Phyre^2

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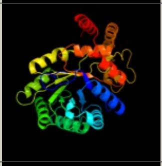
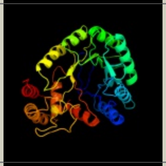
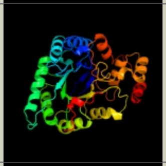
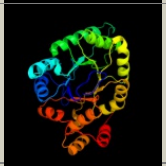
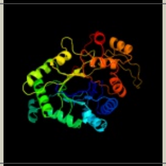
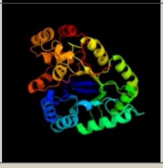
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3n6qF_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**yghz aldo-keto reductase; **PDBTitle:** crystal structure of yghz from e. coli
2	c3erpA_	Alignment		100.0	61	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of idp01002, a putative oxidoreductase from and essential2 gene of salmonella typhimurium
3	d1lqaa_	Alignment		100.0	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
4	d3eaua1	Alignment		100.0	35	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
5	c3lutA_	Alignment		100.0	35	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**voltage-gated potassium channel subunit beta-2; **PDBTitle:** a structural model for the full-length shaker potassium channel kv1.2
6	d1pyfa_	Alignment		100.0	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
7	d1pz1a_	Alignment		100.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
8	d1ur3m_	Alignment		100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
9	c3n2tA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the glycerol dehydrogenase akr11b4 from gluconobacter2 oxydans
10	d1gvea_	Alignment		100.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
11	c2bp1C_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aflatoxin b1 aldehyde reductase member 2; **PDBTitle:** structure of the aflatoxin aldehyde reductase in complex2 with nadph

12	c1ynpA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** aldo-keto reductase akr11c1 from bacillus halodurans (apo form)
13	d1q5ma_	Alignment		100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
14	d1j96a_	Alignment		100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
15	c3h7uA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c9
16	d1afsa_	Alignment		100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
17	c3up8B_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative 2,5-diketo-d-gluconic acid reductase b; **PDBTitle:** crystal structure of a putative 2,5-diketo-d-gluconic acid reductase b
18	d1us0a_	Alignment		100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
19	d1qwka_	Alignment		100.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
20	d1mi3a_	Alignment		100.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
21	d1frba_	Alignment	not modelled	100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
22	d1hqta_	Alignment	not modelled	100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
23	c3f7jB_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**yvgn protein; **PDBTitle:** b.subtilis yvgn
24	d1s1pa_	Alignment	not modelled	100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
25	c3h7rA_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c8
26	c3buvB_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxo-5-beta-steroid 4-dehydrogenase; **PDBTitle:** crystal structure of human delta(4)-3-ketosteroid 5-beta-reductase in2 complex with nadp and hepes. resolution: 1.35 a.
27	d1ah4a_	Alignment	not modelled	100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
28	c1zgdB_	Alignment	not modelled	100.0	23	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**chalcone reductase; **PDBTitle:** chalcone reductase complexed with nadp+ at 1.7 angstrom2 resolution
29	c2wztA	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase;

						PDBTitle: crystal structure of a mycobacterium aldo-keto reductase in2 its apo and liganded form
30	d1c9wa_	Alignment	not modelled	100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
31	d1vp5a_	Alignment	not modelled	100.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
32	d2alra_	Alignment	not modelled	100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
33	d1hw6a_	Alignment	not modelled	100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
34	c3o0kB_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldo/keto reductase; **PDBTitle:** crystal structure of aldo/keto reductase from brucella melitensis
35	d1mzra_	Alignment	not modelled	100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
36	c2bgsA_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldose reductase; **PDBTitle:** holo aldose reductase from barley
37	c3b3dA_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative morphine dehydrogenase; **PDBTitle:** b.subtilis ytbe
38	c1vbjB_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**prostaglandin f synthase; **PDBTitle:** the crystal structure of prostaglandin f synthase from2 trypanosoma brucei
39	c3krbB_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldose reductase; **PDBTitle:** structure of aldose reductase from giardia lamblia at 1.75a resolution
40	c3ln3A_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of putative reductase (np_038806.2) from2 mus musculus at 1.18 a resolution
41	d3bofa2	Alignment	not modelled	73.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
42	c3dx5A_	Alignment	not modelled	60.8	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uncharacterized protein asbf; **PDBTitle:** crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
43	c3bdkB_	Alignment	not modelled	54.4	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-mannonate dehydratase; **PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
44	c3bolB_	Alignment	not modelled	52.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5-methyltetrahydrofolate s-homocysteine **PDBTitle:** cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
45	c3sb1B_	Alignment	not modelled	38.0	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hydrogenase expression protein; **PDBTitle:** hydrogenase expression protein huph from thiobacillus denitrificans2 atcc 25259
46	c3oqbF_	Alignment	not modelled	37.0	14	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
47	c3hf3A_	Alignment	not modelled	35.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
48	d1szna2	Alignment	not modelled	33.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
49	c3a5vA_	Alignment	not modelled	33.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of alpha-galactosidase i from mortierella vinacea
50	c3g8rA_	Alignment	not modelled	32.5	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**probable spore coat polysaccharide biosynthesis protein e; **PDBTitle:** crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
51	c2ph5A_	Alignment	not modelled	31.6	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homospermidine synthase; **PDBTitle:** crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
52	c3ou8B_	Alignment	not modelled	31.1	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosine deaminase; **PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
53	d1ajza_	Alignment	not modelled	30.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
54	c1uasA_	Alignment	not modelled	29.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of rice alpha-galactosidase
						PDB header:hydrolase

55	c3rysA_	Alignment	not modelled	29.8	16	**Chain:** A: **PDB Molecule:**adenosine deaminase 1; **PDBTitle:** the crystal structure of adenine deaminase (aaur1117) from2 arthrobacter aurescens
56	d1jpma1	Alignment	not modelled	26.2	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
57	d1gqna_	Alignment	not modelled	25.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
58	d1h8ba_	Alignment	not modelled	23.1	21	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
59	d2nlya1	Alignment	not modelled	22.2	15	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**Divergent polysaccharide deacetylase
60	d1vp8a_	Alignment	not modelled	19.5	14	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
61	d1bxba_	Alignment	not modelled	19.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
62	c1m0tB_	Alignment	not modelled	19.3	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**glutathione synthetase; **PDBTitle:** yeast glutathione synthase
63	d1tz9a_	Alignment	not modelled	19.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**UxuA-like
64	d1qt1a_	Alignment	not modelled	18.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
65	d1zy9a2	Alignment	not modelled	18.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**YicI catalytic domain-like
66	c2kzhA_	Alignment	not modelled	17.1	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**tryptophan biosynthesis protein trpcf; **PDBTitle:** three-dimensional structure of a truncated phosphoribosylanthranilate2 isomerase (residues 255-384) from escherichia coli
67	c3d0cB_	Alignment	not modelled	17.1	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
68	d1kkoa1	Alignment	not modelled	17.1	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
69	d2hv2a1	Alignment	not modelled	17.0	21	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**EF1021 C-terminal domain-like
70	c3ksmA_	Alignment	not modelled	16.8	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc-type sugar transport system, periplasmic component; **PDBTitle:** crystal structure of abc-type sugar transport system, periplasmic2 component from hahella chejuensis
71	c2yr1B_	Alignment	not modelled	16.3	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of 3-dehydroquinate dehydratase from geobacillus2 kaustophilus hta426
72	d2i00a1	Alignment	not modelled	16.2	14	**Fold:**SCP-like **Superfamily:**SCP-like **Family:**EF1021 C-terminal domain-like
73	c2nvaH_	Alignment	not modelled	16.0	15	**PDB header:**lyase **Chain:** H: **PDB Molecule:**arginine decarboxylase, a207r protein; **PDBTitle:** the x-ray crystal structure of the paramecium bursaria2 chlorella virus arginine decarboxylase bound to agmatine
74	c2gjxE_	Alignment	not modelled	16.0	17	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**beta-hexosaminidase alpha chain; **PDBTitle:** crystallographic structure of human beta-hexosaminidase a
75	c3dnfB_	Alignment	not modelled	15.7	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
76	d1uwka_	Alignment	not modelled	15.5	16	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
77	c2ekcA_	Alignment	not modelled	14.5	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
78	c3sdoB_	Alignment	not modelled	14.4	4	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase; **PDBTitle:** structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
79	d2gjxa1	Alignment	not modelled	14.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
80	d1vyra_	Alignment	not modelled	14.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
						Fold: Hyaluronidase domain-like

81	d2ijqa1	Alignment	not modelled	14.1	10	**Superfamily:**TTHA0068-like **Family:**TTHA0068-like
82	c2wjeA_	Alignment	not modelled	13.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase cpsb; **PDBTitle:** crystal structure of the tyrosine phosphatase cps4b from2 steptococcus pneumoniae tigr4.
83	c2vwtA_	Alignment	not modelled	13.5	14	**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
84	c2ksnA_	Alignment	not modelled	13.5	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin domain-containing protein 2; **PDBTitle:** solution structure of the n-terminal domain of dc-ubp/ubtd2
85	d1ub3a_	Alignment	not modelled	13.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
86	c2fknC_	Alignment	not modelled	12.6	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**urocanate hydratase; **PDBTitle:** crystal structure of urocanase from bacillus subtilis
87	c1t0oA_	Alignment	not modelled	11.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** the structure of alpha-galactosidase from trichoderma reesei complexed2 with beta-d-galactose
88	c2v5jB_	Alignment	not modelled	11.8	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; **PDBTitle:** apo class ii aldolase hpch
89	c1vliA_	Alignment	not modelled	11.5	20	**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
90	c1xeaD_	Alignment	not modelled	11.3	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
91	c3pueA_	Alignment	not modelled	11.1	10	**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
92	c3lmyA_	Alignment	not modelled	10.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-hexosaminidase subunit beta; **PDBTitle:** the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
93	d2zd1b1	Alignment	not modelled	10.8	21	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Reverse transcriptase
94	d2ajta2	Alignment	not modelled	10.7	9	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**AraA N-terminal and middle domain-like
95	d1x87a_	Alignment	not modelled	10.2	16	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
96	c3l2iB_	Alignment	not modelled	10.2	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.85 angstrom crystal structure of the 3-dehydroquinate dehydratase2 (arod) from salmonella typhimurium lt2.
97	c2jwlB_	Alignment	not modelled	10.1	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**protein tolr; **PDBTitle:** solution structure of periplasmic domain of tolr from h.2 influenzae with saxs data
98	c3gh7A_	Alignment	not modelled	10.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-hexosaminidase; **PDBTitle:** crystal structure of beta-hexosaminidase from paenibacillus2 sp. ts12 in complex with galnac
99	d1nowa1	Alignment	not modelled	10.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain