



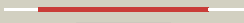






















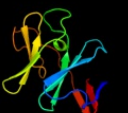





Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2jo6a1</a>	 Alignment		100.0	100	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> NirD-like
2	<a href="#">d2jzaa1</a>	 Alignment		100.0	63	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> NirD-like
3	<a href="#">d3c0da1</a>	 Alignment		100.0	36	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> NirD-like
4	<a href="#">c2qpzA</a>	 Alignment		100.0	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> naphthalene 1,2-dioxygenase system ferredoxin <b>PDBTitle:</b> naphthalene 1,2-dioxygenase rieske ferredoxin
5	<a href="#">d1fqta</a>	 Alignment		100.0	21	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
6	<a href="#">c3gcA</a>	 Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin component of carbazole 1,9a- <b>PDBTitle:</b> ferredoxin of carbazole 1,9a-dioxygenase from nocardioide2 aromaticivorans ic177
7	<a href="#">c3d89A</a>	 Alignment		99.9	18	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rieske domain-containing protein; <b>PDBTitle:</b> crystal structure of a soluble rieske ferredoxin from mus musculus
8	<a href="#">d1z01a1</a>	 Alignment		99.9	13	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
9	<a href="#">d1vm9a</a>	 Alignment		99.9	20	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
10	<a href="#">c2de7E</a>	 Alignment		99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> ferredoxin component of carbazole; <b>PDBTitle:</b> the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
11	<a href="#">d2de6a1</a>	 Alignment		99.9	13	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain

12	<a href="#">c2i7fB_</a>	Alignment		99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin component of dioxygenase; <b>PDBTitle:</b> sphingomonas yanoikuyae b1 ferredoxin
13	<a href="#">c2zylA_</a>	Alignment		99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> possible oxidoreductase; <b>PDBTitle:</b> crystal structure of 3-ketosteroid-9-alpha-hydroxylase2 (ksha) from m. tuberculosis
14	<a href="#">c3gkqB_</a>	Alignment		99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> terminal oxygenase component of carbazole 1,9a- <b>PDBTitle:</b> terminal oxygenase of carbazole 1,9a-dioxygenase from2 novosphingobium sp. ka1
15	<a href="#">c2de7B_</a>	Alignment		99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> terminal oxygenase component of carbazole; <b>PDBTitle:</b> the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
16	<a href="#">c1z01D_</a>	Alignment		99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-oxo-1,2-dihydroquinoline 8-monooxygenase, <b>PDBTitle:</b> 2-oxoquinoline 8-monooxygenase component: active site2 modulation by rieske-[2fe-2s] center oxidation/reduction
17	<a href="#">c3dqyA_</a>	Alignment		99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> toluene 1,2-dioxygenase system ferredoxin <b>PDBTitle:</b> crystal structure of toluene 2,3-dioxygenase ferredoxin
18	<a href="#">c3gcfC_</a>	Alignment		99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> terminal oxygenase component of carbazole 1,9a- <b>PDBTitle:</b> terminal oxygenase of carbazole 1,9a-dioxygenase from2 nocardioidees aromaticivorans ic177
19	<a href="#">c3gteB_</a>	Alignment		99.9	20	<b>PDB header:</b> electron transport, oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ddmc; <b>PDBTitle:</b> crystal structure of dicamba monooxygenase with non-heme2 iron
20	<a href="#">c3n0qA_</a>	Alignment		99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative aromatic-ring hydroxylating dioxygenase; <b>PDBTitle:</b> crystal structure of a putative aromatic-ring hydroxylating2 dioxygenase (tm1040_3219) from silicibacter sp. tm1040 at 1.80 a3 resolution
21	<a href="#">d1ulia1</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
22	<a href="#">d1wqla1</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
23	<a href="#">d1o7na1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
24	<a href="#">d2bmoa1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
25	<a href="#">c1uljA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> biphenyl dioxygenase large subunit; <b>PDBTitle:</b> biphenyl dioxygenase (bpha1a2) in complex with the substrate
26	<a href="#">c1wqlA_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> iron-sulfur protein large subunit of cumene dioxygenase; <b>PDBTitle:</b> cumene dioxygenase (cuma1a2) from pseudomonas fluorescens ip01
27	<a href="#">d2b1xa1</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
28	<a href="#">c2hmnA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> naphthalene 1,2-dioxygenase alpha subunit; <b>PDBTitle:</b> crystal structure of the naphthalene 1,2-dioxygenase f352v2 mutant bound to anthracene.

