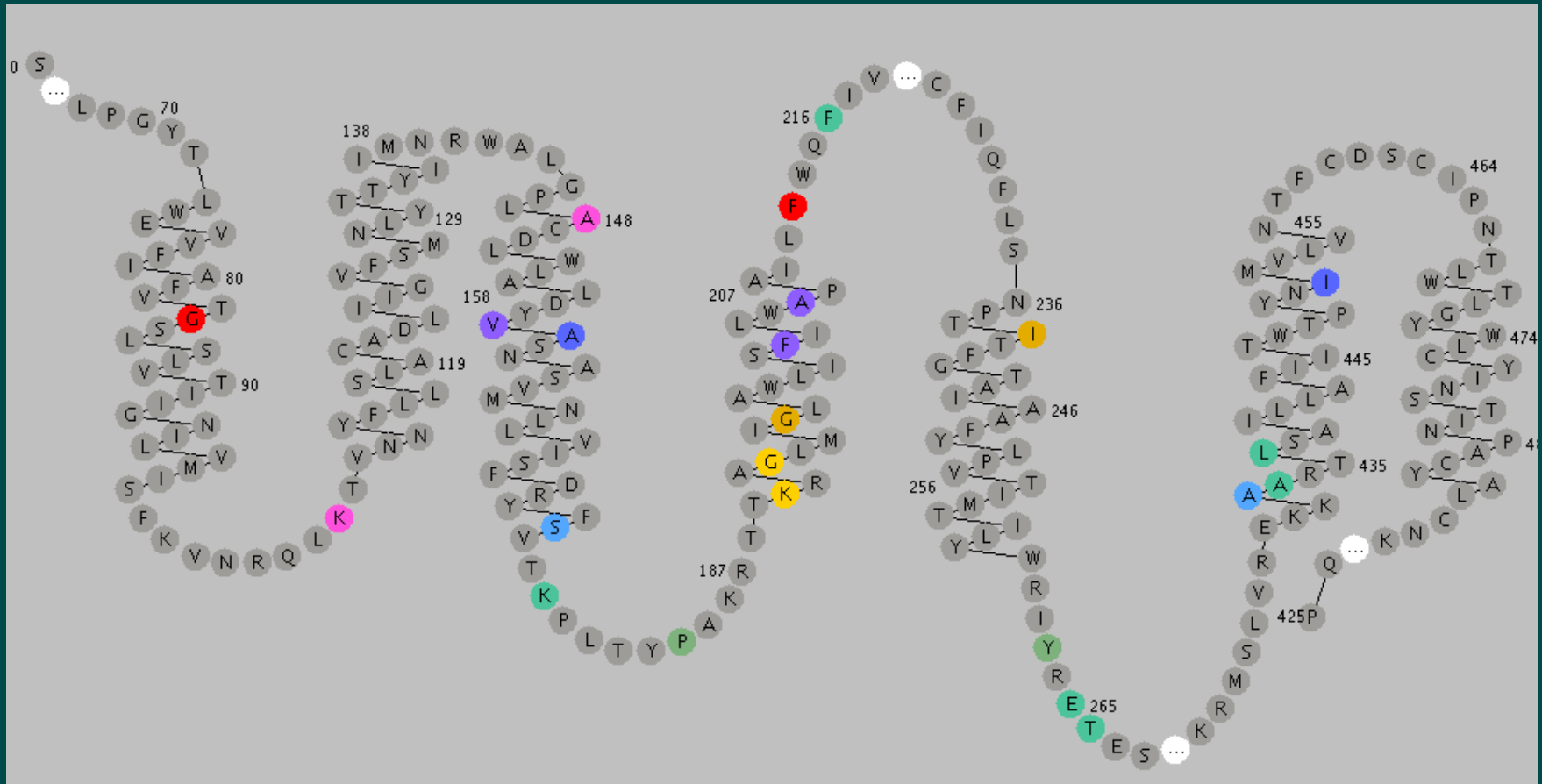


CMA = Correlated mutation analysis



		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	6	7	8	9	0						
64	0	Q	Q	3.05	0.10							27	90	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	E	E	E	E	E	Q	E	E	Q	Q	Q	E	E
136	341	Y	Y	8.00	2.00							27	80	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	W	W	W	W	W	Y	W	W	Y	Y	Y	W	W
273	626	F	F	8.00	2.00							27	80	F	F	F	F	F	F	F	F	F	F	F	W	W	W	W	F	W	W	F	F	F	W	W	

