Table 6

HNF-3 (winged helix-turn-helix, HTH, Not in PDB)

I. MAP(DSSP)						II. MAP(PHD)						III. Threader					
1BIA_I	**27**	α+β	**W-HTH(HTH)**	**73.5**	**100.0**	1r69	8	α	λ-rep(HTH)			2fx2	-3.51	α/β	FLAVO(DWAB)		
3GAPA_II	**13**	α+β	**W-HTH(HTH)**	**87.5**	**100.0**	1avr_IV	0	α	annexin			1cd8	-2.63	β	IG(GKBS)		
1atna_III	8	α+β	actin			4blma_II	0	α+β	β-lactamase			1rn4	-2.38	α+β	ribo		
2end	2	α	T4.endonuclease			1avr_II	-3	α	annexin			1avr_IV	-2.13	α	annexin		
4icb	1	α	EF-HAND			2ts1_II	-4	α	Tyr tRNA synth			1hrha	-1.92	α/β	ribo		
4tnc_II	-3	α	EF-HAND			2c2c	-5	α	CYTOC			2trxa	-1.86	α/β	THIO(DWAB)		
3sdpa	-7	α	EF-HAND			1ycc	-6	α	CYTOC			2npx_II	-1.83	α+β	FAD-BIND		
1gmfa	-8	α	4HB-2(4HB)			1avr_I	-7	α	annexin			1aps	-1.81	α+β	acyl-phosphatase		
1ppn_I	-8	α+β	papain			1lmb3	-11	α	λ-rep(HTH)			5ruba_I	-1.69	α+β	α/β-BARREL		
2aaia_II	-9	α+β	ricin a chain			1cc5	-13	α	CYTOC			1trb_II	-1.66	α+β	FAD-BIND		

Sea Hare Myoglobin (globin-fold, 1MBA)

I. MAP(DSSP)						II. MAP(PHD)						III. Threader					
1HBG	**68**	α	**GLOBIN**	**90.5**	**85.7**	**1HBG**	**33**	α	**GLOBIN**	**51.6**	**85.7**	**1ECA**	**-3.10**	α	**GLOBIN**	**72.2**	**100.0**
1MYGA	**65**	α	**GLOBIN**	**94.2**	**87.5**	**1MYGA**	**22**	α	**GLOBIN**	**31.4**	**87.5**	**1HBG**	**-2.94**	α	**GLOBIN**	**47.0**	**100.0**
1ECA	**49**	α	**GLOBIN**	**59.4**	**75.0**	**1ECA**	**18**	α	**GLOBIN**	**60.4**	**87.5**	1pgd_I	-2.75	α/β	ROSS(DWAB)		
1COLA	**22**	α	**GLOBIN**	**11.3**	**66.7**	**1COLA**	**-9**	α	**GLOBIN**	**0.0**	**33.3**	**1COLA**	**-2.70**	α	**GLOBIN**	**18.1**	**66.7**
1CPCA	**17**	α	**GLOBIN**	**63.0**	**80.0**	**1CPCA**	**-12**	α	**GLOBIN**	**0.0**	**40.0**	1bia_II	-2.34	α+β	SH2-like		
256ba	5	α	4HB-1			1ezm_II	-14	α	thermolysin			3chy	-2.32	α/β	FLAVO(DWAB)		
1gsta_II	5	α	glut-S-trans.			1gsta_II	-16	α	glut-S-trans.			1llda_II	-2.09	α+β	ldh		
1avr_II	2	α	annexin			4blma_II	-17	α+β	β-lactamase			1llda_I	-2.06	α/β	ROSS(DWAB)		
1ezm_II	2	α	thermolysin			2wrpr	-20	α	Trp rep(HTH)			1lfi_II	-2.01	α/β	PBL(DWAB)		
1vsga_II	2	α	surface.glyc.			2scpa	-24	α	EF-hand			1pii_II	-1.95	α/β	α/β-BARREL		

Plastocyanin (CUP, Greek-key-beta-sandwich, 1PLC)

