

Rankings2 - Microsoft Internet Explorer

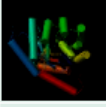
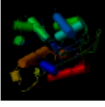
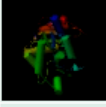
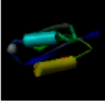
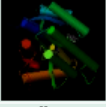
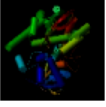
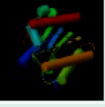
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## Comparer for protein structure rankings

[First 30 records] [Examine table] [focball.all] [Display values] [Display ranks] [total number of functions associated with the fold] [Image size: 50] [70] [100] [120]

	X(func)	total number of functions associated with the fold	interaction types (pdb)
		16	35
		1	1
		1.5	2.7
		211	268
<b>Ranked folds (click on arrows to re-rank)</b>			
beta/alpha (TIM)-barrel d1aj2_...3.1 [SCOP 1.39] A/B		16	22
alpha/beta-Hydrolases d1evl_...3.56 [SCOP 1.39] A/B		9	5
P-loop containing nucleotide triphosphate hydrolases d1dai_...3.29 [SCOP 1.39] A/B		6	23
Ferredoxin-like d2daw0_...4.34 [SCOP 1.39] A+B		6	17
NAD(P)-binding Rossmann-fold domains d1eny_...3.22 [SCOP 1.39] A/B		6	7
Cytochrome P450 d1ept_...1.83 [SCOP 1.39] A		5	1
Flavodoxin-like d1wab_...3.14 [SCOP 1.39] A/B		4	.

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Correlator - Microsoft Internet Explorer

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## Correlator

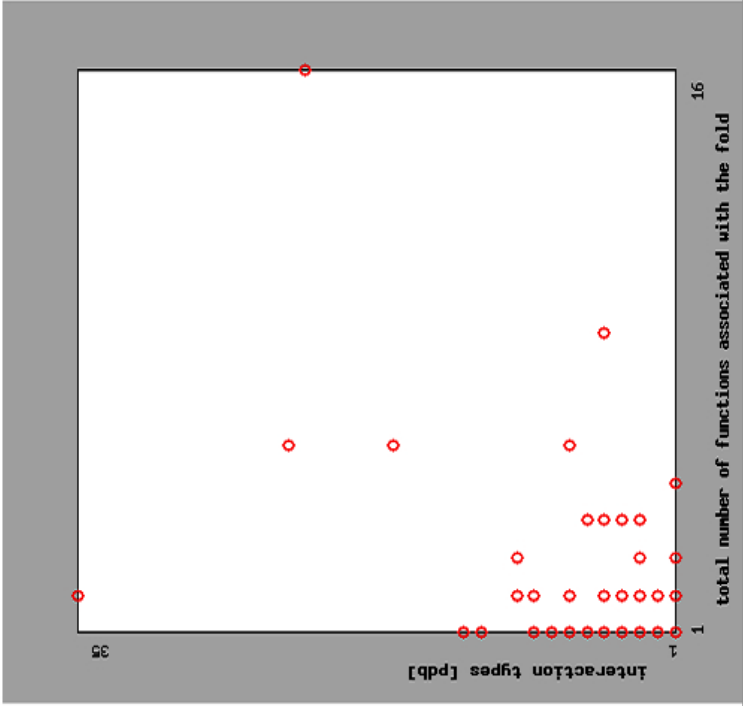
X axis: total number of functions associated with the fold

Y axis: total number of functions associated with the fold

Display the correlation

The linear correlation coefficient and rank correlation coefficient between "total number of functions associated with the fold" and "interaction types [pdb]" are 0.48 and 0.29, respectively. [The coefficient for perfect correlation is 1, for perfect anti-correlation is -1, and for complete uncorrelated is 0]

Mouse-over the points to show information on folds.



Interaction types [pdb]

total number of functions associated with the fold

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