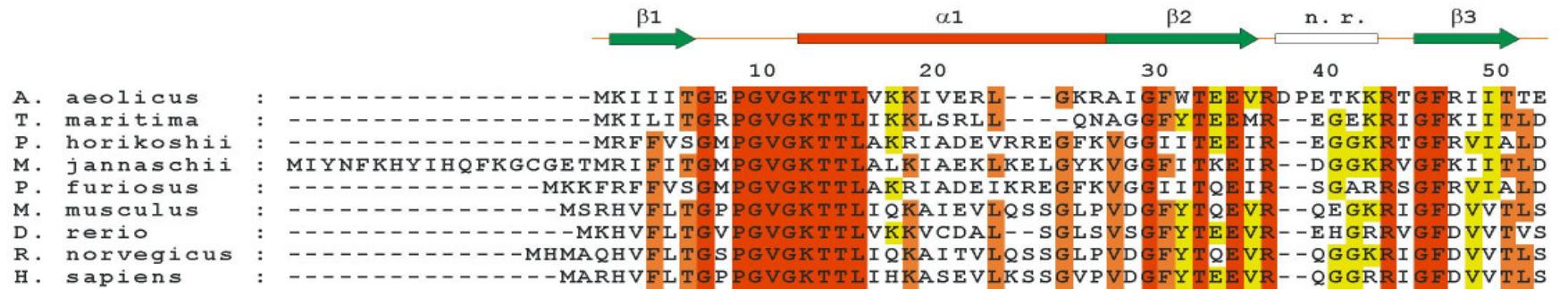
CMA = Correlated mutation analysis

velká -> malá
malá -> velká

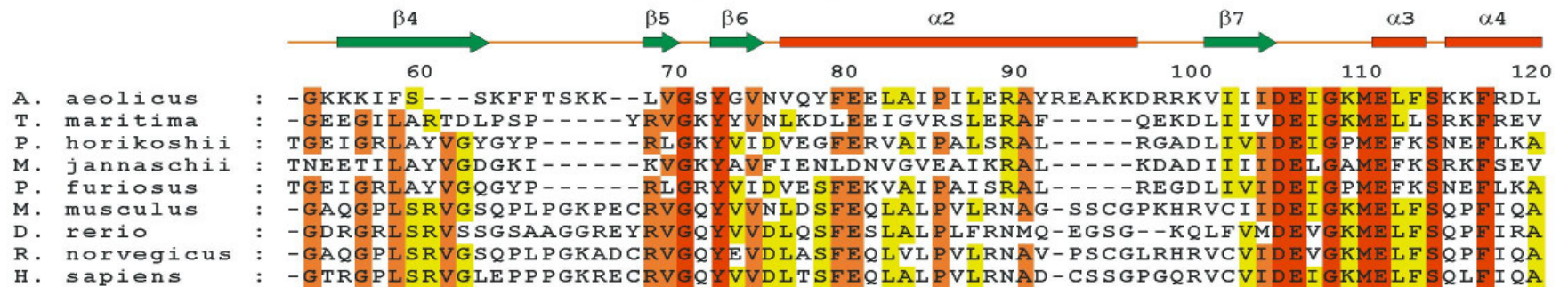
plus -> minus
minus -> plus

Nahrazované aminokyseliny na mutovaných pozicích se často vzájemně fyzikálně nebo chemicky doplňují.

