Phyre^2

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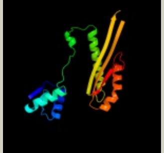
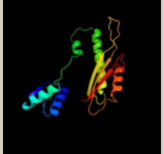
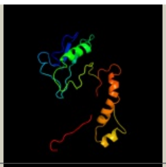
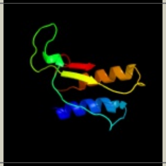
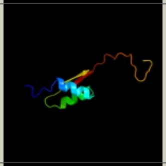
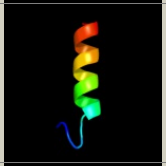
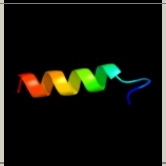
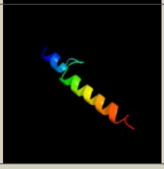
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2y9jt_	Alignment		100.0	21	**PDB header:**protein transport **Chain:** T: **PDB Molecule:**protein prgh; **PDBTitle:** three-dimensional model of salmonella's needle complex at2 subnanometer resolution
2	c1yj7A_	Alignment		100.0	24	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**escj; **PDBTitle:** crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
3	c2hfvA_	Alignment		92.5	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rpa1041; **PDBTitle:** solution nmr structure of protein rpa1041 from pseudomonas2 aeruginosa. northeast structural genomics consortium3 target pat90.
4	d2hfva1	Alignment		86.7	24	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**RPA1041-like
5	d1yqha1	Alignment		80.7	13	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
6	d1lxna_	Alignment		79.1	23	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
7	d1vk8a_	Alignment		78.0	6	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
8	d1lxja_	Alignment		77.8	17	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
9	d2iboa1	Alignment		71.4	8	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
10	c2epiA_	Alignment		63.4	5	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0045 protein mj1052; **PDBTitle:** crystal structure pf hypothetical protein mj1052 from2 methanocaldococcus jannascii (form 2)
11	c2rddB_	Alignment		60.4	19	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.

12	c1oy8A_	Alignment		54.5	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
13	c2flzC_	Alignment		53.9	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cis-3-chloroacrylic acid dehalogenase; **PDBTitle:** the x-ray structure of cis-3-chloroacrylic acid dehalogenase (cis-2 caad) with a sulfate ion bound in the active site
14	d2yzca1	Alignment		52.2	19	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**Urate oxidase (uricase)
15	d1b6ga_	Alignment		48.1	6	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloalkane dehalogenase
16	c2h7xA_	Alignment		47.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**type i polyketide synthase pikaiv; **PDBTitle:** pikromycin thioesterase adduct with reduced triketide2 affinity label
17	d2h7xa1	Alignment		41.8	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
18	c3g7sA_	Alignment		40.8	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**long-chain-fatty-acid--coa ligase (fadd-1); **PDBTitle:** crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
19	d2b61a1	Alignment		40.4	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
20	c3hd7A_	Alignment		37.8	18	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
21	c3n4dF_	Alignment	not modelled	36.4	16	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of cg10062 inactivated by(r)-oxirane-2-carboxylate
22	d1cr6a2	Alignment	not modelled	35.1	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
23	c1zhvA_	Alignment	not modelled	33.7	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu0741; **PDBTitle:** x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8.
24	c2xuaH_	Alignment	not modelled	33.2	0	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**3-oxoadipate enol-lactonase; **PDBTitle:** crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
25	d1otfa_	Alignment	not modelled	33.0	14	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
26	d1zhva2	Alignment	not modelled	32.8	19	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Atu0741-like
27	c3bf7B_	Alignment	not modelled	32.5	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**esterase ybff; **PDBTitle:** 1.1 resolution structure of ybff, a new esterase from2 escherichia coli: a unique substrate-binding crevice3 generated by domain arrangement
28	c3etcB_	Alignment	not modelled	31.7	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**amp-binding protein; **PDBTitle:** 2.1 a structure of acyl-adenylate synthetase from