29	<a href="#">c2b1xE</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> naphthalene dioxygenase large subunit; <b>PDBTitle:</b> crystal structure of naphthalene 1,2-dioxygenase from rhodococcus sp.
30	<a href="#">c2gbxE</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> biphenyl 2,3-dioxygenase alpha subunit; <b>PDBTitle:</b> crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyae b1 bound to biphenyl
31	<a href="#">dlg8kb</a>	Alignment	not modelled	99.8	10	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
32	<a href="#">dlrfsa</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
33	<a href="#">d3cx5e1</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
34	<a href="#">dlq90c</a>	Alignment	not modelled	99.8	11	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
35	<a href="#">dlnya</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
36	<a href="#">d2e74d1</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
37	<a href="#">c2e76D</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> photosynthesis <b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome b6-f complex iron-sulfur subunit; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
38	<a href="#">dlriea</a>	Alignment	not modelled	99.6	10	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
39	<a href="#">c1p84E</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur <b>PDBTitle:</b> hdbt inhibited yeast cytochrome bc1 complex
40	<a href="#">c2fyuE</a>	Alignment	not modelled	99.5	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit, <b>PDBTitle:</b> crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
41	<a href="#">c2fynO</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur <b>PDBTitle:</b> crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
42	<a href="#">c2nvgA</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit; <b>PDBTitle:</b> soluble domain of rieske iron sulfur protein.
43	<a href="#">dljmla</a>	Alignment	not modelled	99.3	16	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
44	<a href="#">d2hf1a1</a>	Alignment	not modelled	58.6	19	<b>Fold:</b> Trm112p-like <b>Superfamily:</b> Trm112p-like <b>Family:</b> Trm112p-like
45	<a href="#">d2jnya1</a>	Alignment	not modelled	56.6	22	<b>Fold:</b> Trm112p-like <b>Superfamily:</b> Trm112p-like <b>Family:</b> Trm112p-like
46	<a href="#">d2pk7a1</a>	Alignment	not modelled	52.9	19	<b>Fold:</b> Trm112p-like <b>Superfamily:</b> Trm112p-like <b>Family:</b> Trm112p-like
47	<a href="#">c2jr6A</a>	Alignment	not modelled	49.4	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0434 protein nma0874; <b>PDBTitle:</b> solution structure of upf0434 protein nma0874. northeast structural2 genomics target mr32
48	<a href="#">c2kpiA</a>	Alignment	not modelled	47.9	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein sco3027; <b>PDBTitle:</b> solution nmr structure of streptomyces coelicolor sco30272 modeled with zn+2 bound, northeast structural genomics3 consortium target rr58
49	<a href="#">c2js4A</a>	Alignment	not modelled	45.6	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0434 protein bb2007; <b>PDBTitle:</b> solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3 bor54
50	<a href="#">c3lasA</a>	Alignment	not modelled	31.5	8	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative carbonic anhydrase; <b>PDBTitle:</b> crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution
51	<a href="#">c2w3nA</a>	Alignment	not modelled	27.5	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carbonic anhydrase 2; <b>PDBTitle:</b> structure and inhibition of the co2-sensing carbonic2 anhydrase can2 from the pathogenic fungus cryptococcus3 neoformans
52	<a href="#">c1ylkA</a>	Alignment	not modelled	27.4	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rv1284/mt1322; <b>PDBTitle:</b> crystal structure of rv1284 from mycobacterium tuberculosis in complex2 with thiocyanate
53	<a href="#">d1ddza1</a>	Alignment	not modelled	26.9	17	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> beta-carbonic anhydrase, cab <b>Family:</b> beta-carbonic anhydrase, cab
						<b>PDB header:</b> structural genomics, unknown function

54	<a href="#">c2kppA</a>	Alignment	not modelled	26.3	3	<b>Chain:</b> A: <b>PDB Molecule:</b> lin0431 protein; <b>PDBTitle:</b> solution nmr structure of lin0431 protein from listeria innocua.2 northeast structural genomics consortium target lkr112
55	<a href="#">c2a8cE</a>	Alignment	not modelled	26.2	17	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> carbonic anhydrase 2; <b>PDBTitle:</b> haemophilus influenzae beta-carbonic anhydrase
56	<a href="#">d1ddza2</a>	Alignment	not modelled	26.2	17	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> beta-carbonic anhydrase, cab <b>Family:</b> beta-carbonic anhydrase, cab
57	<a href="#">c1ddzA</a>	Alignment	not modelled	26.2	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> x-ray structure of a beta-carbonic anhydrase from the red2 alga, porphyridium purpureum r-1
58	<a href="#">c3eyxB</a>	Alignment	not modelled	25.2	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae
59	<a href="#">d1g5ca</a>	Alignment	not modelled	22.0	8	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> beta-carbonic anhydrase, cab <b>Family:</b> beta-carbonic anhydrase, cab
60	<a href="#">d2aqaa1</a>	Alignment	not modelled	22.0	17	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Nop10-like SnoRNP <b>Family:</b> Nucleolar RNA-binding protein Nop10-like
61	<a href="#">c3ucoB</a>	Alignment	not modelled	21.6	18	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> cocomyxa beta-carbonic anhydrase in complex with iodide
62	<a href="#">c2a5vB</a>	Alignment	not modelled	21.6	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carbonic anhydrase (carbonate dehydratase) (carbonic <b>PDBTitle:</b> crystal structure of m. tuberculosis beta carbonic anhydrase, rv3588c, 2 tetrameric form
63	<a href="#">d1i6pa</a>	Alignment	not modelled	21.5	27	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> beta-carbonic anhydrase, cab <b>Family:</b> beta-carbonic anhydrase, cab
64	<a href="#">d1ekja</a>	Alignment	not modelled	21.2	17	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> beta-carbonic anhydrase, cab <b>Family:</b> beta-carbonic anhydrase, cab
65	<a href="#">d1t1ua1</a>	Alignment	not modelled	17.9	15	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
66	<a href="#">c1t7qA</a>	Alignment	not modelled	13.5	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carnitine acetyltransferase; <b>PDBTitle:</b> crystal structure of the f565a mutant of murine carnitine2 acetyltransferase in complex with carnitine and coa
67	<a href="#">c2h4tB</a>	Alignment	not modelled	12.3	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carnitine o-palmitoyltransferase ii, <b>PDBTitle:</b> crystal structure of rat carnitine palmitoyltransferase ii
68	<a href="#">d1xl7a1</a>	Alignment	not modelled	12.2	13	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
69	<a href="#">c2j6aA</a>	Alignment	not modelled	11.7	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein trm112; <b>PDBTitle:</b> crystal structure of s. cerevisiae ynr046w, a zinc finger2 protein from the erf1 methyltransferase complex.
70	<a href="#">c1q6xA</a>	Alignment	not modelled	11.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> choline o-acetyltransferase; <b>PDBTitle:</b> crystal structure of rat choline acetyltransferase
71	<a href="#">d1ubdc1</a>	Alignment	not modelled	11.4	18	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
72	<a href="#">d1ndba1</a>	Alignment	not modelled	11.3	15	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
73	<a href="#">d2j7ja2</a>	Alignment	not modelled	10.5	17	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
74	<a href="#">c2jyeA</a>	Alignment	not modelled	10.4	16	<b>PDB header:</b> cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> granulin a; <b>PDBTitle:</b> human granulin a
75	<a href="#">d2apob1</a>	Alignment	not modelled	9.9	29	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Nop10-like SnoRNP <b>Family:</b> Nucleolar RNA-binding protein Nop10-like
76	<a href="#">d1nm8a1</a>	Alignment	not modelled	9.5	18	<b>Fold:</b> CoA-dependent acyltransferases <b>Superfamily:</b> CoA-dependent acyltransferases <b>Family:</b> Choline/Carnitine O-acyltransferase
77	<a href="#">d2bdra1</a>	Alignment	not modelled	9.3	9	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Ureidoglycolate hydrolase AIIA
78	<a href="#">c2fyoA</a>	Alignment	not modelled	9.1	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carnitine o-palmitoyltransferase ii, <b>PDBTitle:</b> crystal structure of rat carnitine palmitoyltransferase 22 in space group p43212
79	<a href="#">d2nn6g3</a>	Alignment	not modelled	8.9	13	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
80	<a href="#">d2c42a2</a>	Alignment	not modelled	8.8	8	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> PFOR PP module
						<b>PDB header:</b> transferase