I. MAP(DSSP)						II. MAP(PHD)						III. Threader					
2AZAA	**18**	β	**CUP(GKBS)**	**66.7**	**100.0**	1snwa_I	-10	β	ser-prot			**1PAZ**	**-3.16**	β	**CUP(GKBS)**	**29.2**	**100.0**
1hoe	12	β	α-amylase.inh(GKBS)			1cd8	-12	β	IG(GKBS)			6taa_II	-2.83	β	α-amylase.inh(GKBS)		
2bbkl	9	β	met.dehydr(GKBS)			1bova	-13	β	OB-FOLD			3cd4_I	-2.66	β	IG(GKBS)		
2fbjh_II	7	β	IG(GKBS)			6taa_II	-14	β	α-amylase.inh(GKBS)			1tie	-2.56	β	β-TREFOIL		
3cd4_I	6	β	IG(GKBS)			1hoe	-16	β	α-amylase.inh(GKBS)			4fgf	-2.28	β	β-TREFOIL		
1snwa_II	6	β	ser-prot			2sn3	-16	α+β	scorpion.toxin			1tlk	-2.23	β	IG(GKBS)		
2aaib_II	4	β	β-TREFOIL			1hcc	-18	β	factor-H, 16th			2fbjl_I	-2.04	β	IG(GKBS)		
2aaib_I	3	β	β-TREFOIL			1tlk	-18	β	IG(GKBS)			2aaib_I	-2.03	β	β-TREFOIL		
1hsab	2	β	IG(GKBS)			4gcr_I	-18	β	γ–crystallin			2mcm	-2.00	β	macromycin(GKBS)		
1coba	1	β	sod(GKBS)			**2AZAA**	**-20**	β	**CUP(GKBS)**	**37.8**	**100.0**	2paba	-1.98	β	prealbumin(GKBS)		

