Phyre2

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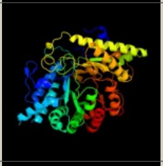
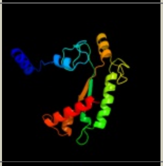
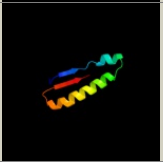
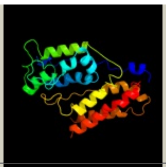
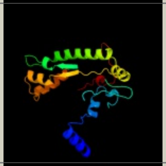
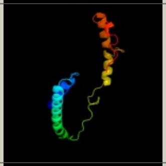
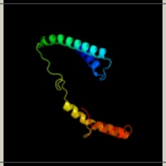
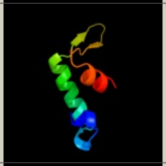
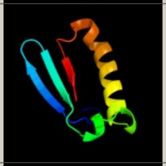
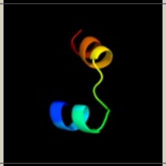
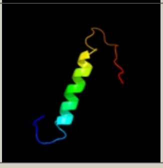
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1h16a_	Alignment		100.0	79	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
2	d1qhma_	Alignment		100.0	77	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
3	d1r9da_	Alignment		100.0	26	**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	24	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pyruvate formate-lyase 2; **PDBTitle:** crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus
6	c1hk8A_	Alignment		99.5	13	**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
7	d1hk8a_	Alignment		99.5	13	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
8	c1xjeA_	Alignment		78.8	15	**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
9	c3hnfA_	Alignment		70.3	19	**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
10	c2cvuA_	Alignment		68.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large chain **PDBTitle:** structures of yeast ribonucleotide reductase i
11	c3gr1A_	Alignment		66.1	22	**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)

12	c3at7B_	Alignment		63.6	14	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**alginate-binding flagellin; **PDBTitle:** crystal structure of bacterial cell-surface alginate-binding protein2 algp7
13	c2wghA_	Alignment		61.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large **PDBTitle:** human ribonucleotide reductase r1 subunit (rrm1) in complex2 with datp and mg.
14	c1fs9A_	Alignment		52.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c nitrite reductase; **PDBTitle:** cytochrome c nitrite reductase from wolinella succinogenes-azide2 complex
15	d1fs7a_	Alignment		52.0	14	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
16	d1dq3a4	Alignment		48.8	17	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
17	c3gr0D_	Alignment		42.5	25	**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)
18	d1jvaa3	Alignment		39.8	16	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
19	c2jobA_	Alignment		37.7	19	**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
20	d1u5tb1	Alignment		37.1	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
21	d2i15a1	Alignment	not modelled	31.1	34	**Fold:**MG296-like **Superfamily:**MG296-like **Family:**MG296-like
22	c3r1rB_	Alignment	not modelled	31.0	16	**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
23	d1ztda1	Alignment	not modelled	28.4	27	**Fold:**RNase III domain-like **Superfamily:**RNase III domain-like **Family:**PF0609-like
24	c2ejeA_	Alignment	not modelled	22.6	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i; **PDBTitle:** solution structure of rsgi ruh-071, a gtf2i domain in human2 cdna
25	c1pemA_	Alignment	not modelled	20.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase 2 alpha **PDBTitle:** ribonucleotide reductase protein r1e from salmonella2 typhimurium
26	d1uj8a1	Alignment	not modelled	18.3	17	**Fold:**Another 3-helical bundle **Superfamily:**IscX-like **Family:**IscX-like
27	c3pcsB_	Alignment	not modelled	16.9	19	**PDB header:**protein transport/transferase **Chain:** B: **PDB Molecule:**espg; **PDBTitle:** structure of espg-pak2 autoinhibitory ialpha3 helix complex
28	d2bgxa1	Alignment	not modelled	16.8	17	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**Peptidoglycan binding domain, PGBD

29	d1aisa1	Alignment	not modelled	16.4	27	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
30	d1jwoa_	Alignment	not modelled	16.4	28	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
31	d1rpya_	Alignment	not modelled	16.3	28	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
32	d1v5ra1	Alignment	not modelled	16.1	33	**Fold:**N domain of copper amine oxidase-like **Superfamily:**GAS2 domain-like **Family:**GAS2 domain
33	c3knyA_	Alignment	not modelled	16.1	10	**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
34	c2a7oA_	Alignment	not modelled	16.1	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**huntingtin interacting protein b; **PDBTitle:** solution structure of the hset2/hypb sri domain
35	c3uo9B_	Alignment	not modelled	16.0	17	**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
36	d1nh2a1	Alignment	not modelled	15.8	17	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
37	d1nh2a2	Alignment	not modelled	15.8	36	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
38	c2q01A_	Alignment	not modelled	15.7	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**uronate isomerase; **PDBTitle:** crystal structure of glucuronate isomerase from caulobacter crescentus
39	c1r8jB_	Alignment	not modelled	15.3	24	**PDB header:**circadian clock protein **Chain:** B: **PDB Molecule:**kaia; **PDBTitle:** crystal structure of circadian clock protein kaia from2 synechococcus elongatus
40	d1qnaa1	Alignment	not modelled	14.9	17	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
41	d1vioa2	Alignment	not modelled	14.7	28	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
42	d1aisa2	Alignment	not modelled	14.5	42	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
43	d1mp9a1	Alignment	not modelled	14.2	29	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
44	d1qnaa2	Alignment	not modelled	14.1	36	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
45	d1k9aa2	Alignment	not modelled	14.1	29	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
46	c2khvA_	Alignment	not modelled	13.8	8	**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.
47	d1cdwa1	Alignment	not modelled	13.2	17	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
48	d1fp3a_	Alignment	not modelled	13.0	8	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**N-acylglucosamine (NAG) epimerase
49	d1rlra2	Alignment	not modelled	12.9	18	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**R1 subunit of ribonucleotide reductase, C-terminal domain
50	d1mp9a2	Alignment	not modelled	12.6	42	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
51	d1w7pd1	Alignment	not modelled	12.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
52	c3d36B_	Alignment	not modelled	12.1	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
53	d1i3za_	Alignment	not modelled	11.4	25	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
54	c2dlzA_	Alignment	not modelled	11.4	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein vav-2; **PDBTitle:** solution structure of the sh2 domain of human protein vav-2
55	c2ci8A	Alignment	not modelled	10.7	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**cytoplasmic protein nck1;

