Phyre2

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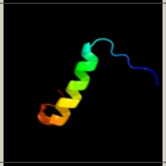
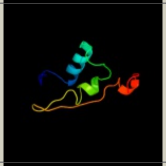
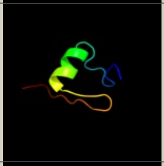
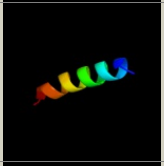
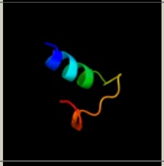
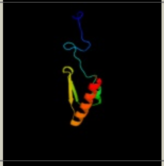
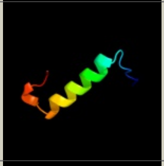
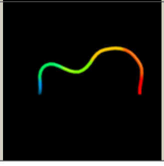
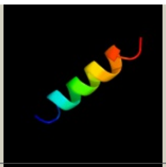
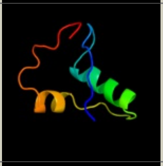
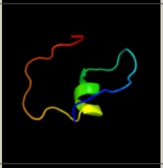
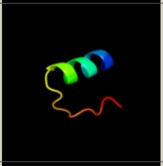
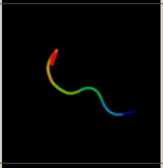
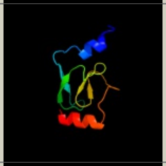
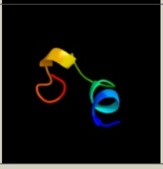
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2r1fB_	Alignment		100.0	97	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**predicted aminodeoxychorismate lyase; **PDBTitle:** crystal structure of predicted aminodeoxychorismate lyase from2 escherichia coli
2	d3bz6a1	Alignment		45.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PSPTO2686-like
3	c2v3sB_	Alignment		44.5	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase osr1; **PDBTitle:** structural insights into the recognition of substrates and2 activators by the osr1 kinase
4	d1l0wa2	Alignment		38.3	29	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
5	d1gjja2	Alignment		36.9	25	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
6	c3r85E_	Alignment		34.5	40	**PDB header:**apoptosis **Chain:** E: **PDB Molecule:**heme-binding protein 2; **PDBTitle:** crystal structure of human soul bh3 domain in complex with bcl-xl
7	d1eg7a_	Alignment		34.4	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
8	d1h9fa_	Alignment		33.9	21	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
9	d1ztwa1	Alignment		33.3	16	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Reverse transcriptase
10	c3bz6A_	Alignment		33.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0502 protein pspto_2686; **PDBTitle:** crystal structure of a conserved protein of unknown function from2 pseudomonas syringae pv. tomato str. dc3000
11	d1jeia_	Alignment		32.5	29	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain

12	c3r85G_	Alignment		32.1	40	**PDB header:**apoptosis **Chain:** G: **PDB Molecule:**heme-binding protein 2; **PDBTitle:** crystal structure of human soul bh3 domain in complex with bcl-xl
13	d1e0ga_	Alignment		29.6	10	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
14	d2fug13	Alignment		26.9	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Nqo1 middle domain-like **Family:**Nqo1 middle domain-like
15	c2exuA_	Alignment		26.7	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription initiation protein spt4/spt5; **PDBTitle:** crystal structure of saccharomyces cerevisiae transcription elongation2 factors spt4-spt5ngn domain
16	c3do6B_	Alignment		26.2	29	**PDB header:**ligase **Chain:** B: **PDB Molecule:**formate--tetrahydrofolate ligase; **PDBTitle:** crystal structure of putative formyltetrahydrofolate2 synthetase (tm1766) from thermotoga maritima at 1.85 a3 resolution
17	c3r85F_	Alignment		26.2	41	**PDB header:**apoptosis **Chain:** F: **PDB Molecule:**heme-binding protein 2; **PDBTitle:** crystal structure of human soul bh3 domain in complex with bcl-xl
18	c1gjjA_	Alignment		25.8	57	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lap2; **PDBTitle:** n-terminal constant region of the nuclear envelope protein2 lap2
19	c3lk2B_	Alignment		25.2	16	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**f-actin-capping protein subunit beta isoforms 1 and 2; **PDBTitle:** crystal structure of capz bound to the uncapping motif from carmil
20	c3f1iH_	Alignment		24.6	30	**PDB header:**protein binding **Chain:** H: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** human escrt-0 core complex
21	c2zktB_	Alignment	not modelled	23.7	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** structure of ph0037 protein from pyrococcus horikoshii
22	d1wxqa2	Alignment	not modelled	23.1	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