						methanosarcina2 acetivorans containing a link between lys256 and cys298
29	d1gksa_	Alignment	not modelled	30.1	10	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
30	d1r3da_	Alignment	not modelled	29.8	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical protein VC1974
31	c2yzbA_	Alignment	not modelled	29.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uricase; **PDBTitle:** crystal structure of uricase from arthrobacter globiformis2 in complex with uric acid (substrate)
32	c3lcrA_	Alignment	not modelled	28.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tautomycetin biosynthetic pks; **PDBTitle:** thioesterase from tautomycetin biosynthhetic pathway
33	c2aj1A_	Alignment	not modelled	28.5	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable cadmium-transporting atpase; **PDBTitle:** solution structure of apocada
34	d1ic8a2	Alignment	not modelled	28.2	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
35	c3l80A_	Alignment	not modelled	27.0	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1393c; **PDBTitle:** crystal structure of smu.1393c from streptococcus mutans ua159
36	c3gacD_	Alignment	not modelled	26.8	13	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** structure of mif with hpp
37	c1y37A_	Alignment	not modelled	26.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fluoroacetate dehalogenase; **PDBTitle:** structure of fluoroacetate dehalogenase from burkholderia sp. fa1
38	d1qlwa_	Alignment	not modelled	26.2	39	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**A novel bacterial esterase
39	d1bjpa_	Alignment	not modelled	26.1	25	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
40	c2kncB_	Alignment	not modelled	25.9	30	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
41	c3fwtA_	Alignment	not modelled	25.6	15	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** crystal structure of leishmania major mif2
42	d1pg4a_	Alignment	not modelled	25.6	17	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
43	c3ol4B_	Alignment	not modelled	25.5	23	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
44	d1mo2a_	Alignment	not modelled	25.3	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
45	c1mo2A_	Alignment	not modelled	25.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**erythronolide synthase, modules 5 and 6; **PDBTitle:** thioesterase domain from 6-deoxyerythronolide synthase2 (debs te), ph 8.5
46	c3ry0A_	Alignment	not modelled	25.1	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tautomerase; **PDBTitle:** crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
47	c3fobA_	Alignment	not modelled	25.1	0	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bromoperoxidase; **PDBTitle:** crystal structure of bromoperoxidase from bacillus anthracis
48	d2rhwa1	Alignment	not modelled	24.7	0	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
49	c1j2gC_	Alignment	not modelled	24.6	10	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**uricase; **PDBTitle:** crystal structure of urate oxidase from bacillus sp. tb-90 co-2 crystallized with 8-azaxanthine
50	c2xmzA_	Alignment	not modelled	24.6	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydrolase, alpha/beta hydrolase fold family; **PDBTitle:** structure of menh from s. aureus
51	c2vavL_	Alignment	not modelled	24.3	13	**PDB header:**transferase **Chain:** L: **PDB Molecule:**acetyl-coa--deacetylcephalosporin c **PDBTitle:** crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak)
52	d2hmfa2	Alignment	not modelled	23.0	8	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
53	c2xczA_	Alignment	not modelled	22.5	13	**PDB header:**immune system **Chain:** A: **PDB Molecule:**possible atls1-like light-inducible protein; **PDBTitle:** crystal structure of macrophage migration inhibitory factor2 homologue from prochlorococcus marinus
54	d1u1ia1	Alignment	not modelled	22.3	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains

54	d1u1fa1	Alignment	not modelled	22.5	12	**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
55	c2op8A_	Alignment	not modelled	21.8	33	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase ywhb; **PDBTitle:** crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
56	d1uaaa2	Alignment	not modelled	21.6	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
57	c2kt2A_	Alignment	not modelled	21.4	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
58	d1eh1a_	Alignment	not modelled	21.0	16	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
59	d2vata1	Alignment	not modelled	20.8	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
60	c1yy7A_	Alignment	not modelled	20.4	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stringent starvation protein a; **PDBTitle:** crystal structure of stringent starvation protein a (sspa),2 an rna polymerase-associated transcription factor
61	d1is1a_	Alignment	not modelled	20.3	11	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
62	c1cr6A_	Alignment	not modelled	20.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
63	c2ronA_	Alignment	not modelled	20.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**surfactin synthetase thioesterase subunit; **PDBTitle:** the external thioesterase of the surfactin-synthetase
64	d1dd5a_	Alignment	not modelled	20.0	5	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
65	c3mlcC_	Alignment	not modelled	20.0	13	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**fg41 malonate semialdehyde decarboxylase; **PDBTitle:** crystal structure of fg41msad inactivated by 3-chloropropiolate
66	c2kkhA_	Alignment	not modelled	19.8	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
67	d1w36b2	Alignment	not modelled	19.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
68	d1z3ea1	Alignment	not modelled	19.4	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
69	d1uk8a_	Alignment	not modelled	19.1	5	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
70	c2cjpA_	Alignment	not modelled	18.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** structure of potato (solanum tuberosum) epoxide hydrolase i2 (steh1)
71	d1ek8a_	Alignment	not modelled	18.7	13	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
72	c2f06B_	Alignment	not modelled	18.3	6	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
73	c3qyjB_	Alignment	not modelled	18.2	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alr0039 protein; **PDBTitle:** crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120.
74	c2rogA_	Alignment	not modelled	18.2	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
75	c3b64A_	Alignment	not modelled	18.2	14	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** macrophage migration inhibitory factor (mif) from2 /leishmania major
76	d1a8qa_	Alignment	not modelled	18.0	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
77	c3h3yF_	Alignment	not modelled	17.8	12	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**baseplate structural protein gp6; **PDBTitle:** fitting of the gp6 crystal structure into 3d cryo-em2 reconstruction of bacteriophage t4 star-shaped baseplate
78	c3a2nF_	Alignment	not modelled	17.4	11	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** crystal structure of dbja (wild type type ii p21)
79	c2g29A_	Alignment	not modelled	17.3	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrate transport protein nrta; **PDBTitle:** crystal structure of the periplasmic nitrate-binding2 protein nrta from synechocystis pcc 6803
						Fold: Ferredoxin-like

80	d1osda_	Alignment	not modelled	17.2	17	**Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
81	c2k2pA_	Alignment	not modelled	17.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1203; **PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
82	c3l78A_	Alignment	not modelled	17.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein spx; **PDBTitle:** the crystal structure of smu.1142c from streptococcus mutans ua159
83	d1gyxa_	Alignment	not modelled	17.0	16	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
84	c3mb2G_	Alignment	not modelled	17.0	25	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**4-oxalocrotonate tautomerase family enzyme - alpha subunit; **PDBTitle:** kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
85	d1sb6a_	Alignment	not modelled	16.6	10	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
86	d2aw0a_	Alignment	not modelled	16.4	33	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
87	c2dahA_	Alignment	not modelled	16.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquilin-3; **PDBTitle:** solution structure of the c-terminal uba domain in the2 human ubiquilin 3
88	c2l3mA_	Alignment	not modelled	16.2	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
89	d2qifa1	Alignment	not modelled	16.1	16	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
90	d2pl5a1	Alignment	not modelled	16.1	6	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
91	d2ddha2	Alignment	not modelled	16.0	23	**Fold:**Bromodomain-like **Superfamily:**Acyl-CoA dehydrogenase C-terminal domain-like **Family:**acyl-CoA oxidase C-terminal domains
92	d1q8la_	Alignment	not modelled	16.0	20	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
93	c1yg0A_	Alignment	not modelled	16.0	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
94	d1n6za_	Alignment	not modelled	15.8	15	**Fold:**Hypothetical protein Yml108w **Superfamily:**Hypothetical protein Yml108w **Family:**Hypothetical protein Yml108w
95	c1sr9A_	Alignment	not modelled	15.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of leua from mycobacterium tuberculosis
96	c2l9bA_	Alignment	not modelled	15.6	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mrna 3'-end-processing protein rna15; **PDBTitle:** heterodimer between rna14p monkeytail domain and rna15p hinge domain2 of the yeast cf ia complex
97	c3fsgC_	Alignment	not modelled	15.6	5	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha/beta superfamily hydrolase; **PDBTitle:** crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
98	d1pyya1	Alignment	not modelled	15.4	13	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
99	d2i52a1	Alignment	not modelled	15.4	17	**Fold:**MK0786-like **Superfamily:**MK0786-like **Family:**MK0786-like