

Modules	PDB code	Order	Tilt	Twist	Skew	Tilt Error	Twist Error	Skew Error
VCP~13-X	1G40	1	4.4	-9.9	66.5	1.6	8.6	8.1
DAF~34-X	1OK3	2	7.6	113.7	59.1	1.5	9.8	3.9
B2GPI~12-X	1QUB	3	10.9	133.8	-139.9	na	na	na
FH~1920-N	2BZM	4	11.1	15.5	149.7	6.4	8.4	ne [†]
DAF~34-X	1H03	5	12	112.6	39	6	5.6	39.5
MASP2~12-X	1ZJK	6	12.5	79.1	119.4	na	na	na
CR1~1617-N	1GKG	7	16.3	110.8	-6.6	9	18.5	41.5
C1r~12-X	1GPZ	8	22.2	97.6	124.9	na	na	na
DAF~24-X	1OK3	9	24.9	-55.8	-54.1	4.8	13.4	1
VCP~23-N	1E5G	10	31.2	144.1	77.6	10.4	11.9	24.7
CR1~1516-N	1GKN	11	31.2	161	-44.9	7.3	13.7	21.5
DAF~23-X	1OK3	12	31.5	-168.5	-63.5	5.3	4.4	2
B2GPI~23-X	1QUB	13	32.9	89.1	60.1	na	na	na
VCP~24-X	1G40	14	35.2	-12.7	-91.5	1.3	3.5	3.6
DAF~13-X	1OK3	15	37	114.7	139.1	2.1	8.2	3.4
CR1~1517-N	1GOP	16	37.6	-81.7	-19.9	na	na	na
C4BPa~12-N	2A55	17	38.4	3.7	-110.2	4.4	5.7	17.9
DAF~14-X	1OK3	18	39.3	-134.1	152.5	0.4	17.7	0.5
DAF~12-X	1OK3	19	41.1	-87	107.4	0.1	2.8	10.4
B2GPI~13-X	1QUB	20	41.9	-139.2	-143.7	na	na	na
DAF~23-N	1NWV	21	45.4	128.7	-127.5	20.9	15.3	24.2
B2GPI~24-X	1QUB	22	48.4	144.1	103.3	na	na	na
FH~1516-N	1HFH	23	50	-130	155	13	17	23
B2GPI~34-X	1QUB	24	53.2	40.2	100.2	na	na	na
B2GPI~14-X	1QUB	25	56.3	-78.5	-121.4	na	na	na
VCP~12-X	1G40	26	62.8	-18.5	69.1	4	9.2	8.5
VCP~23-X	1G40	27	64.6	7.4	-91	1.7	2.6	3.6
VCP~34-N	1VVC	28	67.2	7.2	81.3	6.3	9.2	11
MCP~12-X	1CKL	29	68.3	-158.3	-20.3	5.7	7	2.2
VCP~34-X	1G40	30	97.9	-31.5	66.5	4.1	10	8.2
VCP~14-X	1G40	31	99.7	-19.4	75.4	1.3	2	1.2
CR2~12-X	1LY2	32	142.2	-4.2	43.6	2.6	20.1	2.9

Intermodular angles for all CCP module pairs and larger fragments. Tilt, twist and skew angles plotted for all experimentally determined structures of multiple CCP-module fragments. The values for pairs of modules and for non-consecutive modules (red), in order of increasing tilt angle (°). Modules solved by X-ray diffraction marked with an “-X”, while structures solved by NMR marked with an “-N” and corresponding PDB codes shown. Error values represent the standard deviation of angles observed, calculated for structures where several molecules are present in the unit cell of a crystal or where an ensemble exists for structures solved by NMR (na = not applicable; ne[†] = not entered; value seems to be an overestimation of intermodular flexibility, and could be due to local flexibility).

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.