Phyre2

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Description	P46883
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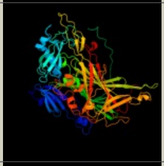
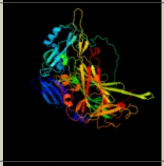
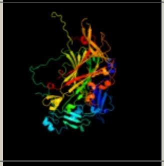
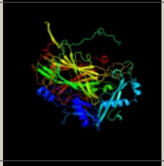
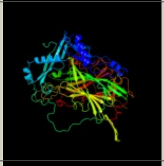
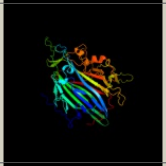
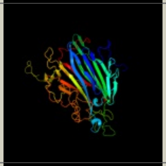
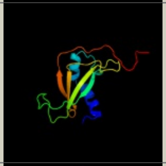
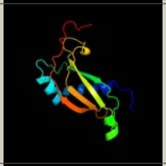
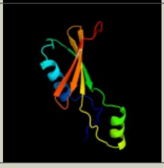
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1d6uB_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure of e. coli amine oxidase anaerobically reduced with2 beta-phenylethylamine
2	c1ksiA_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure of a eukaryotic (pea seedling) copper-containing2 amine oxidase at 2.2a resolution
3	c1ekmC_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure at 2.5 a resolution of zinc-substituted2 copper amine oxidase of hansenula polymorpha expressed in3 escherichia coli
4	c1ui7A_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phenylethylamine oxidase; **PDBTitle:** site-directed mutagenesis of his433 involved in binding of2 copper ion in arthrobacter globiformis amine oxidase
5	c3nbbC_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**peroxisomal primary amine oxidase; **PDBTitle:** crystal structure of mutant y305f expressed in e. coli in the copper2 amine oxidase from hansenula polymorpha
6	c3loyB_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure of a copper-containing benzylamine oxidase from2 hansenula polymorpha
7	c3higB_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**amiloride-sensitive amine oxidase; **PDBTitle:** crystal structure of human diamine oxidase in complex with the2 inhibitor berenil
8	c3pgbA_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of aspergillus nidulans amine oxidase
9	c1n9eA_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysyl oxidase; **PDBTitle:** crystal structure of pichia pastoris lysyl oxidase pplo
10	c1w7cA_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysyl oxidase; **PDBTitle:** pplo at 1.23 angstroms
11	c2pncB_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**copper amine oxidase, liver isozyme; **PDBTitle:** crystal structure of bovine plasma copper-containing amine oxidase in2 complex with clonidine

12	d1d6za1	Alignment		100.0	100	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
13	d1w6ga1	Alignment		100.0	31	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
14	d2oqea1	Alignment		100.0	29	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
15	d1w2za1	Alignment		100.0	32	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
16	d1w7ca1	Alignment		100.0	25	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
17	d1d6za3	Alignment		100.0	100	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
18	d1w6ga3	Alignment		100.0	29	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
19	d1w2za3	Alignment		100.0	20	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
20	d1d6za2	Alignment		99.9	100	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
21	d2oqea2	Alignment	not modelled	99.9	26	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
22	d2oqea3	Alignment	not modelled	99.9	23	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
23	d1w2za2	Alignment	not modelled	99.9	24	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
24	d1w6ga2	Alignment	not modelled	99.8	23	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
25	d1w7ca2	Alignment	not modelled	99.4	19	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
26	d1d6za4	Alignment	not modelled	98.7	100	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Copper amine oxidase, domain N **Family:**Copper amine oxidase, domain N
27	c3mlhA_	Alignment	not modelled	40.0	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** crystal structure of the 2009 h1n1 influenza virus hemagglutinin2 receptor-binding domain
28	d2viua_	Alignment	not modelled	38.5	24	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
29	d1kx5d_	Alignment	not modelled	36.4	24	**Fold:**Histone-fold **Superfamily:**Histone-fold