Table 6

I. MAP(DSSP)						II. MAP(PHD)						III. Threader					
Interleukin-4 (up-up-down-down, four helix bundle, 1RCB)																	
256ba	33	α	4HB-1			1avr_III	9	α	annexin			1pfka_II	-2.89	α/β	pfk(DWAB)		
1bbha	32	α	4HB-1(4HB)			256ba	7	α	4HB-1			5p21	-2.65	α/β	G-PROT(DWAB)		
2ccya	29	α	4HB-1(4HB)			**1GMFA**	**6**	**α**	**4HB-2(4HB)**	**0.0**	**100.0**	1avr_I	-2.48	α	annexin		
2asr	20	α	4HB-1(4HB)			7cata_III	4	α	catalase			1llda_I	-2.44	α/β	ROSS(DWAB)		
1lpe	17	α	4HB-1(4HB)			2hmqa	2	α	4HB-1(4HB)			2mnr_II	-2.25	α/β	α/β-BARREL		
1GMFA	**16**	**α**	**4HB-2(4HB)**	**27.9**	**100.0**	2end	-2	α	T4.endonuclease			2fx2	-2.09	α/β	FLAVO(DWAB)		
1avr_III	16	α	annexin			1utg	-4	α	uteroglobin			6abp_II	-2.05	α/β	PBL(DWAB)		
2hmqa	13	α	4HB-1(4HB)			2yhx_III	-4	α	hexokinase			2trxa	-1.99	α/β	THIO(DWAB)		
7cata_III	11	α	catalase			1avr_II	-5	α	annexin			1ofv	-1.88	α/β	FLAVO(DWAB)		
2end	7	α	T4.endonuclease			1avr_I	-6	α	annexin			1avr_II	-1.88	α	annexin		
SH2 domain (SH2-fold, 1SHAA)																	
1atna_II	-10	α+β	ACTIN-ATPASE			3rubs	-10	α+β	RuBisCO small sub			1i1b	-3.12	β	β-TREFOIL		
1ppn_II	-11	α+β	papain			4blma_I	-14	α+β	β-lactamase			2fbjh_I	-2.99	β	IG(GKBS)		
2npx_III	-13	α+β	nadp.perxidase			1atna_II	-14	α+β	ACTIN-ATPASE			1tie	-2.80	β	β-TREFOIL		
5ruba_I	-14	α+β	α/β-BARREL			1bova	-17	β	OB-FOLD			1cd8	-2.32	β	IG(GKBS)		
1sgt_I	-16	β	ser-prot			1aps	-18	α+β	acyl-phosphatase			3dfr	-2.31	α/β	dhfr(DWAB)		
1thm_II	-17	α/β	subtilase			2fxb	-18	α+β	ferredoxin			1bbt3	-2.09	β	JELLYROLL		
3b5c	-18	α+β	cytoc.b5			2hpr	-18	α+β	HPr			2fbjl_I	-2.00	β	IG(GKBS)		
1aaqb	-18	β	asp-prot			3hsc_II	-18	α+β	ACTIN-ATPASE			6taa_II	-1.91	β	α–amylase.inh (GKBS)		
2rspa	-18	β	asp-prot.			1bia_III	-18	β	SH3-like			5fbpa_II	-1.80	α/β	sugar.phosph(DWAB)		
2fbjl_II	-18	β	IG(GKBS)			5fd1	-19	α+β	ferredoxin			8adh_II	-1.79	α/β	ROSS(DWAB)		
Ubiquitin (β-grasp, 1UBQ)																	
1FXIA	**12**	**α+β**	**β-GRASP**	**47.8**	**80.0**	**1PGX**	**4**	**α+β**	**β-GRASP**	**46.2**	**80.0**	6taa_II	-2.30	β	α-amylase.inh(GKBS)		
1PGX	**11**	**α+β**	**β-GRASP**	**37.0**	**100.0**	1alc_II	-8	α+β	a-lactalbumin			1avr_IV	-1.91	α	annexin		
2sn3	6	α+β	scorpion.toxin			1rn4	-10	α+β	ribo			1bova	-1.79	β	OB-FOLD		
1choi	6	α+β	ovomucoid.inh			2cpke_I	-10	α+β	ser/thr-kinase			**1PGX**	**-1.73**	**α+β**	**β-GRASP**	**43.8**	**80.0**
1bova	5	β	OB-FOLD			2sn3	-11	α+β	scorpion.toxin			2msbb	-1.66	α/β	lectin		
1rn4	4	α+β	ribo			1choi	-11	α+β	Ovomucoid.inh			1cd8	-1.65	β	IG(GKBS)		
1thm_II	3	α/β	subtilase			3monb	-12	α+β	monellin			1gsta_I	-1.52	α/β	THIO(DWAB)		
1fkb	0	α+β	FKBP-like			3sici	-12	α+β	subtilisin.inh			1trb_II	-1.45	α+β	FAD-BIND		
1tgsi	0	α+β	ser-prot.inh.			3il8	-13	α+β	interleukin-8			1aba	-1.33	α/β	THIO(DWAB)		
3sici	-2	α+β	subtilisin.inh			1ltsd	-14	β	OB-FOLD			3chy	-1.31	α/β	FLAVO(DWAB)		

