Phyre^2

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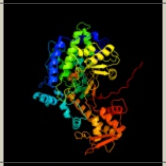
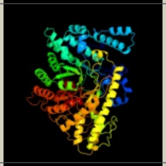
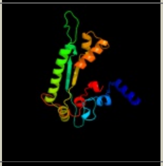
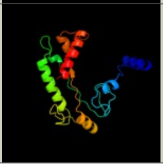
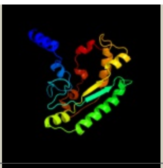
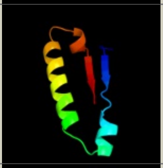
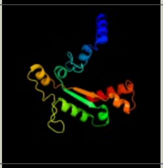
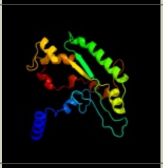
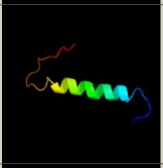
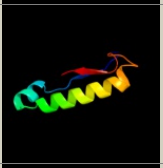
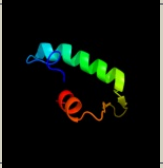
Description	P09373
Date	Thu Jan 5 11:02:15 GMT 2012
Unique Job ID	973cbb7f09cb6b84

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1h16a_	Alignment		100.0	100	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
2	d1qhma_	Alignment		100.0	100	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
3	d1r9da_	Alignment		100.0	28	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
4	c2y8nC_	Alignment		100.0	21	**PDB header:**lyase **Chain:** C: **PDB Molecule:**4-hydroxyphenylacetate decarboxylase large subunit; **PDBTitle:** crystal structure of glycyl radical enzyme
5	c2f3oB_	Alignment		100.0	21	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pyruvate formate-lyase 2; **PDBTitle:** crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus
6	d1hk8a_	Alignment		99.5	16	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
7	c1hk8A_	Alignment		99.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
8	c2cvuA_	Alignment		90.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large chain **PDBTitle:** structures of yeast ribonucleotide reductase i
9	c2wghA_	Alignment		89.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large **PDBTitle:** human ribonucleotide reductase r1 subunit (rrm1) in complex2 with datp and mg.
10	c3hnfA_	Alignment		88.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large subunit; **PDBTitle:** crystal structure of human ribonucleotide reductase 1 bound to the2 effectors ttp and datp
11	c1xjeA_	Alignment		87.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleotide reductase, b12-dependent; **PDBTitle:** structural mechanism of allosteric substrate specificity in a2 ribonucleotide reductase: dttp-gdp complex

12	c3r1rB_	Alignment		84.4	17	**PDB header:**complex (oxidoreductase/peptide) **Chain:** B: **PDB Molecule:**ribonucleotide reductase r1 protein; **PDBTitle:** ribonucleotide reductase r1 protein with amppnp occupying2 the activity site from escherichia coli
13	c3gr1A_	Alignment		71.8	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein prgh; **PDBTitle:** periplamic domain of the t3ss inner membrane protein prgh2 from s.typhimurium (fragment 170-392)
14	c1pemA_	Alignment		69.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase 2 alpha **PDBTitle:** ribonucleotide reductase protein r1e from salmonella2 typhimurium
15	d1rlra2	Alignment		66.9	18	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**R1 subunit of ribonucleotide reductase, C-terminal domain
16	d2bgxa1	Alignment		56.3	20	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**Peptidoglycan binding domain, PGBD
17	d1u5tb1	Alignment		50.3	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
18	c3gr0D_	Alignment		48.9	23	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**protein prgh; **PDBTitle:** periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-362)
19	d1dq3a4	Alignment		46.9	19	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
20	c2jobA_	Alignment		40.5	24	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
21	d1jvaa3	Alignment	not modelled	36.3	10	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
22	d2i15a1	Alignment	not modelled	34.0	28	**Fold:**MG296-like **Superfamily:**MG296-like **Family:**MG296-like
23	c2vkjA_	Alignment	not modelled	28.9	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**tm1634; **PDBTitle:** structure of the soluble domain of the membrane protein2 tm1634 from thermotoga maritima
24	d2di0a1	Alignment	not modelled	24.5	22	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
25	c3gebC_	Alignment	not modelled	23.3	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**eyes absent homolog 2; **PDBTitle:** crystal structure of edeya2
26	d1ztda1	Alignment	not modelled	21.7	25	**Fold:**RNase III domain-like **Superfamily:**RNase III domain-like **Family:**PF0609-like
27	c3uo9B_	Alignment	not modelled	21.4	20	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**glutaminase kidney isoform, mitochondrial; **PDBTitle:** crystal structure of human gac in complex with glutamate and bptes
28	d1nh2a2	Alignment	not modelled	20.3	36	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
						Fold:TBP-like