						Family: Nucleosome core histones
30	d1eqzb_	Alignment	not modelled	34.7	22	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
31	c3qqiB_	Alignment	not modelled	32.0	30	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hemagglutinin; **PDBTitle:** crystal structure of the ha1 receptor binding domain of h22 hemagglutinin
32	d1rvxa_	Alignment	not modelled	30.7	28	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
33	d1s32d_	Alignment	not modelled	30.0	24	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
34	c3imoC_	Alignment	not modelled	29.7	26	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**integron cassette protein; **PDBTitle:** structure from the mobile metagenome of vibrio cholerae.2 integron cassette protein vch_cass14
35	d1rv0h_	Alignment	not modelled	28.5	21	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
36	d1w7ca3	Alignment	not modelled	28.1	16	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
37	c1ha0A_	Alignment	not modelled	27.9	24	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (hemagglutinin precursor); **PDBTitle:** hemagglutinin precursor ha0
38	d2dira1	Alignment	not modelled	26.7	22	**Fold:**THUMP domain **Superfamily:**THUMP domain-like **Family:**Minimal THUMP
39	c1x9yD_	Alignment	not modelled	23.3	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cysteine proteinase; **PDBTitle:** the prostaphopain b structure
40	d1uwwa_	Alignment	not modelled	21.9	17	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 28 carbohydrate binding module, CBM28
41	d1mqma_	Alignment	not modelled	21.2	24	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
42	d1jsda_	Alignment	not modelled	21.0	23	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
43	d2cx1a2	Alignment	not modelled	20.3	20	**Fold:**Cystatin-like **Superfamily:**Pre-PUA domain **Family:**Hypothetical protein APE0525, N-terminal domain
44	c2jssA_	Alignment	not modelled	20.1	23	**PDB header:**chaperone/nuclear protein **Chain:** A: **PDB Molecule:**chimera of histone h2b.1 and histone h2a.z; **PDBTitle:** nmr structure of chaperone chz1 complexed with histone2 h2a.z-h2b
45	d1rd8a_	Alignment	not modelled	20.0	23	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
46	c2cfoA_	Alignment	not modelled	19.5	35	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** non-discriminating glutamyl-trna synthetase from2 thermosynechococcus elongatus in complex with glu
47	d2plga1	Alignment	not modelled	17.6	39	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Tll0839-like
48	c3al0C_	Alignment	not modelled	16.8	27	**PDB header:**ligase/rna **Chain:** C: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit c, glutamyl- **PDBTitle:** crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
49	d2visc_	Alignment	not modelled	16.0	23	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
50	d1nkqa_	Alignment	not modelled	16.0	40	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
51	d1jsma_	Alignment	not modelled	12.9	30	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
52	c2rfuA_	Alignment	not modelled	12.8	24	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**influenza b hemagglutinin (ha); **PDBTitle:** crystal structure of influenza b virus hemagglutinin in complex with2 lstc receptor analog
53	c3rurB_	Alignment	not modelled	12.8	19	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**iron-regulated surface determinant protein b; **PDBTitle:** staphylococcus aureus heme-bound selenomethionine-labeled isdb-n2
54	d1jp4a_	Alignment	not modelled	12.6	31	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
55	c1zxuA_	Alignment	not modelled	12.1	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**at5g01750 protein; **PDBTitle:** x-ray structure of protein from arabidopsis thaliana2 at5g01750

