Phyre2

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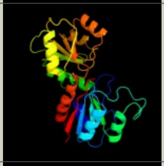
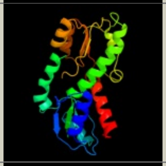
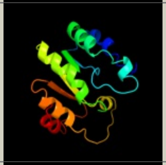
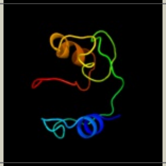
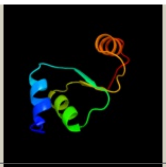
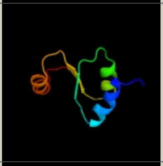
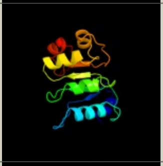
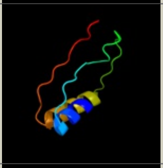
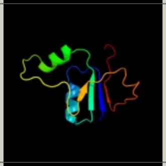
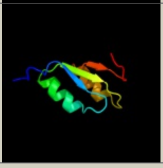
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nmpa_	Alignment		100.0	100	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
2	c2nydB_	Alignment		100.0	23	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**upf0135 protein sa1388; **PDBTitle:** crystal structure of staphylococcus aureus hypothetical protein sa1388
3	c2gx8B_	Alignment		100.0	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**nif3-related protein; **PDBTitle:** the crystal stucture of bacillus cereus protein related to nif3
4	d2gx8a1	Alignment		100.0	25	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
5	c2yybA_	Alignment		100.0	37	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1606; **PDBTitle:** crystal structure of ttha1606 from thermus thermophilus hb8
6	d2fywa1	Alignment		100.0	24	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
7	c3rxyA_	Alignment		99.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nif3 protein; **PDBTitle:** crystal structure of nif3 superfamily protein from sphaerobacter2 thermophilus
8	c2yx6C_	Alignment		85.0	12	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein ph0822; **PDBTitle:** crystal structure of ph0822
9	c3qc3B_	Alignment		83.4	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-ribulose-5-phosphate-3-epimerase; **PDBTitle:** crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
10	c2am1A_	Alignment		79.3	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramoylalanine-d-glutamyl-lysine-d-alanyl-d- **PDBTitle:** sp protein ligand 1
11	d1w0ma_	Alignment		77.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)

12	d1t3va_	Alignment		75.8	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
13	d1eo1a_	Alignment		75.4	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
14	c3e96B_	Alignment		70.8	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
15	c2wfbA_	Alignment		67.3	20	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein orp; **PDBTitle:** high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
16	c3d0cB_	Alignment		66.0	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
17	c3aamA_	Alignment		65.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease iv; **PDBTitle:** crystal structure of endonuclease iv from thermus thermophilus hb8
18	c3c6kC_	Alignment		64.4	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**spermine synthase; **PDBTitle:** crystal structure of human spermine synthase in complex2 with spermidine and 5-methylthioadenosine
19	c3ct7E_	Alignment		64.1	17	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**d-allulose-6-phosphate 3-epimerase; **PDBTitle:** crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
20	d1p3da1	Alignment		63.9	17	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
21	c3jr2D_	Alignment	not modelled	61.3	14	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**hexulose-6-phosphate synthase sgbh; **PDBTitle:** x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961
22	d1afsa_	Alignment	not modelled	59.8	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
23	c2yw3E_	Alignment	not modelled	59.3	16	**PDB header:**lyase **Chain:** E: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- **PDBTitle:** crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
24	d1u83a_	Alignment	not modelled	58.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
25	c1u83A_	Alignment	not modelled	58.1	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphosulfolactate synthase; **PDBTitle:** psl synthase from bacillus subtilis
26	d1us0a_	Alignment	not modelled	57.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
27	d1xp3a1	Alignment	not modelled	55.8	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Endonuclease IV
28	d1e7wa_	Alignment	not modelled	55.5	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases

29	d1rdua_	Alignment	not modelled	52.5	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
30	d2flia1	Alignment	not modelled	52.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
31	c3o26A_	Alignment	not modelled	51.5	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**salutaridine reductase; **PDBTitle:** the structure of salutaridine reductase from papaver somniferum.