29	d1aisa1	Alignment	not modelled	19.9	36	**Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
30	d1nh2a1	Alignment	not modelled	19.7	25	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
31	c1r8jB_	Alignment	not modelled	19.7	24	**PDB header:**circadian clock protein **Chain:** B: **PDB Molecule:**kaia; **PDBTitle:** crystal structure of circadian clock protein kaia from2 synechococcus elongatus
32	d1qnaa2	Alignment	not modelled	19.1	36	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
33	d1mp9a1	Alignment	not modelled	19.0	29	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
34	d1aisa2	Alignment	not modelled	18.8	36	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
35	c2khvA_	Alignment	not modelled	18.3	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of protein nmul_a0922 from2 nitrosospira multiformis. northeast structural genomics3 consortium target nmr38b.
36	d1v5ra1	Alignment	not modelled	17.8	33	**Fold:**N domain of copper amine oxidase-like **Superfamily:**GAS2 domain-like **Family:**GAS2 domain
37	d1rpya_	Alignment	not modelled	17.7	17	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
38	d1qnaa1	Alignment	not modelled	17.6	25	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
39	d1jwoa_	Alignment	not modelled	17.4	39	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
40	d1mp9a2	Alignment	not modelled	17.3	42	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
41	d1w7pd1	Alignment	not modelled	16.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
42	c2q01A_	Alignment	not modelled	16.4	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**uronate isomerase; **PDBTitle:** crystal structure of glucuronate isomerase from caulobacter crescentus
43	c2hjhB_	Alignment	not modelled	16.1	44	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nad-dependent histone deacetylase sir2; **PDBTitle:** crystal structure of the sir2 deacetylase
44	d1uj8a1	Alignment	not modelled	15.8	22	**Fold:**Another 3-helical bundle **Superfamily:**IscX-like **Family:**IscX-like
45	d1vioa2	Alignment	not modelled	15.5	17	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
46	d1cdwa1	Alignment	not modelled	15.5	25	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
47	c3knyA_	Alignment	not modelled	14.9	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bt_3535; **PDBTitle:** crystal structure of a two domain protein with unknown function2 (bt_3535) from bacteroides thetaiotaomicron vpi-5482 at 2.60 a3 resolution
48	d1k9aa2	Alignment	not modelled	14.6	29	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
49	c2a7oA_	Alignment	not modelled	14.2	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**huntingtin interacting protein b; **PDBTitle:** solution structure of the hset2/hypb sri domain
50	d1bf5a3	Alignment	not modelled	13.9	12	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
51	c2k5eA_	Alignment	not modelled	13.6	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195
52	c2zcyM_	Alignment	not modelled	13.1	28	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**proteasome component pre4; **PDBTitle:** yeast 20s proteasome:syringolin a-complex
53	d1i3za_	Alignment	not modelled	13.0	25	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
54	c3vjjA_	Alignment	not modelled	12.9	23	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**p9-1; **PDBTitle:** crystal structure analysis of the p9-1
55	d1xlya_	Alignment	not modelled	12.9	22	**Fold:**RNA-binding protein She2p **Superfamily:**RNA-binding protein She2p **Family:**RNA-binding protein She2p

