| CCP-containing protein | PDB code(s) | Module 1 | Module 2 | Bimodule | Buried |
| :---: | :---: | :---: | :---: | :---: | :---: |
| C4BP $\alpha$ | $2 \mathrm{~A} 55^{*}{ }_{1,2}$ | 4340.74 | 4365.78 | 8194.07 | 512.45 |
| factor H | $1 \mathrm{HFH}^{*}{ }_{15,16}$ | 4161.13 | 3843.43 | 7431.17 | 573.39 |
|  | $2 \mathrm{BZM}^{\text {+ }}{ }_{19,20}$ | 3920.47 | 4388.50 | 7576.76 | 732.21 |
| DAF | $1 \mathrm{H}^{\text {( }}{ }_{3,4}$ | 4072.09 | 4303.13 | 7864.32 | 510.90 |
|  | $1 \mathrm{NWV}^{*, 3}$ | 4684.01 | 4044.11 | 8275.20 | 452.92 |
|  | $1 \mathrm{OK} 3^{\wedge}{ }_{1,2}$ | 4314.42 | 4306.75 | 8141.22 | 479.95 |
|  | $1 \mathrm{OK} 3^{\wedge}{ }_{2,3}$ | 4403.66 | 3992.75 | 7793.96 | 602.45 |
|  | $1 \mathrm{OK} 3^{\wedge}{ }_{3,4}$ | 4033.63 | 4350.62 | 7848.45 | 535.80 |
| MCP | $\mathrm{CKKL}^{1,2}$ | 4576.91 | 4220.77 | 8340.89 | 456.79 |
| CR1 | $1 \mathrm{GKN}^{*}{ }_{15,16}$ | 4489.55 | 3976.54 | 7971.51 | 494.58 |
|  | $1 \mathrm{GKG}^{*}{ }_{16,17}$ | 4068.81 | 4809.27 | 8380.24 | 497.84 |
| CR2 | 1LY2 ${ }_{1,2}$ | 4700.86 | 4180.76 | 7897.61 | 984.01 |
| VCP | $1 \mathrm{G40}{ }_{1,2}$ | 5341.84 | 4201.85 | 8653.74 | 889.95 |
|  | $1 \mathrm{G} 40{ }^{\wedge}{ }_{2,3}$ | 4103.66 | 3979.33 | 7492.39 | 590.60 |
|  | $1 \mathrm{G40}{ }_{3,4}$ | 3988.90 | 4083.96 | 7261.93 | 810.93 |
|  | $1 \mathrm{VVC}_{3,4}$ | 3686.33 | 3785.37 | 7080.40 | 391.30 |
|  | $1 \mathrm{E}^{\text {G }}{ }^{*}{ }_{2,3}$ | 3961.39 | 3454.97 | 7146.18 | 270.18 |
| C1r | $\mathrm{IGPZ}_{1,2}^{\wedge}$ | 4672.76 | 4759.40 | 8954.35 | 477.81 |
| $\beta 2$-GPI | $\mathrm{IQUB}^{1,2}$ | 4173.13 | 3942.93 | 7619.73 | 496.33 |
|  | $\mathrm{LQUB}^{\text {2,3 }}$ | 3928.82 | 4134.70 | 7700.87 | 362.65 |
|  | $1 \mathrm{QUB}^{\text {(,4 }}$ | 4186.09 | 3874.36 | 7491.51 | 568.94 |
| MASP-2 | $1 \mathrm{ZJK}_{1,2}^{\wedge}$ | 4178.72 | 4244.20 | 7987.84 | 435.08 |

Calculated buried surface area among CCP bimodules. All units are in $\AA^{2}$. Experimentally determined structure pairs up to $17^{\text {th }}$ April 2006 included.

## Notes:

- The web server "GETAREA 1.1 " was used for surface area calculations: http://pauli.utmb.edu/cgi-bin/get_a_form.tcl in all cases.
- The surface area (SA) that was buried, was calculated as:
(SA Module ${ }^{\mathrm{i}}+$ SA Module $^{\mathrm{j}}$ ) - SA Bimodule ${ }^{\mathrm{ij}}$
- All units in $\AA^{2}$
- To obtain the Interaction Surface Area per module, divide the Buried Surface Area by 2.
- Linker length was defined as the number of residues between the C-terminal CYS of the preceding CCP module and the N-terminal CYS of the following CCP module.
- For Module 1 (in 4 residue linker protein), boundaries were considered from one residue before the first CYS till two residues after the last CYS.
- For Module 2 (in 4 residue linker protein), boundaries were considered from two residues before the first CYS till one residue after the last CYS.
- For Bimodules, boundaries were considered from one residue before the first CYS of Module 1 to one residue after the last CYS of Module 2.
- All linker lengths for solved structures $=4$ residues, except in the cases of CR2~1,2 (where linker length $=8$ residues), DAF~1,2 and FH~19,20 (where linker length $=3$ residues).
- For CR2~1,2, four residues after the last CYS of Module 1 and four residues before the first CYS of Module 2 were taken as boundaries for individual modules.
- For DAF~1,2 and FH~19,20, two residues after the last CYS of Module 1 and one residue before the first CYS of Module 2 were taken as boundaries for individual modules.
- For structures solved by X-ray diffraction ( ${ }^{\wedge}$ ), the best resolved structure was used or in cases where unliganded and structures in complex available, the unliganded form was used for surface area calculation
- In the case of structures solved by NMR (*), the closest to mean, average minimised structure or the lowest energy structure was used as appropriate.
- X-ray structures were protonated before calculations.

Reference: D. C. Soares, P. N. Barlow, Complement control protein modules in the regulators of complement activation; in Structural Biology of the Complement System. D. Morikis, J. D. Lambris, Eds. (CRC Press, Taylor \& Francis Group, Boca Raton, 2005) pp. 19-62.