55	c2ci8A_	Alignment	not modelled	10.7	18	**PDBTitle:** sh2 domain of human nck1 adaptor protein - uncomplexed
56	d1l8na1	Alignment	not modelled	10.6	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
57	c2bh7A_	Alignment	not modelled	10.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** crystal structure of a semet derivative of amid at 2.22 angstroms
58	d1bf5a3	Alignment	not modelled	10.6	12	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
59	c1x6cA_	Alignment	not modelled	10.4	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase, non-receptor type **PDBTitle:** solution structures of the sh2 domain of human protein-2 tyrosine phosphatase shp-1
60	c3d2rB_	Alignment	not modelled	10.4	17	**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
61	c3gd5D_	Alignment	not modelled	10.4	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
62	d1etea_	Alignment	not modelled	10.3	16	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
63	d1qada_	Alignment	not modelled	10.2	24	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
64	d1yqea1	Alignment	not modelled	10.1	8	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
65	d1ayaa_	Alignment	not modelled	10.1	16	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
66	d1p9ka_	Alignment	not modelled	10.1	21	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
67	c2q82A_	Alignment	not modelled	9.9	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
68	d1yuaa2	Alignment	not modelled	9.9	11	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Prokaryotic DNA topoisomerase I, a C-terminal fragment
69	c3cekA_	Alignment	not modelled	9.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dual specificity protein kinase ttk; **PDBTitle:** crystal structure of human dual specificity protein kinase (ttk)
70	d1xlya_	Alignment	not modelled	9.4	33	**Fold:**RNA-binding protein She2p **Superfamily:**RNA-binding protein She2p **Family:**RNA-binding protein She2p
71	d2nlua1	Alignment	not modelled	9.4	39	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**PWWP domain
72	c3hp7A_	Alignment	not modelled	9.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hemolysin, putative; **PDBTitle:** putative hemolysin from streptococcus thermophilus.
73	c3gebC_	Alignment	not modelled	9.3	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**eyes absent homolog 2; **PDBTitle:** crystal structure of edeya2
74	d1cdwa2	Alignment	not modelled	9.3	25	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
75	c2hx6A_	Alignment	not modelled	9.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease; **PDBTitle:** solution structure analysis of the phage t42 endoribonuclease regb
76	c3vjjA_	Alignment	not modelled	9.3	23	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**p9-1; **PDBTitle:** crystal structure analysis of the p9-1
77	d1fhsa_	Alignment	not modelled	9.0	24	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
78	d1a81e1	Alignment	not modelled	9.0	18	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
79	d1a81e2	Alignment	not modelled	9.0	9	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
80	d2oq1a1	Alignment	not modelled	8.8	24	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
81	d1f2fa_	Alignment	not modelled	8.8	12	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain

82	d1l1la_	Alignment	not modelled	8.7	9	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**B12-dependent (class II) ribonucleotide reductase
83	c3gxxB_	Alignment	not modelled	8.7	33	**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
84	c2pmzV_	Alignment	not modelled	8.7	12	**PDB header:**translation, transferase **Chain:** V: **PDB Molecule:**dna-directed rna polymerase subunit h; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
85	d1v0ea2	Alignment	not modelled	8.6	18	**Fold:**Triple-stranded beta-helix **Superfamily:**Phage fibre proteins **Family:**Endo-alpha-sialidase
86	d1jyra_	Alignment	not modelled	8.5	25	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
87	d1h41a1	Alignment	not modelled	8.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
88	d1luia_	Alignment	not modelled	8.5	11	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
89	d2oq1a2	Alignment	not modelled	8.4	11	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
90	c3ajfA_	Alignment	not modelled	8.4	39	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** structural insigths into dsrna binding and rna silencing suppression2 by ns3 protein of rice hoja blanca tenuivirus
91	d1iruc_	Alignment	not modelled	8.4	20	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
92	d1dwka2	Alignment	not modelled	8.4	21	**Fold:**Cyanase C-terminal domain **Superfamily:**Cyanase C-terminal domain **Family:**Cyanase C-terminal domain
93	d1qcfa2	Alignment	not modelled	8.4	12	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
94	c2dm0A_	Alignment	not modelled	8.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase txk; **PDBTitle:** solution structure of the sh2 domain of human tyrosine-2 protein kinase txk
95	d1rjaa_	Alignment	not modelled	8.4	19	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
96	d1dzfa2	Alignment	not modelled	8.3	16	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
97	c2vpmB_	Alignment	not modelled	8.2	6	**PDB header:**ligase **Chain:** B: **PDB Molecule:**trypanothione synthetase; **PDBTitle:** trypanothione synthetase
98	c3jvdA_	Alignment	not modelled	8.1	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcription regulation repressor (laci2 family) from corynebacterium glutamicum
99	d1duvg1	Alignment	not modelled	8.0	16	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase