Phyre2

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Description	P0A8C1
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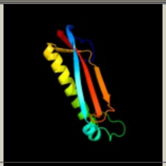
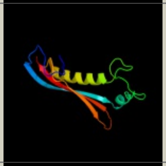
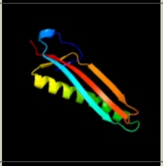
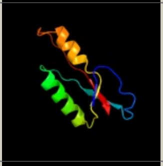
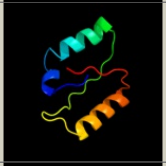
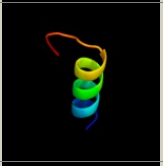
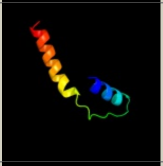
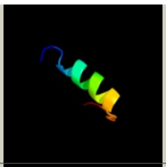
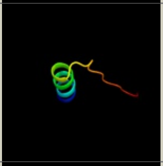
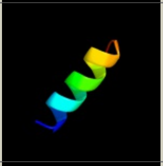
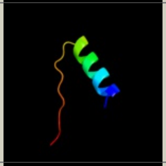
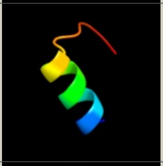
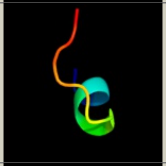
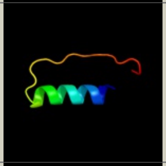
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1y2iC_	Alignment		100.0	97	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein s0862; **PDBTitle:** crystal structure of mcsg target apc27401 from shigella2 flexneri
2	d1y2ia_	Alignment		100.0	97	**Fold:**Dodecin subunit-like **Superfamily:**YbjQ-like **Family:**YbjQ-like
3	d1vr4a1	Alignment		100.0	55	**Fold:**Dodecin subunit-like **Superfamily:**YbjQ-like **Family:**YbjQ-like
4	c3qkbB_	Alignment		99.9	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
5	c2y1bA_	Alignment		97.7	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative outer membrane protein, signal; **PDBTitle:** crystal structure of the e. coli outer membrane lipoprotein2 rcsf
6	c2jz7A_	Alignment		97.7	22	**PDB header:**selenium-binding protein **Chain:** A: **PDB Molecule:**selenium binding protein; **PDBTitle:** solution nmr structure of selenium-binding protein from2 methanococcus vannielii
7	c3bfjK_	Alignment		23.9	12	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**1,3-propanediol oxidoreductase; **PDBTitle:** crystal structure analysis of 1,3-propanediol oxidoreductase
8	c1xuzA_	Alignment		18.0	33	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
9	c1vliA_	Alignment		16.8	39	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
10	c1zvaA_	Alignment		16.6	24	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** a structure-based mechanism of sars virus membrane fusion
11	c2cx8B_	Alignment		16.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyl transferase; **PDBTitle:** crystal structure of methyltransferase with ligand(sah)

12	d1vhka2	Alignment		15.2	24	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
13	d1gefa_	Alignment		14.5	17	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
14	d1vlia2	Alignment		13.8	39	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
15	d1hh1a_	Alignment		13.5	24	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
16	d1w96a2	Alignment		13.1	25	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
17	c2qjhH_	Alignment		12.8	46	**PDB header:**lyase **Chain:** H: **PDB Molecule:**putative aldolase mj0400; **PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
18	c1z85B_	Alignment		12.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein tm1380; **PDBTitle:** crystal structure of a predicted rna methyltransferase (tm1380) from2 thermotoga maritima msb8 at 2.12 a resolution
19	d2j5ya1	Alignment		12.0	40	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**GA module, an albumin-binding domain
20	d1to3a_	Alignment		11.9	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
21	c3gndC_	Alignment	not modelled	11.9	31	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
22	c3jzdA_	Alignment	not modelled	11.6	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of putative alcohol dehedrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution
23	c2wj0B_	Alignment	not modelled	11.6	32	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**archaeal hjc; **PDBTitle:** crystal structures of holliday junction resolvases from2 archaeoglobus fulgidus bound to dna substrate
24	d1v6za2	Alignment	not modelled	11.3	18	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
25	d2zdra2	Alignment	not modelled	10.8	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
26	c2v9dB_	Alignment	not modelled	10.5	47	**PDB header:**lyase **Chain:** B: **PDB Molecule:**yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
27	c3iv7B_	Alignment	not modelled	10.4	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alcohol dehydrogenase iv; **PDBTitle:** crystal structure of iron-containing alcohol dehydrogenase2 (np_602249.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.07 a resolution
28	d1a53a_	Alignment	not modelled	10.2	46	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes

29	c2rdcA_	Alignment	not modelled	10.2	26	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative lipid binding protein (gsu0061) from2 geobacter sulfurreducens pca at 1.80 a resolution
30	c3cmgA_	Alignment	not modelled	10.1	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
31	d2je8a5	Alignment	not modelled	10.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
32	c3d0cB_	Alignment	not modelled	9.8	53	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
33	c3ox4D_	Alignment	not modelled	9.5	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alcohol dehydrogenase 2; **PDBTitle:** structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
34	c2r94B_	Alignment	not modelled	9.4	40	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxy-(6-phospho-)gluconate aldolase; **PDBTitle:** crystal structure of kd(p)ga from t.tenax
35	d1ulza2	Alignment	not modelled	9.3	31	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
36	c3mtjA_	Alignment	not modelled	9.2	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
37	d1uf3a_	Alignment	not modelled	9.0	37	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
38	c2egwB_	Alignment	not modelled	8.6	23	**PDB header:**rna methyltransferase **Chain:** B: **PDB Molecule:**upf0088 protein aq_165; **PDBTitle:** crystal structure of rrna methyltransferase with sah ligand
39	c3sz8D_	Alignment	not modelled	8.4	33	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 2; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
40	d1xxxa1	Alignment	not modelled	8.3	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
41	c2nuxB_	Alignment	not modelled	7.8	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate **PDBTitle:** 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
42	d1rrma_	Alignment	not modelled	7.6	24	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
43	d1vlja_	Alignment	not modelled	7.5	24	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
44	c3jrkG_	Alignment	not modelled	7.4	33	**PDB header:**lyase **Chain:** G: **PDB Molecule:**tagatose 1,6-diphosphate aldolase 2; **PDBTitle:** a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
45	c2rfgB_	Alignment	not modelled	7.4	40	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
46	c2vc6A_	Alignment	not modelled	7.4	33	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
47	d1o5ka_	Alignment	not modelled	7.4	37	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
48	d1hl2a_	Alignment	not modelled	7.3	40	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
49	d2j9ga2	Alignment	not modelled	7.2	31	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
50	c2hdlA_	Alignment	not modelled	7.2	24	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**small inducible cytokine b14; **PDBTitle:** solution structure of brak/cxcl14
51	c3stgA_	Alignment	not modelled	7.2	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
52	d1p5dx4	Alignment	not modelled	7.1	21	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
53	c3dz1A_	Alignment	not modelled	7.1	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
54	c2ehhE_	Alignment	not modelled	7.0	26	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase;

		Alignment	not modelled			**PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
55	c3e96B_	Alignment	not modelled	6.8	58	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
56	d2noca1	Alignment	not modelled	6.8	31	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
57	d2a6na1	Alignment	not modelled	6.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
58	d1o2da_	Alignment	not modelled	6.7	24	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
59	c3hl0B_	Alignment	not modelled	6.7	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**maleylacetate reductase; **PDBTitle:** crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
60	c1vhkA_	Alignment	not modelled	6.7	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yqeu; **PDBTitle:** crystal structure of an hypothetical protein
61	c3lerA_	Alignment	not modelled	6.4	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
62	d1geqa_	Alignment	not modelled	6.4	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
63	c2r8wB_	Alignment	not modelled	6.3	37	**PDB header:**lyase **Chain:** B: **PDB Molecule:**agr_c_1641p; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
64	c3lciA_	Alignment	not modelled	6.2	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
65	c3g0sA_	Alignment	not modelled	6.1	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
66	d1nxza2	Alignment	not modelled	6.1	14	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
67	d1ejxb_	Alignment	not modelled	6.0	57	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
68	c3fkkA_	Alignment	not modelled	6.0	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
69	c3fluD_	Alignment	not modelled	6.0	26	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
70	c3cprB_	Alignment	not modelled	5.8	32	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
71	d2g7oa1	Alignment	not modelled	5.8	21	**Fold:**TraM-like **Superfamily:**TraM-like **Family:**TraM-like
72	c3b4uB_	Alignment	not modelled	5.7	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
73	d1w3ia_	Alignment	not modelled	5.7	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
74	c3gjxD_	Alignment	not modelled	5.6	22	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**exportin-1; **PDBTitle:** crystal structure of the nuclear export complex crm1-2 snurportin1-rangtp
75	c3n2xB_	Alignment	not modelled	5.6	37	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uncharacterized protein yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
76	c3pueA_	Alignment	not modelled	5.5	42	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
77	c2yxgD_	Alignment	not modelled	5.4	42	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
78	c2hmcA_	Alignment	not modelled	5.4	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
79	c3bi8A_	Alignment	not modelled	5.4	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
80	c3na8A_	Alignment	not modelled	5.3	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate

						synthetase from2 pseudomonas aeruginosa
81	d1x51a1	Alignment	not modelled	5.3	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
82	c2kxhB_	Alignment	not modelled	5.2	29	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**peptide of far upstream element-binding protein 1; **PDBTitle:** solution structure of the first two rrm domains of fir in the complex2 with fbp nbox peptide
83	d1tvga_	Alignment	not modelled	5.0	25	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**APC10-like