23	c2dhkA_	Alignment	not modelled	20.6	8	**PDB header:**immune system **Chain:** A: **PDB Molecule:**tbc1 domain family member 2; **PDBTitle:** solution structure of the ph domain of tbc1 domain family2 member 2 protein from human
24	c3r85H_	Alignment	not modelled	18.8	39	**PDB header:**apoptosis **Chain:** H: **PDB Molecule:**heme-binding protein 2; **PDBTitle:** crystal structure of human soul bh3 domain in complex with bcl-xl
25	c3lwfD_	Alignment	not modelled	18.3	15	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
26	c2yztA_	Alignment	not modelled	17.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha1756; **PDBTitle:** crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
27	d2zd1b1	Alignment	not modelled	16.1	15	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Reverse transcriptase
28	c3fwlA_	Alignment	not modelled	15.9	11	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**penicillin-binding protein 1b; **PDBTitle:** crystal structure of the full-length transglycosylase pbp1b2 from escherichia coli

29	d1hara_	Alignment	not modelled	14.2	15	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Reverse transcriptase
30	d2ysca1	Alignment	not modelled	13.8	100	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
31	d1nr6a_	Alignment	not modelled	12.8	56	**Fold:**Cytochrome P450 **Superfamily:**Cytochrome P450 **Family:**Cytochrome P450
32	c3e4eA_	Alignment	not modelled	11.8	56	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome p450 2e1; **PDBTitle:** human cytochrome p450 2e1 in complex with the inhibitor 4-2 methylpyrazole
33	d1dt9a3	Alignment	not modelled	10.9	9	**Fold:**N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 **Superfamily:**N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 **Family:**N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1
34	c2k9xA_	Alignment	not modelled	10.7	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of urm1 from trypanosoma brucei
35	d1oq1a_	Alignment	not modelled	10.4	41	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Hypothetical protein YesU
36	c2h8kA_	Alignment	not modelled	10.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sult1c3 splice variant d; **PDBTitle:** human sulfotranferase sult1c3 in complex with pap
37	c2ps3A_	Alignment	not modelled	9.9	7	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** structure and metal binding properties of znua, a2 periplasmic zinc transporter from escherichia coli
38	d1ujpa_	Alignment	not modelled	9.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
39	c3ed4A_	Alignment	not modelled	9.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylsulfatase; **PDBTitle:** crystal structure of putative arylsulfatase from escherichia coli
40	c1ezjA_	Alignment	not modelled	9.5	12	**PDB header:**viral protein, transferase **Chain:** A: **PDB Molecule:**nucleocapsid phosphoprotein; **PDBTitle:** crystal structure of the multimerization domain of the phosphoprotein2 from sendai virus
41	d1plsa_	Alignment	not modelled	9.5	21	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
42	c1d0rA_	Alignment	not modelled	9.2	13	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon-like peptide-1-(7-36)-amide; **PDBTitle:** solution structure of glucagon-like peptide-1-(7-36)-amide2 in trifluoroethanol/water
43	c2qieB_	Alignment	not modelled	9.2	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**molybdopterin synthase small subunit; **PDBTitle:** staphylococcus aureus molybdopterin synthase in complex2 with precursor z
44	c1us7B_	Alignment	not modelled	9.2	14	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**hsp90 co-chaperone cdc37; **PDBTitle:** complex of hsp90 and p50
45	d1us7b_	Alignment	not modelled	9.2	14	**Fold:**Hsp90 co-chaperone CDC37 **Superfamily:**Hsp90 co-chaperone CDC37 **Family:**Hsp90 co-chaperone CDC37
46	d1vjka_	Alignment	not modelled	8.8	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
47	c3f5fA_	Alignment	not modelled	8.7	14	**PDB header:**transport, transferase **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, heparan **PDBTitle:** crystal structure of heparan sulfate 2-o-sulfotransferase2 from gallus gallus as a maltose binding protein fusion.