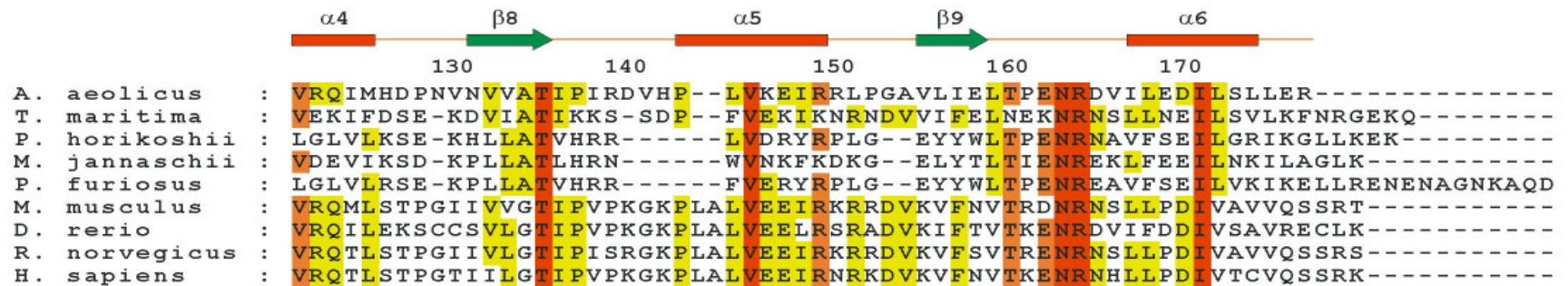
Multiple sequence alignment



|Walker A|



|Walker B|