Table 6

I. MAP(DSSP)						II. MAP(PHD)						III. Threader					
Tryptophan synthase (α/β barrel, 1WSYA)†																	
2TMDA_I	**-19**	α/β	**α/β-BARREL**	**0.0**	**0.0**	1pfka_I	15	α/β	pfk(DWAB)			2liv_I	-3.15	α/β	PBL(DWAB)		
1XIS	**-70**	α/β	**α/β-BARREL**	**0.0**	**18.2**	1pgd_I	14	α/β	ROSS(DWAB)			1pgd_I	-2.92	α/β	ROSS(DWAB)		
						2MNR_II	**6**	α/β	**α/β-BARREL**	**62.8**	**81.8**	**1PII_I**	**-2.61**	α/β	**α/β-BARREL**	**0.0**	**0.0**
						2hsda	1	α/β	ROSS(DWAB)			2pmga_I	-2.53	α/β	P-glucomutase(DWAB)		
						3pgk_II	-2	α/β	pgk(DWAB)			3chy	-2.51	α/β	FLAVO(DWAB)		
						1akea	-9	α/β	p-loop.NTP.hydrolase			2fx2	-2.23	α/β	FLAVO(DWAB)		
						8acn_I	-11	α/β	aconitase			1lap_II	-2.19	α/β	ROSS(DWAB)		
						1wsyb_II	-22	α/β	Trp.synthase(DWAB)			5p21	-2.13	α/β	G-PROT(DWAB)		
						1gky	-23	α/β	guanylate.kinase(DWAB)			1ofv	-2.10	α/β	FLAVO(DWAB)		
						2pmga_II	-32	α/β	p-glucomutase(DWAB)			8adh_II	-2.01	α/β	ROSS(DWAB)		
Hemerythrin (4HB1, 4HB, four helix bundle, 2HMQA)																	
256BA	**28**	α	**4HB-1**	**50.0**	**100.0**	1avr_III	-2	α	annexin			8adh_II	-2.56	α/β	ROSS(DWAB)		
1prcm_II	19	α	prc memb. dom.			**256BA**	**-7**	α	**4HB-1**	**0.0**	**25.0**	3chy	-2.51	α/β	FLAVO(DWAB)		
1utg	18	α	uteroglobin			7cata_III	-11	α	catalase			1pgd_I	-2.49	α/β	ROSS(DWAB)		
1avr_III	18	α	annexin			1utg	-12	α	uteroglobin			2npx_IV	-2.37	α+β	nadp.peroxidase		
7cata_III	16	α	catalase			1avr_II	-12	α	annexin			1ofv	-2.18	α/β	FLAVO(DWAB)		
1avr_II	11	α	annexin			1avr_I	-13	α	annexin			2rsla	-2.17	α/β	γδ-resolvase		
1LPE	**10**	α	**4HB-1(4HB)**	**0.0**	**100.0**	2ts1_II	-13	α	Tyr.tRNA.synth			2tmda_III	-2.12	α/β	tri-metam.dehydr.(DWAB)		
1gsta_II	7	α	glut-S-trans.			1prcc_I	-17	α	prc.cyt.dom.			2npx_II	-1.98	α+β	FAD-BIND		
2yhx_III	7	α	hexokinase			1fiaa	-18	α	fis.protein			1avr_IV	-1.95	α	annexin		
1BBHA	**6**	α	**4HB-1(4HB)**	**30.4**	**100.0**	1avr_IV	-19	α	annexin			1trb_II	-1.91	α+β	FAD-BIND		
6-phosphogluconate dehydrogenase (Rossmann fold, 2PGD domain I)																	
3chy	41	α/β	FLAVO(DWAB)			**1LLDA_I**	**1**	α/β	**ROSS(DWAB)**	**31.4**	**70.0**	1pii_II	-2.80	α/β	α/β-BARREL		
4MDHA_I	**40**	α/β	**ROSS(DWAB)**	**60.4**	**87.5**	3chy	-1	α/β	FLAVO(DWAB)			2liv_II	-2.73	α/β	PBL(DWAB)		
1LLDA_I	**37**	α/β	**ROSS(DWAB)**	**40.4**	**80.0**	**4MDHA_I**	**-7**	α/β	**ROSS(DWAB)**	**21.4**	**62.5**	1pfka_II	-2.70	α/β	pfk(DWAB)		
3PGK_I	**32**	α/β	**ROSS(DWAB)**	**38.9**	**100.0**	5p21	-8	α/β	G-PROT(DWAB)			3chy	-2.33	α/β	FLAVO(DWAB)		
8ADH_II	**29**	α/β	**ROSS(DWAB)**	**60.4**	**90.0**	1pfka_II	-10	α/β	pfk(DWAB)			2pmga_II	-2.20	α/β	p-glucomutase(DWAB)		
1pfka_I	24	α/β	pfk(DWAB)			2fx2	-12	α/β	FLAVO(DWAB)			1gpr	-2.01	β	glucose.permease		
1lfi_III	24	α/β	PBL(DWAB)			2tmvp	-17	α	4HB-1(4HB)			2npx_II	-1.97	α+β	FAD-BIND		
2tmda_II	20	α/β	tri-metam.dehydr(DWAB)			1rhd_II	-17	α/β	rhodanese			1trb_II	-1.79	α+β	FAD-BIND		
1etu	19	α/β	G-PROT(DWAB)			1etu	-19	α/β	G-PROT(DWAB)			1grca	-1.75	α/β	glyc.ribo.trans.(DWAB)		
2liv_II	17	α/β	PBL(DWAB)			2liv_II	-23	α/β	PBL(DWAB)			1drf	-1.69	α/β	dhfr(DWAB)		

