

**Table 6. Native recognition scores obtained using the profile computed from the designed sequences for each protein in conjunction with the PSI-BLAST procedure, with standard settings**

<b>Fold</b>	<b>PDB ID</b>	<b><i>E</i> value</b>
Cold-shock	1mjc	1e-07
	1c9o	0.009
	1csp	9.4
	1csq	9e-05
HTH	1per	3e-04
	1r69	5e-04
Protein G	2igd	1.2
SH3	1abo	5e-05
	1cka	3e-05
	1ckb	2e-08
	1shf	0.10
	1sem	4e-05
	1pwt	2.4
	1shg	7.6
	2src	6.2
Homeobox	9ant	0.082
	1enh	8.1
	2hdd	8.3
	1fjl	1.1
	1b72	1.4
CI2	1coa	4e-04
	1ypc	5e-05
	2ci2	0.011
	1acb	6e-04
	1cse	7e-05
	2sec	0.017
	2tec	0.002

The PSI-BLAST searches were performed in the SWISS-PROT database, and limiting the number of iterations to one, to prevent contribution from natural sequences to the profile. The fold name is given in the first column, the protein PDB ID code is given in the second column, and the *E* value computed by PSI-BLAST is given in the third. For any further information, see text of main paper.