Phyre^2

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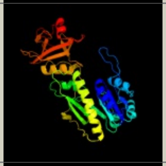
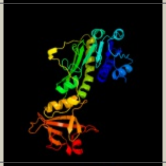
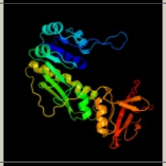
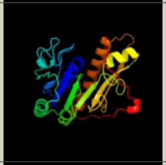
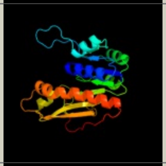
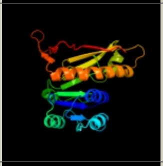
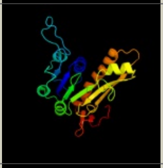
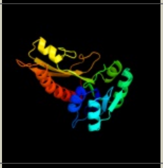
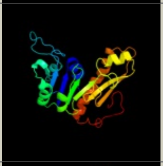
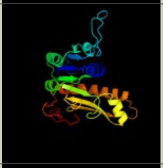
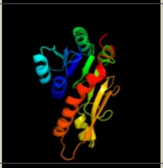
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1fmtA_	Alignment		100.0	100	**PDB header:**formyltransferase **Chain:** A: **PDB Molecule:**methionyl-trna fmet formyltransferase; **PDBTitle:** methionyl-trnafmet formyltransferase from escherichia coli
2	c3rfoA_	Alignment		100.0	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** crystal structure of methyionyl-trna formyltransferase from bacillus2 anthracis
3	c3q0iA_	Alignment		100.0	62	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** methionyl-trna formyltransferase from vibrio cholerae
4	c3tqqA_	Alignment		100.0	51	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** structure of the methionyl-trna formyltransferase (fmt) from coxiella2 burnetii
5	c1z7eC_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of full length arna
6	c1yrwA_	Alignment		100.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of e.coli arna transformylase domain
7	c1s3iA_	Alignment		100.0	33	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**10-formyltetrahydrofolate dehydrogenase; **PDBTitle:** crystal structure of the n terminal hydrolase domain of 10-2 formyltetrahydrofolate dehydrogenase
8	d1fmta2	Alignment		100.0	100	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
9	d2blna2	Alignment		100.0	30	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
10	d2bw0a2	Alignment		100.0	36	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
11	d1s3ia2	Alignment		100.0	39	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase

12	c1zghA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** methionyl-trna formyltransferase from clostridium thermocellum
13	c3kcqA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
14	d1jkxa_	Alignment		100.0	20	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
15	c3dcjA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable 5'-phosphoribosylglycinamide **PDBTitle:** crystal structure of glycinamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3 6,7,8-tetrahydrofolic acid derivative
16	c2ywrA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of gar transformylase from aquifex2 aeolicus
17	c3tqrA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
18	c3p9xB_	Alignment		100.0	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
19	d1meoa_	Alignment		100.0	23	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
20	c3n0vD_	Alignment		100.0	20	**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
21	c3o1lB_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
22	c3louB_	Alignment	not modelled	100.0	18	**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
23	c3obiC_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
24	c3nrbD_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
25	d1zgha2	Alignment	not modelled	100.0	19	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
26	d1fmta1	Alignment	not modelled	100.0	100	**Fold:**FMT C-terminal domain-like **Superfamily:**FMT C-terminal domain-like **Family:**Post formyltransferase domain
27	d2blna1	Alignment	not modelled	99.9	28	**Fold:**FMT C-terminal domain-like **Superfamily:**FMT C-terminal domain-like **Family:**Post formyltransferase domain
						Fold:FMT C-terminal domain-like

