

Table S2. True positives and false positives in Cliquery's cliques for CheA compared to KEGG's bacterial chemotaxis pathway (pathway 02030). *Probability (P_{co})* is Cliquery's probability cutoff; Number of proteins is the clique size; the columns *Che*, *MCP*, *Fli* and *Mot* give the number of proteins from each of these groups appearing in the identified clique; *True positive* is the percentage of proteins in Cliquery's clique that are part of the KEGG pathway. *False positive* is the percentage of proteins in Cliquery's clique that do not appear in the KEGG pathway. The pathway can be viewed at <https://www.genome.jp/pathway/map02030+K03407>.

Probability (P_{co})	Number of proteins in the clique	Che	MCP	Fli	Mot	True positive	False positive
0.85	3	1	2	0	0	100%	0%
0.8	12	1	0	6	1	67%	33%
	6	4	2	0	0	100%	0%
0.75	17	2	0	7	2	65%	35%
	22	1	0	11	2	64%	36%
	18	3	1	7	2	72%	28%
	18	4	2	7	1	78%	22%
	5	4	1	0	0	100%	0%
0.7	27	4	2	11	2	70%	30%
	21	3	3	7	2	71%	29%
	8	5	2	0	0	88%	13%
	8	4	3	0	0	88%	13%
	26	3	2	11	2	69%	31%
0.65	30	4	2	11	2	63%	37%
	30	4	3	12	2	70%	30%
	30	5	3	12	2	73%	27%
	29	3	4	12	2	72%	28%
	28	2	2	11	2	61%	39%
0.6	32	1	2	10	3	50%	50%
	30	1	2	8	3	47%	53%
	29	1	2	6	3	41%	59%
	29	1	2	6	3	41%	59%
	28	1	2	5	3	39%	61%

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The table demonstrate that as *Pco* decreases, Cliquely identifies more cliques, and the number of proteins per cliques increases (in this example, an average of 3, 9, 16, 18, 29, 30 proteins per clique were identified for *Pco* values of 0.85, 0.8, 0.75, 0.65, 0.6, respectively). True positive percentage decreases with *Pco* (an average of 100%, 83%, 76%, 77%, 68%, 44% for *Pco* values of 0.85, 0.8, 0.75, 0.65, 0.6, respectively), and false positive percentage increases (an average of 0%, 17%, 24%, 32%, 56% on average for *Pco* values of 0.85, 0.8, 0.75, 0.65, 0.6, respectively). A false positive here does necessarily imply an erroneous identification, but rather that the protein identified by Cliquely as connected to CheA does not appear in the small KEGG pathway 02030.