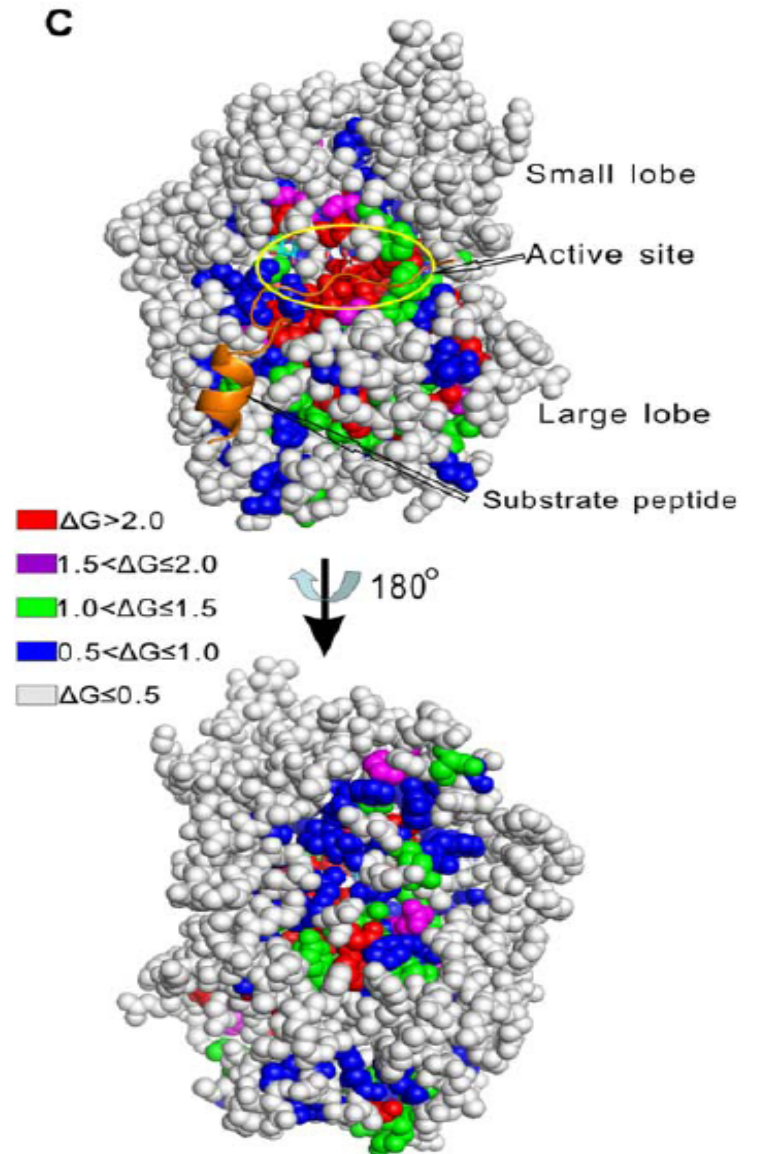
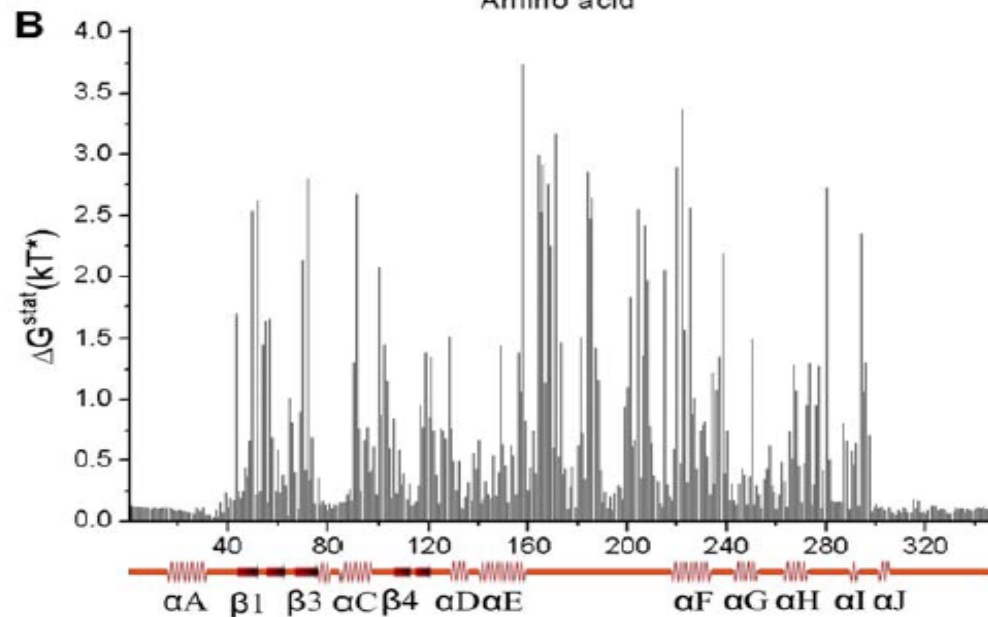
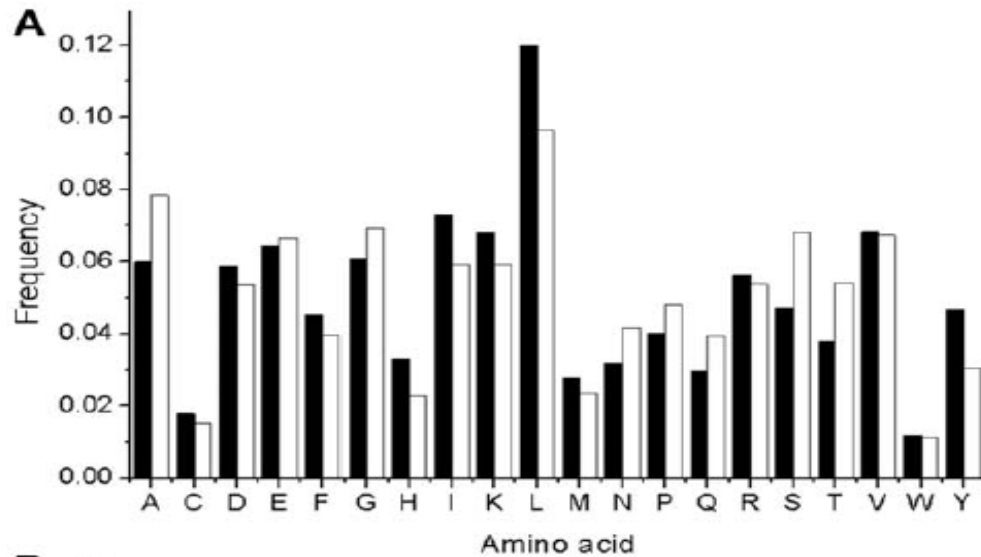
CLUSTALW