28	d1s3ia1	Alignment	not modelled	99.9	25	**Superfamily:**FMT C-terminal domain-like **Family:**Post formyltransferase domain
29	d2bw0a1	Alignment	not modelled	99.9	20	**Fold:**FMT C-terminal domain-like **Superfamily:**FMT C-terminal domain-like **Family:**Post formyltransferase domain
30	c3rbvA_	Alignment	not modelled	96.5	26	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sugar 3-ketoreductase; **PDBTitle:** crystal structure of kijd10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
31	c3ceaA_	Alignment	not modelled	96.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**myo-inositol 2-dehydrogenase; **PDBTitle:** crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
32	c3db2C_	Alignment	not modelled	96.4	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative nadph-dependent oxidoreductase; **PDBTitle:** crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
33	d1vlva2	Alignment	not modelled	96.4	23	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
34	c3euwB_	Alignment	not modelled	96.3	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase; **PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
35	c3e18A_	Alignment	not modelled	96.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of nad-binding protein from listeria innocua
36	c3q2kB_	Alignment	not modelled	95.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of the wlba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaca
37	c3v5nA_	Alignment	not modelled	95.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** the crystal structure of oxidoreductase from sinorhizobium meliloti
38	c3e9mC_	Alignment	not modelled	95.9	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
39	c2p2gD_	Alignment	not modelled	95.9	25	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
40	c3ec7C_	Alignment	not modelled	95.7	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dehydrogenase; **PDBTitle:** crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
41	c3nt5B_	Alignment	not modelled	95.7	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; **PDBTitle:** crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
42	c1zh8B_	Alignment	not modelled	95.6	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
43	d1lssa_	Alignment	not modelled	95.6	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
44	c3ezyB_	Alignment	not modelled	95.5	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima
45	c2ho3D_	Alignment	not modelled	95.3	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
46	d1pvva2	Alignment	not modelled	95.3	17	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
47	d1a9xa4	Alignment	not modelled	95.3	18	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
48	d1zh8a1	Alignment	not modelled	95.2	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
49	c3m2tA_	Alignment	not modelled	95.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from chromobacterium2 violaceum
50	c3ic5A_	Alignment	not modelled	95.2	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
51	c3eywA_	Alignment	not modelled	95.1	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
52	c2pzlB_	Alignment	not modelled	95.1	17	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme2 wbmg in complex with nad and udp
						PDB header:transferase

53	c1ml4A_	Alignment	not modelled	95.1	25	**Chain:** A: **PDB Molecule:**aspartate transcarbamoylase; **PDBTitle:** the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
54	d1ekxa2	Alignment	not modelled	95.0	19	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
55	c2p5uC_	Alignment	not modelled	95.0	21	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** crystal structure of thermus thermophilus hb8 udp-glucose 4-2 epimerase complex with nad
56	d1kewa_	Alignment	not modelled	95.0	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
57	d1qh8b_	Alignment	not modelled	94.9	17	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
58	d1ml4a2	Alignment	not modelled	94.9	25	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
59	c2o48X_	Alignment	not modelled	94.9	26	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**dimeric dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of mammalian dimeric dihydrodiol dehydrogenase
60	d2nu7a1	Alignment	not modelled	94.8	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
61	c2pk3B_	Alignment	not modelled	94.8	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gdp-6-deoxy-d-lyxo-4-hexulose reductase; **PDBTitle:** crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
62	d1zgha1	Alignment	not modelled	94.8	15	**Fold:**FMT C-terminal domain-like **Superfamily:**FMT C-terminal domain-like **Family:**Post formyltransferase domain
63	d1ek6a_	Alignment	not modelled	94.7	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
64	c3l4bG_	Alignment	not modelled	94.7	18	**PDB header:**transport protein **Chain:** G: **PDB Molecule:**trka k+ channel protien tm1088b; **PDBTitle:** crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
65	c1ofgF_	Alignment	not modelled	94.6	14	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** glucose-fructose oxidoreductase
66	c1h6dL_	Alignment	not modelled	94.5	16	**PDB header:**protein translocation **Chain:** L: **PDB Molecule:**precursor form of glucose-fructose **PDBTitle:** oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
67	c3dtyA_	Alignment	not modelled	94.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from pseudomonas2 syringae
68	c3moiA_	Alignment	not modelled	94.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
69	d1miob_	Alignment	not modelled	94.5	14	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
70	c1vm6B_	Alignment	not modelled	94.5	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** crystal structure of dihydrodipicolinate reductase (tm1520) from2 thermotoga maritima at 2.27 a resolution
71	d1m1nb_	Alignment	not modelled	94.3	21	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
72	c3gfgB_	Alignment	not modelled	94.2	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized oxidoreductase yvaa; **PDBTitle:** structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
73	d1tuga1	Alignment	not modelled	94.1	23	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
74	c1vlvA_	Alignment	not modelled	94.1	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
75	c2hunB_	Alignment	not modelled	94.0	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**336aa long hypothetical dtdp-glucose 4,6-dehydratase; **PDBTitle:** crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3
76	c3grfA_	Alignment	not modelled	94.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** x-ray structure of ornithine transcarbamoylase from giardia2 lamblia
77	c2q4eB_	Alignment	not modelled	94.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable oxidoreductase at4g09670; **PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670
78	d2nvwa1	Alignment	not modelled	93.9	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain

79	c3uuwB_	Alignment	not modelled	93.8	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase with nad(p)-binding rossmann-fold **PDBTitle:** 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
80	c1a1sA_	Alignment	not modelled	93.8	21	**PDB header:**transcarbamylase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine carbamoyltransferase from pyrococcus furiosus
81	d1pg5a2	Alignment	not modelled	93.7	21	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
82	c2ph5A_	Alignment	not modelled	93.6	14	**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
83	c2nvwB_	Alignment	not modelled	93.5	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal sctucture of transcriptional regulator gal80p from2 kluyveromymes lactis
84	d1o6ca_	Alignment	not modelled	93.5	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
85	c2glxD_	Alignment	not modelled	93.5	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1,5-anhydro-d-fructose reductase; **PDBTitle:** crystal structure analysis of bacterial 1,5-af reductase
86	c3fd8A_	Alignment	not modelled	93.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
87	c1drwA_	Alignment	not modelled	93.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** escherichia coli dhpr/nhdh complex
88	c3sc6F_	Alignment	not modelled	93.4	22	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**dtdp-4-dehydrorhamnose reductase; **PDBTitle:** 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
89	c2ixaA_	Alignment	not modelled	93.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
90	c1kjjA_	Alignment	not modelled	93.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
91	c1pg5A_	Alignment	not modelled	93.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** crystal structure of the unligated (t-state) aspartate2 transcarbamoylase from the extremely thermophilic archaeon sulfolobus3 acidocaldarius
92	c3tpfF_	Alignment	not modelled	93.2	16	**PDB header:**transferase **Chain:** F: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of anabolic ornithine carbamoyltransferase from2 campylobacter jejuni subsp. jejuni nctc 11168
93	c3kuxA_	Alignment	not modelled	93.2	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the ypo2259 putative oxidoreductase from yersinia pestis
94	c3evnA_	Alignment	not modelled	93.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
95	c2ys6A_	Alignment	not modelled	93.1	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide synthetase; **PDBTitle:** crystal structure of gar synthetase from geobacillus kaustophilus
96	c3dapB_	Alignment	not modelled	93.1	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**diaminopimelic acid dehydrogenase; **PDBTitle:** c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
97	d1ru8a_	Alignment	not modelled	92.9	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
98	d1ydwa1	Alignment	not modelled	92.9	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
99	c3ot5D_	Alignment	not modelled	92.9	10	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
100	c2axqA_	Alignment	not modelled	92.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
101	c2qx7A_	Alignment	not modelled	92.8	16	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**eugenol synthase 1; **PDBTitle:** structure of eugenol synthase from ocimum basilicum
102	d1bxka_	Alignment	not modelled	92.8	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
103	c3enkB_	Alignment	not modelled	92.7	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-glucose 4-epimerase;

103	c3enkB_	Alignment	not modelled	92.7	15	**PDBTitle:** 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei
104	c2xdqA_	Alignment	not modelled	92.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
105	c1i36A_	Alignment	not modelled	92.4	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein mth1747; **PDBTitle:** structure of conserved protein mth1747 of unknown function2 reveals structural similarity with 3-hydroxyacid3 dehydrogenases
106	c2rgwD_	Alignment	not modelled	92.4	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
107	c2dzdB_	Alignment	not modelled	92.4	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase
108	d1f06a1	Alignment	not modelled	92.4	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
109	c3nklA_	Alignment	not modelled	92.2	10	**PDB header:**oxidoreductase/lyase **Chain:** A: **PDB Molecule:**udp-d-quinovosamine 4-dehydrogenase; **PDBTitle:** crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri
110	c3gd5D_	Alignment	not modelled	92.2	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
111	d1vl0a_	Alignment	not modelled	92.2	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
112	c1xeaD_	Alignment	not modelled	92.1	21	**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
113	d1qh8a_	Alignment	not modelled	92.1	11	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
114	c2yy7B_	Alignment	not modelled	92.1	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-threonine dehydrogenase; **PDBTitle:** crystal structure of thermolabile l-threonine dehydrogenase from2 flavobacterium frigidimaris kuc-1
115	d1udca_	Alignment	not modelled	92.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
116	c2q1uA_	Alignment	not modelled	92.1	16	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme wbmf in2 complex with nad+ and udp
117	c2ggsB_	Alignment	not modelled	92.1	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**273aa long hypothetical dtdp-4-dehydrorhamnose **PDBTitle:** crystal structure of hypothetical dtdp-4-dehydrorhamnose2 reductase from sulfolobus tokodaii
118	c1fvoB_	Alignment	not modelled	91.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine transcarbamylase; **PDBTitle:** crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
119	d1gsoa2	Alignment	not modelled	91.9	18	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
120	c2p2sA_	Alignment	not modelled	91.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution