

S5 Table. Common blocks /patterns among Na⁺-ATPase family members in two groups.

Seq. Nos.	Similarity (%)	Pattern
		341444344444448451444474746474742264228644284144174477774671274747882674426331
1	100	317-WLEAVIFLIGIIVANVPEGLLATVTVCLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDDKTGTLTQNRMTVAHMWFD
2	100	315-WLEAVIFLIGIIVANVPEGLLATVTVCLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDDKTGTLTQNRMTVAHMWFD
3	100	307-WLEAVIFLIGIIVANVPEGLLATVTVCLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDDKTGTLTQNRMTVAHMWFD
4	100	325-WLEAVIFLIGIIVANVPEGLLATVTVCLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDDKTGTLTQNRMTVAHMWFD
Seq. Nos.	Similarity (%)	3353342
5	100	242-YYPYGG
6	100	227-YFPYGG
7	100	214-YFPYGG
8	100	295-YYPYGG
Domain		E1-E2_ATPase