48	d1rd5a_	Alignment	not modelled	8.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
49	c3b5qB_	Alignment	not modelled	8.5	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative sulfatase yidj; **PDBTitle:** crystal structure of a putative sulfatase (np_810509.1)2 from bacteroides thetaiotaomicron vpi-5482 at 2.40 a3 resolution
50	c3s2wB_	Alignment	not modelled	8.5	7	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the crystal structure of a marr transcriptional regulator from2 methanosarcina mazei go1
51	d1c0aa2	Alignment	not modelled	8.4	13	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
52	d1seia_	Alignment	not modelled	8.3	10	**Fold:**Ribosomal protein S8 **Superfamily:**Ribosomal protein S8 **Family:**Ribosomal protein S8
53	c3szzA_	Alignment	not modelled	8.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonoacetate hydrolase; **PDBTitle:** crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
54	c3po0A_	Alignment	not modelled	8.2	4	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small archaeal modifier protein 1;

						PDBTitle: crystal structure of samp1 from haloferax volcanii
55	c3ebsA_	Alignment	not modelled	8.1	56	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome p450 2a6; **PDBTitle:** human cytochrome p450 2a6 i208s/i300f/g301a/s369g in complex2 with phenacetin
56	c3lggA_	Alignment	not modelled	8.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase cecr1; **PDBTitle:** crystal structure of human adenosine deaminase growth factor,2 adenosine deaminase type 2 (ada2) complexed with transition state3 analogue, coformycin
57	c3jviA_	Alignment	not modelled	8.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein tyrosine phosphatase; **PDBTitle:** product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
58	c3bbnH_	Alignment	not modelled	8.0	8	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**ribosomal protein s8; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
59	c2ogwB_	Alignment	not modelled	7.9	7	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**high-affinity zinc uptake system protein znua **PDBTitle:** structure of abc type zinc transporter from e. coli
60	d1a9xa1	Alignment	not modelled	7.8	42	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
61	c3e20C_	Alignment	not modelled	7.7	15	**PDB header:**translation **Chain:** C: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** crystal structure of s.pombe erf1/erf3 complex
62	c2qzuA_	Alignment	not modelled	7.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sulfatase yidj; **PDBTitle:** crystal structure of the putative sulfatase yidj from bacteroides2 fragilis. northeast structural genomics consortium target bfr123
63	d2joya1	Alignment	not modelled	7.5	8	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L14e
64	c2uzhB_	Alignment	not modelled	7.5	7	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2c-methyl-d-erythritol 2,4-cyclodiphosphate **PDBTitle:** mycobacterium smegmatis 2c-methyl-d-erythritol-2,4-2 cyclodiphosphate synthase (ispf)
65	d1gx1a_	Alignment	not modelled	7.5	23	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
66	c3thaB_	Alignment	not modelled	7.4	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni.
67	c2dt7A_	Alignment	not modelled	7.4	67	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**splicing factor 3a subunit 3; **PDBTitle:** solution structure of the second surp domain of human2 splicing factor sf3a120 in complex with a fragment of3 human splicing factor sf3a60
68	c2jugB_	Alignment	not modelled	7.3	17	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**tubc protein; **PDBTitle:** multienzyme docking in hybrid megasynthetases
69	d2ouxa2	Alignment	not modelled	7.3	4	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
70	d1i94h_	Alignment	not modelled	7.2	8	**Fold:**Ribosomal protein S8 **Superfamily:**Ribosomal protein S8 **Family:**Ribosomal protein S8
71	c2e0yB_	Alignment	not modelled	7.2	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** crystal structure of the samarium derivative of mature gamma-2 glutamyltranspeptidase from escherichia coli
72	c2c1tC_	Alignment	not modelled	7.0	35	**PDB header:**protein transport/membrane protein **Chain:** C: **PDB Molecule:**nucleoporin nup2; **PDBTitle:** structure of the kap60p:nup2 complex
73	c2yvsA_	Alignment	not modelled	7.0	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycolate oxidase subunit glce; **PDBTitle:** crystal structure of glycolate oxidase subunit glce from thermus2 thermophilus hb8
74	d1s6la1	Alignment	not modelled	6.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
75	c2pmpA_	Alignment	not modelled	6.9	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; **PDBTitle:** structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate synthase from2 the isoprenoid biosynthetic pathway of arabidopsis thaliana
76	c2o1eB_	Alignment	not modelled	6.8	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ycdh; **PDBTitle:** crystal structure of the metal-dependent lipoprotein ycdh2 from bacillus subtilis, northeast structural genomics3 target sr583
77	c3f0gA_	Alignment	not modelled	6.7	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; **PDBTitle:** co-crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase with cmp
78	c2ngoB	Alignment	not modelled	6.6	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**gamma-glutamyltranspeptidase;

78	c2nqoB_	Alignment	not modelled	6.6	25	**PDBTitle:** crystal structure of helicobacter pylori gamma-glutamyltranspeptidase
79	d1iuga_	Alignment	not modelled	6.6	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
80	d1ecfa1	Alignment	not modelled	6.6	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
81	d1gph11	Alignment	not modelled	6.5	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
82	c2iirJ_	Alignment	not modelled	6.4	16	**PDB header:**transferase **Chain:** J: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase from a hypothermophile thermotoga maritima
83	d1an7a_	Alignment	not modelled	6.4	8	**Fold:**Ribosomal protein S8 **Superfamily:**Ribosomal protein S8 **Family:**Ribosomal protein S8
84	c2j98A_	Alignment	not modelled	6.4	100	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**replicase polyprotein 1ab; **PDBTitle:** human coronavirus 229e non structural protein 9 cys69ala2 mutant (nsp9)
85	c1w9qB_	Alignment	not modelled	6.3	3	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**syntenin 1; **PDBTitle:** crystal structure of the pdz tandem of human syntenin in2 complex with tnefaf peptide
86	d2nnja1	Alignment	not modelled	6.3	56	**Fold:**Cytochrome P450 **Superfamily:**Cytochrome P450 **Family:**Cytochrome P450
87	c3izcN_	Alignment	not modelled	6.2	16	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein rpl14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
88	d1a6qa1	Alignment	not modelled	6.0	71	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
89	d1i6ua_	Alignment	not modelled	6.0	4	**Fold:**Ribosomal protein S8 **Superfamily:**Ribosomal protein S8 **Family:**Ribosomal protein S8
90	c3cqxD_	Alignment	not modelled	5.9	33	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**bag family molecular chaperone regulator 2; **PDBTitle:** chaperone complex
91	c3lp9C_	Alignment	not modelled	5.9	27	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**ls-24; **PDBTitle:** crystal structure of ls24, a seed albumin from lathyrus2 sativus
92	c2vqrA_	Alignment	not modelled	5.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sulfatase; **PDBTitle:** crystal structure of a phosphonate monoester hydrolase2 from rhizobium leguminosarum: a new member of the3 alkaline phosphatase superfamily
93	c3iz5N_	Alignment	not modelled	5.8	8	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein l14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
94	d2gy9h1	Alignment	not modelled	5.7	16	**Fold:**Ribosomal protein S8 **Superfamily:**Ribosomal protein S8 **Family:**Ribosomal protein S8
95	d1b74a1	Alignment	not modelled	5.7	15	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
96	d1okra_	Alignment	not modelled	5.7	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
97	c2b5dX_	Alignment	not modelled	5.6	8	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima
98	d1iv3a_	Alignment	not modelled	5.6	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
99	d2crfa1	Alignment	not modelled	5.5	8	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Ran-binding domain