56	d1fs7a_	Alignment	not modelled	12.8	13	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
57	c1fs9A_	Alignment	not modelled	12.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c nitrite reductase; **PDBTitle:** cytochrome c nitrite reductase from wolinella succinogenes-azide2 complex
58	d2nlua1	Alignment	not modelled	12.4	44	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**PWWP domain
59	d1dwka2	Alignment	not modelled	12.3	21	**Fold:**Cyanase C-terminal domain **Superfamily:**Cyanase C-terminal domain **Family:**Cyanase C-terminal domain
60	d1cdwa2	Alignment	not modelled	12.3	25	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
61	c3pkiF_	Alignment	not modelled	12.3	32	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
62	c3gd5D_	Alignment	not modelled	12.2	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
63	c2ci8A_	Alignment	not modelled	12.2	24	**PDB header:**translation **Chain:** A: **PDB Molecule:**cytoplasmic protein nck1; **PDBTitle:** sh2 domain of human nck1 adaptor protein - uncomplexed
64	c3k35D_	Alignment	not modelled	12.1	32	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
65	c2q82A_	Alignment	not modelled	11.9	35	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**core protein p7; **PDBTitle:** crystal structure of core protein p7 from pseudomonas phage2 phi12. northeast structural genomics target oc1
66	d1u8sa1	Alignment	not modelled	11.9	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
67	c2hx6A_	Alignment	not modelled	11.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** solution structure analysis of the phage t42 endoribonuclease regb
68	d1p9ka_	Alignment	not modelled	11.9	14	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
69	c2ksgA_	Alignment	not modelled	11.8	28	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**dermcidin; **PDBTitle:** solution structure of dermcidin-1l, a human antibiotic2 peptide
70	c3d36B_	Alignment	not modelled	11.7	13	**PDB header:**transferase/transferase inhibitor **Chain:** B: **PDB Molecule:**sporulation kinase b; **PDBTitle:** how to switch off a histidine kinase: crystal structure of2 geobacillus stearothermophilus kinb with the inhibitor sda
71	c2pmzV_	Alignment	not modelled	11.7	12	**PDB header:**translation, transferase **Chain:** V: **PDB Molecule:**dna-directed rna polymerase subunit h; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
72	c3df1R_	Alignment	not modelled	11.6	19	**PDB header:**ribosome **Chain:** R: **PDB Molecule:**30s ribosomal protein s18; **PDBTitle:** crystal structure of the bacterial ribosome from escherichia2 coli in complex with hygromycin b. this file contains the3 30s subunit of the first 70s ribosome, with hygromycin b4 bound. the entire crystal structure contains two 70s5 ribosomes.
73	c3d2rB_	Alignment	not modelled	11.4	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**[pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; **PDBTitle:** crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp
74	c2vpmB_	Alignment	not modelled	11.4	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**trypanothione synthetase; **PDBTitle:** trypanothione synthetase
75	d1hmja_	Alignment	not modelled	11.3	9	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
76	c3pcsB_	Alignment	not modelled	11.2	18	**PDB header:**protein transport/transferase **Chain:** B: **PDB Molecule:**espg; **PDBTitle:** structure of espg-pak2 autoinhibitory ialpha3 helix complex
77	d1yuaa2	Alignment	not modelled	11.1	11	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Prokaryotic DNA topoisomerase I, a C-terminal fragment
78	d1dzfa2	Alignment	not modelled	11.0	14	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
79	d1etea_	Alignment	not modelled	10.9	10	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
80	d1qada_	Alignment	not modelled	10.8	12	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
81	c2i6lB_	Alignment	not modelled	10.8	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mitogen-activated protein kinase 6; **PDBTitle:** crystal structure of human mitogen activated protein kinase2 6 (mapk6)
						Fold:SH2-like

82	d1a81e1	Alignment	not modelled	10.6	29	**Superfamily:**SH2 domain **Family:**SH2 domain
83	c3sohB_	Alignment	not modelled	10.6	29	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**flagellar motor switch protein flig; **PDBTitle:** architecture of the flagellar rotor
84	c2uval_	Alignment	not modelled	10.6	12	**PDB header:**transferase **Chain:** I: **PDB Molecule:**fatty acid synthase beta subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
85	c2kj8A_	Alignment	not modelled	10.4	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative prophage cps-53 integrase; **PDBTitle:** nmr structure of fragment 87-196 from the putative phage2 integrase ints of e. coli: northeast structural genomics3 consortium target er652a, psi-2
86	d2uubr1	Alignment	not modelled	10.4	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein S18 **Family:**Ribosomal protein S18
87	d1eika_	Alignment	not modelled	10.3	16	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
88	c3t4aG_	Alignment	not modelled	10.1	33	**PDB header:**immune system **Chain:** G: **PDB Molecule:**fibrinogen-binding protein; **PDBTitle:** structure of a truncated form of staphylococcal complement inhibitor b2 bound to human c3c at 3.4 angstrom resolution
89	d2b4ya1	Alignment	not modelled	10.1	22	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
90	d1jyra_	Alignment	not modelled	10.1	38	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
91	c3ol0C_	Alignment	not modelled	10.1	50	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
92	c3hp7A_	Alignment	not modelled	10.0	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hemolysin, putative; **PDBTitle:** putative hemolysin from streptococcus thermophilus.
93	c1mqrA_	Alignment	not modelled	10.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-d-glucuronidase; **PDBTitle:** the crystal structure of alpha-d-glucuronidase (e386q) from bacillus2 stearothermophilus t-6
94	c3dxnA_	Alignment	not modelled	9.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calmodulin-like domain protein kinase isoform 3; **PDBTitle:** crystal structure of the calcium-dependent kinase from toxoplasma2 gondii, 541.m00134, kinase domain.
95	d1yc5a1	Alignment	not modelled	9.8	32	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
96	c3cekA_	Alignment	not modelled	9.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dual specificity protein kinase ttk; **PDBTitle:** crystal structure of human dual specificity protein kinase (ttk)
97	c3nzqB_	Alignment	not modelled	9.6	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**biosynthetic arginine decarboxylase; **PDBTitle:** crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
98	c3gxxB_	Alignment	not modelled	9.5	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** structure of the sh2 domain of the candida glabrata2 transcription elongation factor spt6, crystal form b
99	c2vkzH_	Alignment	not modelled	9.4	13	**PDB header:**transferase **Chain:** H: **PDB Molecule:**fatty acid synthase subunit beta; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex