYDKGNDYICNKYKNIHDRMKK----NNGNFVTDNFVKKSW-----E-I---2360
3D7-DBL6 2323 HHEYD-KGNDYI--C-NKY-----KNINVNMKKNNDDTW--TD-LVKNSSD----2361
             HHEYD-KGNDYI--C-NKY-----KNINVNMKKNNDDTW--TD-LVKNSSD---- 2361
            A4-DBL3X 1260 --TN-GACTPPRTONLCVGELWDKSYGGRSNIKNDT---KELLKEKIKNAIHKETELLYEY 1314
3D7-DBL3X 1251 --TN-GAC<mark>I</mark>PPRTON<mark>LC</mark>VGELWDKRYGGRSNIKNDT---KESLKOKIKNAIOKETELLYEY 1305
3D7-DBL6: 2362 --INKGVL<mark>I</mark>PPRRKNIFLKIDESD----ICKYKRD---PKLFKDFIYSSAISEVER<mark>L</mark>KKV- 2412
                               ------
A4-DBL3X 1315 HDTGTAIISKNDKKGQKGK----NDPNGLPKGFCHAVQRSFIDYKNMTLGTSV---NIYEH 1368
3D7-DBL3X 1306 HDKGTAIISRNPMKGQKEKEEKNNDSNGLPKGFCHAVQRSFIDYKNMTLGTSV---NIYEY 1363
3D7-DBL5g 2077 Y-----NEDKDK-------EKALEAMKNS YDYBYIIKGSDM---LTNIQ 2111
        2411 Y-----GGARAKVVHAMKYSFTDIGSIIKGDDMMEKNSSDK 2446
A4-DBL6ε
3D7-DBL6 2413 Y--GEA------KTKVVHAMKYS AD IGS I KG DDMMENNSSDK 2443
            ннининининини
A4-DBL3X 1369 IGKLQEDIKKIIEKGTPQQKDK------IGGVGSSTENVNAWKGIEREMDAVRCAITKI 1422
3D7-DBL3X 1364 IGKLQEDIKKIIEKGTTKQNGK-----T--VGSGAENVNAWKGIEGEMADAVRCAITKI 1416
3D7-DBL2X 668 TKDLELNLQKIFGKLFRKYIKKNNTAEQDTSYSSLDELRESWUNTNKKYIKLAMKHGAGMN 728
A4-DBL2X 670 TKDLELNLQ<mark>N</mark>NFG<mark>K</mark>LFGKYIKKNNTAEQDTSYSSLDELRESW<mark>W</mark>NTNKKYIWTAMKHGAEMN 730
A4-DBL5 2118 FKDIKIKLDRLLEKET-N-----NTKKAEDWWKTNKKSIWNAMLCGYKKS 2161
3D7-DBL5 2112 FKDIKRKLDRLLEKET-N-----NTEKVDDWWETNKKSIWNAMLCGYKK 2154
A4-DBL6s 2447 IGKILGD-----TDGQ-----N-EKRKKWWDMNKYHIWESMLCGYRE-2482
3D7-DBL6 2444 IGKILGD------GVGN-------EKRKKWWDMNKYHIWESMLCGYKHA 2485
            нн------нининининининининининин
A4-DBL3X 1423 NK---KNNNSIFN-GDECGVS--PPTGNDEDQSVSWFKEWGEQFCIERLRYEQNIREACT 11478
3D7-DBL3X 1417 NKK--QKKNGTF-SIDECGIF--PPTGNDEDQSVSWFKEWSEQFCIERLQYEKNIRDACTN 1473
_____
A4-DBL3X 1479 NGKNEKKCINSKSGQGDKI-QGACKRKCEKYKKYISEKKQEWDKQKTKTENK-----Y 1530
3D7-DBL2X 784 ----KSCKES-GGT NGECKTECKNKCEVYKKFIEDCKGGDGTAGSS VKRWDQIYKRYS 838
A4-DBL2X 786 ----KSCKESGNK KTEC-KTKCKDECEKYKKFIEACGTAGGGIGTAGSPWSKRWDQIYK 840
3D7-DBL68 2537 AKCNT------sngsvdkkecteacknysnfilikkkeyqslnsq<del>y</del>dmn---yketka 2585
A4-DBL3X 1531 ----VGKS-------ASDLLKEN---YPECISAN-----FDFIFND----NIEY 1561 3D7-DBL3X 1514 ----VGKS--------ASDLLKEN---YPECISAN-----FDFIFND-----NIEY 1543
A4-DBL6 2575 KNKN SNDKD-----APDYLKEK-----CNDNKCEC--LNKHIDDKNKTWKNPYETLED 2620
3D7-DBL6: 2586 EKKE -----SPEYFKDKENGECSCLSEY----FKDETRW----KNEVKNN-- 2622
            ННН---ННН-----
A4-DBL3X 1562 KTYYPYGDYSSICSCE----- 1577
3D7-DBL3X 1544 KTYYPYGDYSSICSCE------1559
3D7-DBL2X 890 -SYLSIVLDDNICGADK-APWTTYTTYTTEKEN------921
A4-DBL2X 883 SFFKHLIDIGLTTPSSYLSNVLDDNICGADKAPWTTYTTYTTTEKCN 930
3D7-DBL5ε
            _____
A4-DBL5ε
A4-DBL6ε 2621 T--FKSKCDCPKP----- 2631
3D7-DBL6g 2623 ______2628
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