32	c3p19A_	Alignment	not modelled	51.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative blue fluorescent protein; **PDBTitle:** improved nadph-dependent blue fluorescent protein
33	d1p90a_	Alignment	not modelled	50.5	6	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**Nitrogenase accessory factor
34	d3clsc1	Alignment	not modelled	47.9	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
35	c2re2A_	Alignment	not modelled	47.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized protein ta1041; **PDBTitle:** crystal structure of a putative iron-molybdenum cofactor (femo-co)2 dinitrogenase (ta1041m) from thermoplasma acidophilum dsm 1728 at3 1.30 a resolution
36	d1p33a_	Alignment	not modelled	47.1	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
37	d1h1ya_	Alignment	not modelled	46.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
38	c3pdiB_	Alignment	not modelled	46.2	17	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nifn; **PDBTitle:** precursor bound nifen
39	d1j6ua1	Alignment	not modelled	46.1	14	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
40	c2foiB_	Alignment	not modelled	44.6	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** synthesis, biological activity, and x-ray crystal structural analysis2 of diaryl ether inhibitors of malarial enoyl acp reductase.
41	c2nq8B_	Alignment	not modelled	44.6	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** malarial enoyl acyl acp reductase bound with inh-nad adduct
42	c2wtzC_	Alignment	not modelled	44.6	14	**PDB header:**ligase **Chain:** C: **PDB Molecule:**udp-n-acetylmuramoyl-l-alanyl-d-glutamate- **PDBTitle:** mure ligase of mycobacterium tuberculosis
43	c3ppiA_	Alignment	not modelled	43.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase type-2; **PDBTitle:** crystal structure of 3-hydroxyacyl-coa dehydrogenase type-2 from2 mycobacterium avium
44	d2pv7a2	Alignment	not modelled	42.7	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
45	d1uh5a_	Alignment	not modelled	41.9	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
46	d1km4a_	Alignment	not modelled	41.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
47	d1rpxa_	Alignment	not modelled	40.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
48	c1zcjA_	Alignment	not modelled	40.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxisomal bifunctional enzyme; **PDBTitle:** crystal structure of 3-hydroxyacyl-coa dehydrogenase
49	c3lf2B_	Alignment	not modelled	40.3	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short chain oxidoreductase q9hya2; **PDBTitle:** nadph bound structure of the short chain oxidoreductase q9hya2 from2 pseudomonas aeruginosa pao1 containing an atypical catalytic center
50	d1o13a_	Alignment	not modelled	39.6	7	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
51	c3inpA_	Alignment	not modelled	39.5	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-ribulose-phosphate 3-epimerase; **PDBTitle:** 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
52	c3t4xA_	Alignment	not modelled	39.0	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family; **PDBTitle:** short chain dehydrogenase/reductase family oxidoreductase from2 bacillus anthracis str. ames ancestor
53	d1gega_	Alignment	not modelled	38.8	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
						Fold:NAD(P)-binding Rossmann-fold domains

54	d1yxma1	Alignment	not modelled	38.7	33	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
55	c3l77A_	Alignment	not modelled	38.6	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain alcohol dehydrogenase; **PDBTitle:** x-ray structure alcohol dehydrogenase from archaeon thermococcus2 sibiricus complexed with 5-hydroxy-nadp
56	c3dhnA_	Alignment	not modelled	38.2	17	**PDB header:**isomerase, lyase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
57	c3noeA_	Alignment	not modelled	38.1	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
58	c2ehhE_	Alignment	not modelled	37.8	14	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
59	d2hmva1	Alignment	not modelled	37.7	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
60	d1nu0a_	Alignment	not modelled	36.3	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
61	d1fjha_	Alignment	not modelled	36.3	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
62	d1dvja_	Alignment	not modelled	36.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
63	c2ntnB_	Alignment	not modelled	35.3	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of maba-c60v/g139a/s144l
