Phyre2

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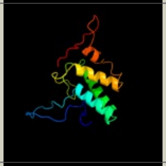
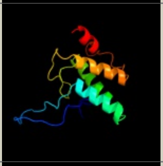
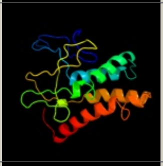
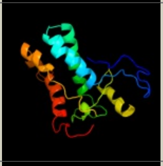
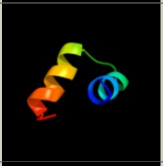
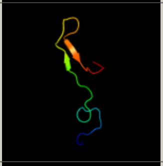
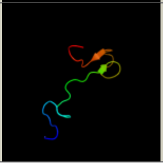
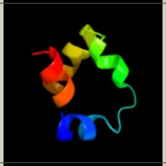
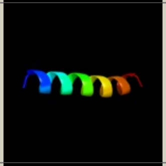
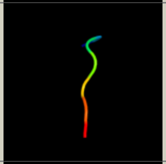
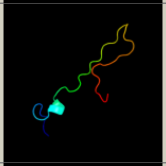
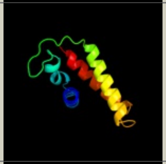
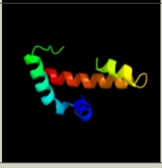
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ulva1	Alignment		97.3	25	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Bacterial glucoamylase C-terminal domain-like
2	d1lf6a1	Alignment		97.3	19	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Bacterial glucoamylase C-terminal domain-like
3	d2fbaa1	Alignment		95.4	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glucoamylase
4	c1lf6A_	Alignment		94.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucoamylase; **PDBTitle:** crystal structure of bacterial glucoamylase
5	d1gaia_	Alignment		94.1	19	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glucoamylase
6	c2vn4A_	Alignment		93.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucoamylase; **PDBTitle:** glycoside hydrolase family 15 glucoamylase from hypocrea2 jecorina
7	c1ug9A_	Alignment		62.8	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucodextranase; **PDBTitle:** crystal structure of glucodextranase from arthrobacter globiformis i42
8	c2jnhA_	Alignment		37.3	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of the uba domain from cbl-b
9	c2ov2O_	Alignment		36.5	34	**PDB header:**protein binding/transferase **Chain:** O: **PDB Molecule:**serine/threonine-protein kinase pak 4; **PDBTitle:** the crystal structure of the human rac3 in complex with the crib2 domain of human p21-activated kinase 4 (pak4)
10	c2ae3A_	Alignment		33.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutaryl 7-aminocephalosporanic acid acylase; **PDBTitle:** glutaryl 7-aminocephalosporanic acid acylase: mutational study of2 activation mechanism
11	c2odbB_	Alignment		32.0	34	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak 6; **PDBTitle:** the crystal structure of human cdc42 in complex with the crib domain2 of human p21-activated kinase 6 (pak6)

12	c2lioA_	Alignment		31.8	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of bfr322 from bacteroides fragilis, northeast2 structural genomics consortium target bfr322
13	d2ixna1	Alignment		29.4	13	**Fold:**PTPA-like **Superfamily:**PTPA-like **Family:**PTPA-like
14	d2g7oa1	Alignment		29.3	36	**Fold:**TraM-like **Superfamily:**TraM-like **Family:**TraM-like
15	d2pp6a1	Alignment		28.8	71	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**gpFII-like
16	c1e0aB_	Alignment		28.5	31	**PDB header:**signalling protein **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** cdc42 complexed with the gtpase binding domain of p212 activated kinase
17	c2do6A_	Alignment		25.8	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of rsgi ruh-065, a uba domain from human2 cdna
18	c2d9sA_	Alignment		25.4	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cbl e3 ubiquitin protein ligase; **PDBTitle:** solution structure of rsgi ruh-049, a uba domain from mouse2 cdna
19	d2d5xb1	Alignment		25.3	14	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
20	d1oj6a_	Alignment		24.0	12	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
21	d1wmub_	Alignment	not modelled	23.0	17	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
22	c3k3wA_	Alignment	not modelled	22.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**penicillin g acylase; **PDBTitle:** thermostable penicillin g acylase from alcaligence faecalis2 in orthorhombic form
23	d1fhjb_	Alignment	not modelled	22.3	16	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
24	d1cg5b_	Alignment	not modelled	22.2	10	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
25	d1qpwb_	Alignment	not modelled	21.9	19	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
26	c2z07A_	Alignment	not modelled	21.8	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0978; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 thermus thermophilus hb8
27	c3bomC_	Alignment	not modelled	20.2	13	**PDB header:**oxygen storage/transport **Chain:** C: **PDB Molecule:**hemoglobin subunit alpha-4; **PDBTitle:** crystal structure of trout hemoglobin at 1.35 angstrom2 resolution
28	d2dn3b1	Alignment	not modelled	20.2	16	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins

29	d1a4fb_	Alignment	not modelled	19.3	16	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
30	c1ceeB_	Alignment	not modelled	18.7	13	**PDB header:**structural protein regulation **Chain:** B: **PDB Molecule:**wiskott-aldrich syndrome protein wasp; **PDBTitle:** solution structure of cdc42 in complex with the gtpase2 binding domain of wasp
31	c2cqtA_	Alignment	not modelled	18.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cellobiose phosphorylase; **PDBTitle:** crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
32	d2eppa1	Alignment	not modelled	18.0	67	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
33	d1shrb_	Alignment	not modelled	17.1	18	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
34	d3bj1b1	Alignment	not modelled	16.6	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
35	c2zs1D_	Alignment	not modelled	16.4	14	**PDB header:**oxygen storage, oxygen transport **Chain:** D: **PDB Molecule:**extracellular giant hemoglobin major globin subunit b1; **PDBTitle:** structural basis for the heterotropic and homotropic interactions of2 invertebrate giant hemoglobin
36	d2ixma1	Alignment	not modelled	16.3	14	**Fold:**PTPA-like **Superfamily:**PTPA-like **Family:**PTPA-like
37	c1oqzB_	Alignment	not modelled	15.7	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glutaryl acylase; **PDBTitle:** crystal structures of glutaryl 7-aminocephalosporanic acid acylase:2 insight into autoproteolytic activation
38	d2aa1b1	Alignment	not modelled	15.5	10	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
39	c1cp9A_	Alignment	not modelled	15.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**penicillin amidohydrolase; **PDBTitle:** crystal structure of penicillin g acylase from the bro12 mutant strain of providencia rettgeri
40	c1k3rA_	Alignment	not modelled	15.2	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein mt0001; **PDBTitle:** crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
41	d2qssb1	Alignment	not modelled	14.9	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
42	d1u9da_	Alignment	not modelled	14.6	33	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**VC0714-like
43	d1fqva1	Alignment	not modelled	14.5	88	**Fold:**F-box domain **Superfamily:**F-box domain **Family:**F-box domain
44	c3s1jC_	Alignment	not modelled	14.5	13	**PDB header:**oxygen transport, oxygen storage **Chain:** C: **PDB Molecule:**hemoglobin-like flavoprotein; **PDBTitle:** crystal structure of acetate-bound hell's gate globin i
45	c2g62A_	Alignment	not modelled	13.8	14	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**protein phosphatase 2a, regulatory subunit b' (pr 53); **PDBTitle:** crystal structure of human ptpa
46	d1hbga_	Alignment	not modelled	13.5	14	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
47	c2v5jB_	Alignment	not modelled	13.2	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; **PDBTitle:** apo class ii aldolase hpch
48	d1h5wa_	Alignment	not modelled	13.2	21	**Fold:**Upper collar protein gp10 (connector protein) **Superfamily:**Upper collar protein gp10 (connector protein) **Family:**Upper collar protein gp10 (connector protein)
49	d1dxea_	Alignment	not modelled	12.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
50	d1i3da_	Alignment	not modelled	12.8	16	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
51	d3dtoa1	Alignment	not modelled	12.3	17	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
52	c1yhuX_	Alignment	not modelled	12.3	12	**PDB header:**oxygen storage/transport **Chain:** X: **PDB Molecule:**hemoglobin b2 chain; **PDBTitle:** crystal structure of riftia pachyptila c1 hemoglobin reveals novel2 assembly of 24 subunits.
53	c1f3mB_	Alignment	not modelled	12.2	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** crystal structure of human serine/threonine kinase pak1
54	d1hdsa_	Alignment	not modelled	12.1	12	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
55	c3eu8D_	Alignment	not modelled	12.1	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative glucoamylase; **PDBTitle:** crystal structure of putative glucoamylase (yp_210071.1)