- globální zarovnání všech párů (Needleman-Wunsch)
- shlukováním vytvoříme vodící strom
- budujeme mnohočetné zarovnání podle stromu od nejpodobnějších sekvencí

CMA

- SCA (Statistical Coupling Analysis)
- MI (Mutual Information)
- RCA (Residue Correlation Analysis)

CMA



CMA

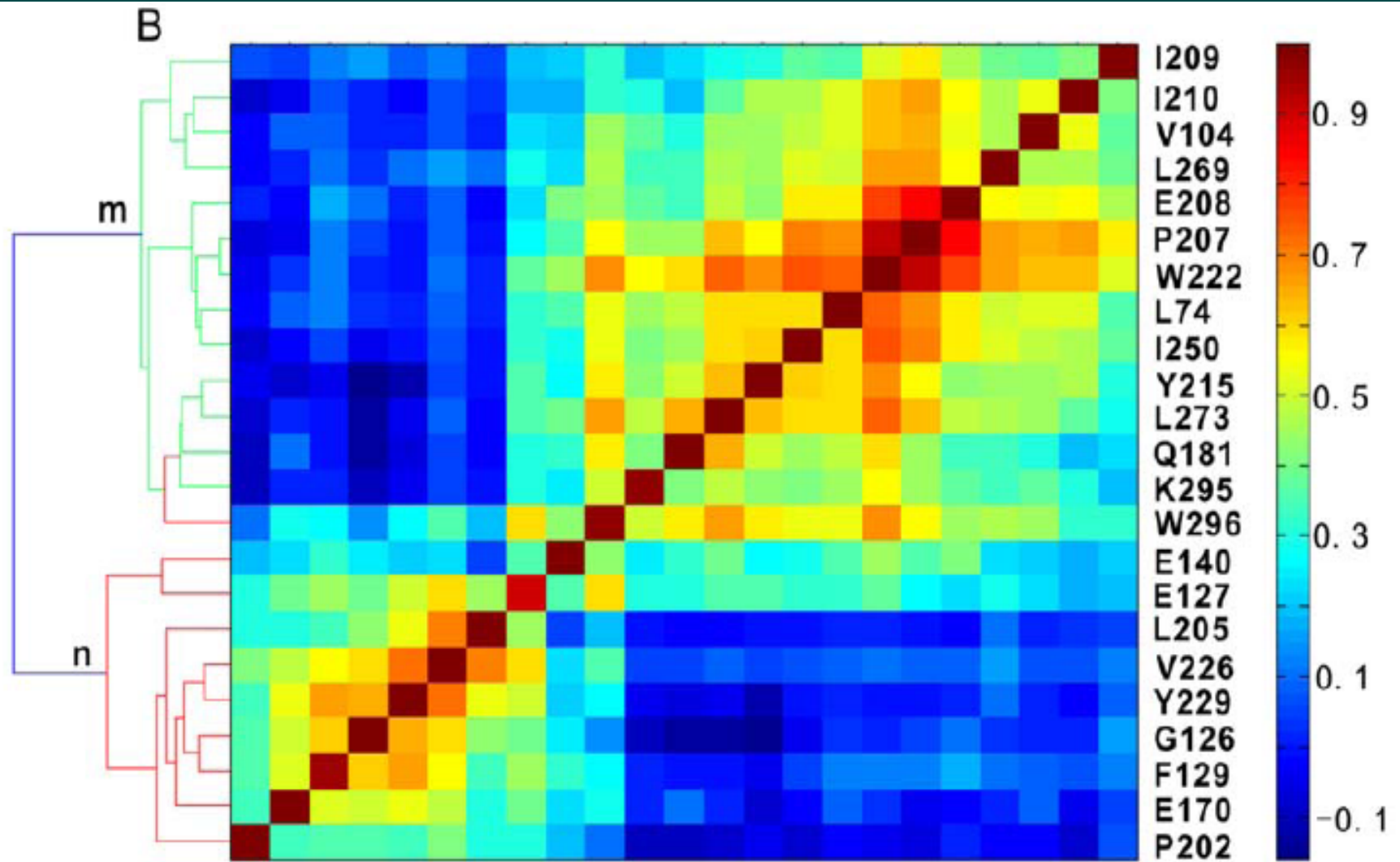


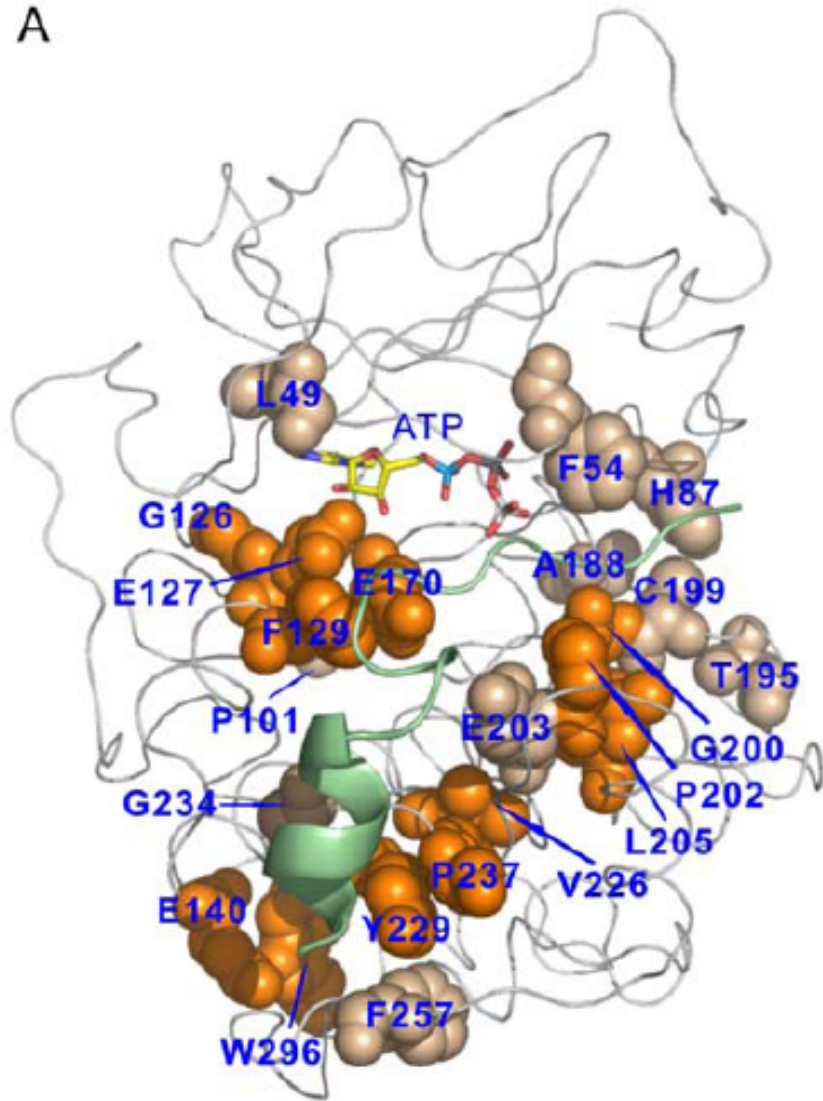
Table 1. Highly coupled sites identified by SCA, RCA and MI analysis.

RCA	MI	SCA	RCA	MI	SCA	RCA	MI	SCA
		L49		T195		Y229	Y229	Y229
		F54			C199			G234
L74				G200	G200		P237	P237
	H87		P202	P202	P202		F238	F238
		P101		E203		I250	I250	I250
V104			L205	L205				F257
G126	G126	G126	P207	P207	P207			D267
E127	E127	E127	E208	E208	E208	L269		
F129	F129	F129	I209			L273	L273	L273
E140		E140	I210				H294	H294
E170	E170	E170	Y215	Y215	Y215	K295		
Q181	Q181	Q181	W222	W222	W222	W296	W296	W296
		A188	V226	V226	V226			

doi:10.1371/journal.pone.0005913.t001

CMA

A



B