64	c3s55F_	Alignment	not modelled	34.9	41	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of a putative short-chain dehydrogenase/reductase2 from mycobacterium abscessus bound to nad
65	d2gv8a1	Alignment	not modelled	34.2	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
66	d1uaya_	Alignment	not modelled	34.1	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
67	c3bmrA_	Alignment	not modelled	33.7	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pteridine reductase; **PDBTitle:** structure of pteridine reductase 1 (ptr1) from trypanosoma2 brucei in ternary complex with cofactor (nadp+) and3 inhibitor (compound ax6)
68	c3un1D_	Alignment	not modelled	33.5	25	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**probable oxidoreductase; **PDBTitle:** crystal structure of an oxidoreductase from sinorhizobium meliloti2 1021
69	d1vhxa_	Alignment	not modelled	33.3	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
70	c2x58B_	Alignment	not modelled	33.2	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxisomal bifunctional enzyme; **PDBTitle:** the crystal structure of mfe1 liganded with coa
71	c2vdcI_	Alignment	not modelled	32.9	12	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**glutamate synthase [nadph] small chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
72	d2gdza1	Alignment	not modelled	32.8	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
73	c3gk3D_	Alignment	not modelled	32.5	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**acetoacetyl-coa reductase; **PDBTitle:** crystal structure of acetoacetyl-coa reductase from2 burkholderia pseudomallei 1710b
74	c3g0sA_	Alignment	not modelled	32.5	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
75	c3tfoD_	Alignment	not modelled	31.9	26	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative 3-oxoacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of a putative 3-oxoacyl-(acyl-carrier-protein)2 reductase from sinorhizobium meliloti
76	c3dz1A_	Alignment	not modelled	31.7	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
77	c2p91A_	Alignment	not modelled	31.5	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadh]; **PDBTitle:** crystal structure of enoyl-[acyl-carrier-protein] reductase (nadh)2 from aquifex aeolicus vf5
78	c2nm0B_	Alignment	not modelled	31.5	36	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable 3-oxacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of sco1815: a beta-ketoacyl-acyl carrier

						protein2 reductase from streptomyces coelicolor a3(2)
79	d1xq1a_	Alignment	not modelled	31.5	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
80	c3k6jA_	Alignment	not modelled	31.2	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein f01g10.3, confirmed by transcript evidence; **PDBTitle:** crystal structure of the dehydrogenase part of multifuctional enzyme 12 from c.elegans
81	d2d1ya1	Alignment	not modelled	30.8	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
82	c2pv7B_	Alignment	not modelled	30.6	17	**PDB header:**isomerase, oxidoreductase **Chain:** B: **PDB Molecule:**t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) **PDBTitle:** crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
83	d1xg5a_	Alignment	not modelled	30.2	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
84	c2qhxB_	Alignment	not modelled	30.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pteridine reductase 1; **PDBTitle:** structure of pteridine reductase from leishmania major2 complexed with a ligand
85	c3i1jB_	Alignment	not modelled	29.9	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase, short chain **PDBTitle:** structure of a putative short chain dehydrogenase from2 pseudomonas syringae
86	d1f6ya_	Alignment	not modelled	29.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
87	c2vt2A_	Alignment	not modelled	29.1	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** structure and functional properties of the bacillus2 subtilis transcriptional repressor rex
88	c3rihB_	Alignment	not modelled	28.7	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short chain dehydrogenase or reductase; **PDBTitle:** crystal structure of a putative short chain dehydrogenase or reductase2 from mycobacterium abscessus
89	d1ah4a_	Alignment	not modelled	28.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
90	c3f5sA_	Alignment	not modelled	28.5	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of putatitve short chain dehydrogenase from shigella2 flexneri 2a str. 301