56	d2q4ma1	Alignment	not modelled	12.1	7	**Fold:**Tubby C-terminal domain-like **Superfamily:**Tubby C-terminal domain-like **Family:**At5g01750-like
57	d1pfsa_	Alignment	not modelled	10.2	50	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Phage ssDNA-binding proteins
58	c2ka6B_	Alignment	not modelled	9.8	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** nmr structure of the cbp-taz2/stat1-tad complex
59	d1r5ya_	Alignment	not modelled	9.6	4	**Fold:**TIM beta/alpha-barrel **Superfamily:**tRNA-guanine transglycosylase **Family:**tRNA-guanine transglycosylase
60	c3k1tA_	Alignment	not modelled	9.5	55	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase gsha; **PDBTitle:** crystal structure of putative gamma-glutamylcysteine synthetase2 (yp_546622.1) from methylobacillus flagellatus kt at 1.90 a3 resolution
61	c2ja2A_	Alignment	not modelled	9.4	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** mycobacterium tuberculosis glutamyl-trna synthetase
62	c3acgA_	Alignment	not modelled	9.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-1,4-endoglucanase; **PDBTitle:** crystal structure of carbohydrate-binding module family 282 from clostridium josui cel5a in complex with cellobiose
63	d2d9ra1	Alignment	not modelled	9.3	8	**Fold:**Double-split beta-barrel **Superfamily:**AF2212/PG0164-like **Family:**PG0164-like
64	d1xxxa1	Alignment	not modelled	9.2	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
65	c3bbnI_	Alignment	not modelled	9.2	26	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**ribosomal protein s9; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
66	d2vqei1	Alignment	not modelled	9.0	42	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
67	d2cs7a1	Alignment	not modelled	8.9	35	**Fold:**IL8-like **Superfamily:**PhtA domain-like **Family:**PhtA domain-like
68	d2ibxa1	Alignment	not modelled	8.8	29	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
69	c2xfyA_	Alignment	not modelled	8.8	52	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-amylase; **PDBTitle:** crystal structure of barley beta-amylase complexed with2 alpha-cyclodextrin
70	d1hcza1	Alignment	not modelled	8.7	22	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
71	c3cu4A_	Alignment	not modelled	8.6	16	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** omcf, outer membrance cytochrome f from geobacter2 sulfurreducens
72	d2o8ra4	Alignment	not modelled	8.6	7	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
73	c1flIA_	Alignment	not modelled	8.5	17	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tnf receptor associated factor 3; **PDBTitle:** molecular basis for cd40 signaling mediated by traf3
74	d1jjcb4	Alignment	not modelled	8.4	4	**Fold:**Ferredoxin-like **Superfamily:**Anticodon-binding domain of PheRS **Family:**Anticodon-binding domain of PheRS
75	d2dy1a4	Alignment	not modelled	8.4	26	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
76	c3gr0D_	Alignment	not modelled	8.2	14	**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)
77	c1zljE_	Alignment	not modelled	8.1	28	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
78	d1ejxb_	Alignment	not modelled	8.1	27	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
79	c2yxgD_	Alignment	not modelled	8.1	20	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
80	c1g59A_	Alignment	not modelled	8.1	45	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** glutamyl-trna synthetase complexed with trna(glu).
81	c3afhA_	Alignment	not modelled	8.0	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase 2; **PDBTitle:** crystal structure of thermotoga maritima nondiscriminating glutamyl-2 trna synthetase in complex with a glutamyl-amp analog
82	c3iz6I	Alignment	not modelled	7.8	42	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**40s ribosomal protein s16 (s9p);

						PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
83	c3sbrF_	Alignment	not modelled	7.6	8	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nitrous-oxide reductase; **PDBTitle:** pseudomonas stutzeri nitrous oxide reductase, p1 crystal form with2 substrate
84	c2xzml_	Alignment	not modelled	7.6	42	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**rps16e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
85	d2oo3a1	Alignment	not modelled	7.6	7	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**LPG1296-like
86	d2gy9i1	Alignment	not modelled	7.5	37	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
87	c3si9B_	Alignment	not modelled	7.5	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
88	c3luzA_	Alignment	not modelled	7.5	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**extragenic suppressor protein suhb; **PDBTitle:** crystal structure of extragenic suppressor protein suhb from2 bartonella henselae, via combined iodide sad molecular replacement
89	d1owxa_	Alignment	not modelled	7.5	17	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
90	c1y4hA_	Alignment	not modelled	7.4	12	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**cysteine protease; **PDBTitle:** wild type staphopain-staphostatin complex
91	c2ehhE_	Alignment	not modelled	7.4	20	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
92	c3pueA_	Alignment	not modelled	7.4	20	**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
93	d1a6ca1	Alignment	not modelled	7.3	29	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
94	c1kzzA_	Alignment	not modelled	7.3	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tnf receptor associated factor 3; **PDBTitle:** downstream regulator tank binds to the cd40 recognition2 site on traf3
95	c2vc6A_	Alignment	not modelled	7.3	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
96	c3fluD_	Alignment	not modelled	7.2	32	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
97	d1xi6a_	Alignment	not modelled	6.9	38	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
98	d1lbva_	Alignment	not modelled	6.9	38	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
99	d1w0pa2	Alignment	not modelled	6.9	12	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Vibrio cholerae sialidase, N-terminal and insertion domains