						from2 bacteroides fragilis nctc 9343 at 2.12 a resolution
56	d2ixoa1	Alignment	not modelled	11.9	9	**Fold:**PTPA-like **Superfamily:**PTPA-like **Family:**PTPA-like
57	c2wybA_	Alignment	not modelled	11.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-homoserine lactone acylase pvdq subunit **PDBTitle:** the quorum quenching n-acyl homoserine lactone acylase pvdq2 with a covalently bound dodecanoic acid
58	d1gph11	Alignment	not modelled	11.7	25	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
59	c2gl7C_	Alignment	not modelled	11.3	33	**PDB header:**transcription **Chain:** C: **PDB Molecule:**b-cell lymphoma 9 protein; **PDBTitle:** crystal structure of a beta-catenin/bcl9/tcf4 complex
60	d1hdsb_	Alignment	not modelled	11.2	11	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
61	c1cfgA_	Alignment	not modelled	11.0	67	**PDB header:**coagulation factor **Chain:** A: **PDB Molecule:**coagulation factor viii; **PDBTitle:** membrane-binding peptide from the c2 domain of factor viii2 forms an amphipathic structure as determined by nmr3 spectroscopy
62	d2d5xa1	Alignment	not modelled	10.9	14	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
63	d1spgb_	Alignment	not modelled	10.8	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
64	c2e67D_	Alignment	not modelled	10.3	21	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein tthb029; **PDBTitle:** crystal structure of the hypothetical protein tthb029 from thermus2 thermophilus hb8
65	d1jl6a_	Alignment	not modelled	10.1	13	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
66	d2bt6a1	Alignment	not modelled	10.1	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
67	c1ajnA_	Alignment	not modelled	9.8	13	**PDB header:**antibiotic resistance **Chain:** A: **PDB Molecule:**penicillin amidohydrolase; **PDBTitle:** penicillin acylase complexed with p-nitrophenylacetic acid
68	c1gph1_	Alignment	not modelled	9.6	25	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
69	d1izca_	Alignment	not modelled	9.6	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
70	c1izcA_	Alignment	not modelled	9.6	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**macrophomate synthase intermolecular diels-alderase; **PDBTitle:** crystal structure analysis of macrophomate synthase
71	d1ecfa1	Alignment	not modelled	9.4	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
72	d1a4fa_	Alignment	not modelled	9.4	16	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
73	d2dlqa3	Alignment	not modelled	9.4	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
74	c3on0D_	Alignment	not modelled	9.3	25	**PDB header:**dna binding protein/dna **Chain:** D: **PDB Molecule:**protein tram; **PDBTitle:** crystal structure of the ped208 tram-sbma complex
75	c3qz6A_	Alignment	not modelled	9.3	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hpch/hpai aldolase; **PDBTitle:** the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
76	d1qpwa_	Alignment	not modelled	9.2	14	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
77	d1spga_	Alignment	not modelled	9.2	10	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
78	c2pohA_	Alignment	not modelled	9.1	27	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**head completion protein; **PDBTitle:** structure of phage p22 tail needle gp26
79	c2i7gA_	Alignment	not modelled	8.7	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monooxygenase; **PDBTitle:** crystal structure of monooxygenase from agrobacterium tumefaciens
80	d1b0ba_	Alignment	not modelled	8.6	13	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
81	d2bl8a1	Alignment	not modelled	8.6	21	**Fold:**Bromodomain-like **Superfamily:**Bacteriocin immunity protein-like **Family:**EntA-Im

82	d1seda_	Alignment	not modelled	8.6	26	**Fold:**Hypothetical protein YhaI **Superfamily:**Hypothetical protein YhaI **Family:**Hypothetical protein YhaI
83	c3pt8B_	Alignment	not modelled	8.6	7	**PDB header:**oxygen transport **Chain:** B: **PDB Molecule:**hemoglobin iii; **PDBTitle:** structure of hbii-iii-cn from lucina pectinata at ph 5.0
84	d1k3ra2	Alignment	not modelled	8.5	20	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**Hypothetical protein MTH1 (MT0001), dimerisation domain
85	c1ijgE_	Alignment	not modelled	8.4	18	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**upper collar protein; **PDBTitle:** structure of the bacteriophage phi29 head-tail connector2 protein
86	c3bq4G_	Alignment	not modelled	8.4	18	**PDB header:**viral protein **Chain:** G: **PDB Molecule:**fiber; **PDBTitle:** crystal structure of ad35 fiber knob
87	c2vwtA_	Alignment	not modelled	8.3	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**yfau, 2-keto-3-deoxy sugar aldolase; **PDBTitle:** crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
88	c2d2mC_	Alignment	not modelled	7.9	17	**PDB header:**oxygen storage/transport **Chain:** C: **PDB Molecule:**giant hemoglobin, b2(c) globin chain; **PDBTitle:** structure of an extracellular giant hemoglobin of the2 gutless beard worm oligobrachia mashikoi
89	d5pnta_	Alignment	not modelled	7.8	6	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
90	d1luca_	Alignment	not modelled	7.7	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
91	d2h8fb1	Alignment	not modelled	7.7	16	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
92	c2cwdA_	Alignment	not modelled	7.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight phosphotyrosine protein phosphatase; **PDBTitle:** crystal structure of tt1001 protein from thermus thermophilus hb8
93	c2dafA_	Alignment	not modelled	7.6	67	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**flj35834 protein; **PDBTitle:** solution structure of the novel identified ubiquitin-like2 domain in the human hypothetical protein flj35834
94	c3h87D_	Alignment	not modelled	7.5	24	**PDB header:**toxin/antitoxin **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
95	d1v4wb_	Alignment	not modelled	7.4	11	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
96	c3if4C_	Alignment	not modelled	7.4	33	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**integron cassette protein hfx_cass5; **PDBTitle:** structure from the mobile metagenome of north west arm2 sewage outfall: integron cassette protein hfx_cass5
97	c2b81D_	Alignment	not modelled	7.2	40	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**luciferase-like monooxygenase; **PDBTitle:** crystal structure of the luciferase-like monooxygenase from bacillus2 cereus
98	d3d1ka1	Alignment	not modelled	7.2	20	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
99	c3huiA_	Alignment	not modelled	7.1	26	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** crystal structure of the mutant a105r of [2fe-2s] ferredoxin2 in the class i cyp199a2 system from rhodopseudomonas3 palustris