91	c3n2xB_	Alignment	not modelled	28.4	18	**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
92	c3uxyC_	Alignment	not modelled	28.1	30	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** the crystal structure of short chain dehydrogenase from rhodobacter2 sphaeroides
93	c3n0vD_	Alignment	not modelled	28.1	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
94	d2h7ma1	Alignment	not modelled	28.1	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
95	d1zk4a1	Alignment	not modelled	28.0	41	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
96	c1zmoF_	Alignment	not modelled	28.0	15	**PDB header:**lyase **Chain:** F: **PDB Molecule:**halohydrin dehalogenase; **PDBTitle:** apo structure of haloalcohol dehalogenase hhea of2 arthrobacter sp. ad2
97	d2bela_	Alignment	not modelled	27.8	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
98	d1vqta1	Alignment	not modelled	27.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
99	d1s1pa_	Alignment	not modelled	27.3	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
100	c3louB_	Alignment	not modelled	27.2	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
101	c3sc4A_	Alignment	not modelled	27.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short chain dehydrogenase (a0qtm2 homolog); **PDBTitle:** crystal structure of a short chain dehydrogenase (a0qtm2 homolog)2 mycobacterium thermoresistibile
102	c3qivA_	Alignment	not modelled	26.8	41	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain dehydrogenase or 3-oxoacyl-[acyl-carrier- **PDBTitle:** crystal structure of a putative short-chain dehydrogenase or 3-2 oxoacyl-[acyl-carrier-protein] reductase from

						mycobacterium3 paratuberculosis atcc baa-968 / k-10
103	c2ydyA_	Alignment	not modelled	26.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine adenosyltransferase 2 subunit beta; **PDBTitle:** crystal structure of human s-adenosylmethionine synthetase2 2, beta subunit in orthorhombic crystal form
104	d1vjda_	Alignment	not modelled	26.7	15	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
105	c2dknA_	Alignment	not modelled	26.4	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-alpha-hydroxysteroid dehydrogenase; **PDBTitle:** crystal structure of the 3-alpha-hydroxysteroid dehydrogenase from2 pseudomonas sp. b-0831 complexed with nadh
106	c2w1vA_	Alignment	not modelled	26.1	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nitrilase homolog 2; **PDBTitle:** crystal structure of mouse nitrilase-2 at 1.4a resolution
107	d1xcfa_	Alignment	not modelled	26.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
108	c3ezlA_	Alignment	not modelled	26.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acetoacetyl-coa reductase; **PDBTitle:** crystal structure of acetyacetyl-coa reductase from2 burkholderia pseudomallei 1710b
109	c1yb1B_	Alignment	not modelled	25.8	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**17-beta-hydroxysteroid dehydrogenase type xi; **PDBTitle:** crystal structure of human 17-beta-hydroxysteroid dehydrogenase type2 xi
110	d1xu9a_	Alignment	not modelled	25.8	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
111	c2x7vA_	Alignment	not modelled	25.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable endonuclease 4; **PDBTitle:** crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
112	c3tfxB_	Alignment	not modelled	25.4	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**orotidine 5'-phosphate decarboxylase; **PDBTitle:** crystal structure of orotidine 5'-phosphate decarboxylase from2 lactobacillus acidophilus
113	d1o94c_	Alignment	not modelled	25.3	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
114	d1gtea3	Alignment	not modelled	25.3	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**C-terminal domain of adrenodoxin reductase-like
115	c3rd5A_	Alignment	not modelled	25.1	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mypaa.01249.c; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium paratuberculosis
116	c3q2oB_	Alignment	not modelled	24.8	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
117	d1rd5a_	Alignment	not modelled	24.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
118	d1x1ta1	Alignment	not modelled	24.6	37	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
119	c3uvzB_	Alignment	not modelled	24.4	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
120	c2hjwA_	Alignment	not modelled	24.3	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** crystal structure of the bc domain of acc2