Table 6

I. MAP(DSSP)						II. MAP(PHD)						III. Threader					
Thioredoxin (THIO, DWAB, 2TRXA)																	
1EGO	**9**	α/β	**THIO(DWAB)**	**38.5**	**100.0**	**1GSTA_I**	**3**	α/β	**THIO(DWAB)**	**0.0**	**60.0**	**1GSTA_I**	**-3.36**	α/β	**THIO(DWAB)**	**0.0**	**40.0**
1GSTA_I	**5**	α/β	**THIO(DWAB)**	**27.3**	**100.0**	3chy	2	α/β	FLAVO(DWAB)			1snc	-2.75	β	OB-FOLD		
3grs_III	4	α+β	glutathione.red			5fbpa_II	1	α/β	sugar.phosph(DWAB)			2fbjh_I	-2.64	β	IG(GKBS)		
1ABA	**-4**	α/β	**THIO(DWAB)**	**30.4**	**100.0**	2fx2	-1	α/β	FLAVO(DWAB)			1ofv	-2.24	α/β	FLAVO(DWAB)		
4mdha_I	-4	α/β	ROSS(DWAB)			4mdha_I	-1	α/β	ROSS(DWAB)			1llda_I	-2.03	α/β	ROSS(DWAB)		
6abp_I	-8	α/β	PBL(DWAB)			1pfka_II	-5	α/β	pfk(DWAB)			2msbb	-1.96	α/β	lectin		
2fx2	-10	α/β	FLAVO(DWAB)			**1EGO**	**-6**	α/β	**THIO(DWAB)**	**0.0**	**20.0**	4fgf	-1.92	β	β–TREFOIL		
1GP1A	**-10**	α/β	**THIO(DWAB)**	**34.7**	**100.0**	6abp_I	-7	α/β	PBL(DWAB)			2rsla	-1.88	α/β	γδ-resolvase		
1ezm_I	-10	α+β	thermolysin			**1ABA**	**-8**	α/β	**THIO(DWAB)**	**57.9**	**60.0**	1ltsd	-1.88	β	OB-FOLD		
1llda_I	-11	α/β	ROSS(DWAB)			1llda_I	-8	α/β	ROSS(DWAB)			4mdha_I	-1.76	α/β	ROSS(DWAB)		
Fibroblast growth factor (β-TREFOIL, 4FGF)																	
1I1B	**23**	β	**β-TREFOIL**	**35.9**	**100.0**	1cd8	-16	β	IG(GKBS)			1trb_II	-4.18	α+β	FAD-BIND		
1TIE	**21**	β	**β-TREFOIL**	**35.4**	**100.0**	1hoe	-18	β	α-amylase.inh(GKBS)			1cd8	-2.79	β	IG(GKBS)		
2AAIB_II	**19**	β	**β-TREFOIL**	**0.0**	**10.0**	1coba	-18	β	sod(GKBS)			3chy	-2.34	α/β	FLAVO(DWAB)		
2AAIB_I	**12**	β	**β-TREFOIL**	**53.9**	**70.0**	2mcm	-21	β	macromycin(GKBS)			2npx_II	-2.20	α+β	FAD-BIND		
3cd4_I	8	β	IG(GKBS)			1snwa_I	-22	β	ser-prot			2rsla	-2.12	α/β	γδ-resolvase		
1coba	2	β	sod(GKBS)			2fbjh_I	-22	β	IG(GKBS)			**1TIE**	**-2.06**	β	**β-TREFOIL**	**0.0**	**10.0**
1gpr	-3	β	glucose.permease			6taa_II	-22	β	α-amylase.inh(GKBS)			2msbb	-1.99	α/β	lectin		
2fbjh_I	-7	β	IG(GKBS)			2bbkl	-23	β	met.dehydr.(GKBS)			1bbt3	-1.94	β	JELLYROLL		
1tlk	-9	β	IG(GKBS)			4sbva	-23	β	JELLYROLL			1rnba	-1.83	α+β	ribo		
2mcm	-11	β	macromycin(GKBS)			**2AAIB_II**	**-23**	β	**β-TREFOIL**	**13.3**	**40.0**	1gpr	-1.79	β	glucose.permease		