

# The number of times when a method was the best or in the best class or when it failed<sup>a</sup>

<b>f(0) including immunoglobulins</b>				<b>f(8) including immunoglobulins</b>			
Method <sup>b</sup>	Unique top <sup>c</sup>	Top Class <sup>d</sup>	Failure <sup>e</sup>	Method	Unique top	Top Class	Failure
ce	169	1869	828	ce	282	3354	152
da	<i>440</i>	<i>3348</i>	<i>126</i>	da	187	<i>3542</i>	27
fa	123	2733	252	fa	18	3057	32
lo	51	2641	488	lo	5	3316	47
ma	283	2966	346	ma	258	3399	94
sn	81	2658	414	sn	27	3067	62
va	120	2179	201	va	139	2795	73
<b>f(0) without immunoglobulins</b>				<b>f(8) without immunoglobulins</b>			
ce	157	1435	282	ce	239	1944	149
da	<i>234</i>	<i>2048</i>	<i>41</i>	da	172	<i>2119</i>	27
fa	96	1805	48	fa	12	1935	23
lo	32	1768	91	lo	5	2066	28
ma	194	1884	108	ma	201	1989	90
sn	65	1798	79	sn	26	1892	36
va	99	1536	87	va	137	1834	68

<sup>a</sup>The best number in each category is italicized. All methods achieved less than 0.5 of  $f_{\text{car}}(0)$ , for 15 pairs from cd00096 and 2 pairs from cd00105. For only one pair from cd00105,  $f_{\text{car}}(8)$  values of all methods are less than 0.5, probably because one of the structure has relatively large fraction of coordinate-missing residues and the structures are small. The five outlier superfamilies from Figure 11 were excluded, leaving 3591 pairs in total.

<sup>b</sup>The method is indicated by the first two letters of its name.

<sup>c</sup>The score of the second best method is lower than that of the best one by at least 0.1

<sup>d</sup>The score difference of each method from the best one is 0.1 or less.

<sup>e</sup>The score of the method is 0.5 or less.