81	<a href="#">c2fy2A_</a>	Alignment	not modelled	8.8	15	<b>Chain:</b> A: <b>PDB Molecule:</b> choline o-acetyltransferase; <b>PDBTitle:</b> structures of ligand bound human choline acetyltransferase2 provide insight into regulation of acetylcholine synthesis
82	<a href="#">d2ey4e1</a>	Alignment	not modelled	8.7	21	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Nop10-like SnoRNP <b>Family:</b> Nucleolar RNA-binding protein Nop10-like
83	<a href="#">c3izbP_</a>	Alignment	not modelled	8.1	20	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 40s ribosomal protein rps11 (s17p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
84	<a href="#">c2k5rA_</a>	Alignment	not modelled	7.9	32	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein xf2673; <b>PDBTitle:</b> solution nmr structure of xf2673 from xylella fastidiosa.2 northeast structural genomics consortium target xfr39
85	<a href="#">c3iz6P_</a>	Alignment	not modelled	7.8	20	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 40s ribosomal protein s11 (s17p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
86	<a href="#">d1l1oc_</a>	Alignment	not modelled	7.6	9	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
87	<a href="#">c2xznQ_</a>	Alignment	not modelled	6.7	20	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> ribosomal protein s17 containing protein; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
88	<a href="#">d1xsqa_</a>	Alignment	not modelled	6.3	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Ureidoglycolate hydrolase AIIA
89	<a href="#">d2ct7a1</a>	Alignment	not modelled	6.2	15	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> IBR domain
90	<a href="#">c2ak1A_</a>	Alignment	not modelled	6.1	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phna-like protein pa0128; <b>PDBTitle:</b> solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
91	<a href="#">d1hyoa1</a>	Alignment	not modelled	5.9	13	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Fumarylacetoacetate hydrolase, FAH, N-terminal domain <b>Family:</b> Fumarylacetoacetate hydrolase, FAH, N-terminal domain
92	<a href="#">c2c3yA_</a>	Alignment	not modelled	5.8	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate-ferredoxin oxidoreductase; <b>PDBTitle:</b> crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
93	<a href="#">d2ja9a2</a>	Alignment	not modelled	5.7	13	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
94	<a href="#">c1skzA_</a>	Alignment	not modelled	5.5	9	<b>PDB header:</b> serine protease inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> antistasin; <b>PDBTitle:</b> protease inhibitor
95	<a href="#">d1mdah_</a>	Alignment	not modelled	5.3	14	<b>Fold:</b> 7-bladed beta-propeller <b>Superfamily:</b> YVTN repeat-like/Quinoprotein amine dehydrogenase <b>Family:</b> Methylamine dehydrogenase, H-chain
96	<a href="#">d1gpca_</a>	Alignment	not modelled	5.2	27	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Phage ssDNA-binding proteins