Phyre2

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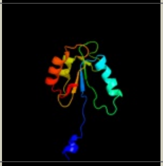
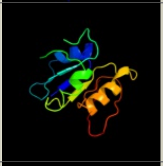
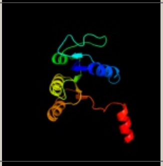
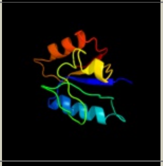
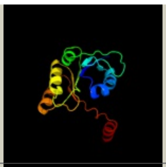
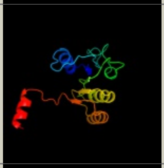
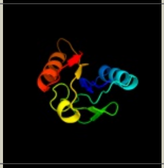
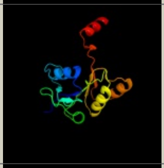
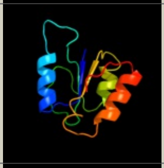
Description	P71241
Date	Thu Jan 5 12:12:36 GMT 2012
Unique Job ID	8f82f087a9b3ebf2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nklA_	Alignment		99.3	19	**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
2	c3ketA_	Alignment		98.2	9	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
3	c2dt5A_	Alignment		98.1	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**at-rich dna-binding protein; **PDBTitle:** crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
4	c2vt2A_	Alignment		97.8	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** structure and functional properties of the bacillus2 subtilis transcriptional repressor rex
5	d2dt5a2	Alignment		97.5	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Transcriptional repressor Rex, C-terminal domain
6	c3evnA_	Alignment		97.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
7	d1euca1	Alignment		96.9	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
8	c2yv1A_	Alignment		96.8	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**succinyl-coa ligase [adp-forming] subunit alpha; **PDBTitle:** crystal structure of succinyl-coa synthetase alpha chain from2 methanocaldococcus jannaschii dsm 2661
9	c2o48X_	Alignment		96.8	13	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**dimeric dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of mammalian dimeric dihydrodiol dehydrogenase
10	c3db2C_	Alignment		96.8	14	**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
11	d1oi7a1	Alignment		96.6	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain

12	c3kuxA_	Alignment		96.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the ypo2259 putative oxidoreductase from yersinia pestis
13	c3ec7C_	Alignment		96.6	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dehydrogenase; **PDBTitle:** crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
14	d2nu7a1	Alignment		96.5	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
15	c3m2tA_	Alignment		96.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from chromobacterium2 violaceum
16	c1lc3A_	Alignment		96.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**biliverdin reductase a; **PDBTitle:** crystal structure of a biliverdin reductase enzyme-cofactor2 complex
17	d2py6a1	Alignment		96.5	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**FkbM-like
18	c3euwB_	Alignment		96.4	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase; **PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
19	c2glxD_	Alignment		96.4	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1,5-anhydro-d-fructose reductase; **PDBTitle:** crystal structure analysis of bacterial 1,5-af reductase
20	c3e18A_	Alignment		96.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of nad-binding protein from listeria innocua
21	c3e82A_	Alignment	not modelled	96.3	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
22	c2fpgA_	Alignment	not modelled	96.3	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**succinyl-coa ligase [gdp-forming] alpha-chain, **PDBTitle:** crystal structure of pig gtp-specific succinyl-coa2 synthetase in complex with gdp
23	c2q4eB_	Alignment	not modelled	96.2	14	**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
24	c2ho3D_	Alignment	not modelled	96.1	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
25	c3q2kB_	Alignment	not modelled	96.1	10	**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
26	d1kjqa2	Alignment	not modelled	96.1	19	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
27	c3e9mC_	Alignment	not modelled	96.1	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
28	c3ezyB_	Alignment	not modelled	96.1	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima

29	c2nu8D_	Alignment	not modelled	96.1	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**succinyl-coa ligase [adp-forming] subunit alpha; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase
30	c1zh8B_	Alignment	not modelled	96.1	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
31	c3fd8A_	Alignment	not modelled	96.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
32	c3rbvA_	Alignment	not modelled	96.0	15	**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
33	d1ydwa1	Alignment	not modelled	96.0	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
34	c3ceaA_	Alignment	not modelled	96.0	10	**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
35	d1zh8a1	Alignment	not modelled	95.9	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
36	d2nvwa1	Alignment	not modelled	95.9	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
37	c3fhlC_	Alignment	not modelled	95.9	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
38	d1a9xa4	Alignment	not modelled	95.8	20	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
39	c3dapB_	Alignment	not modelled	95.8	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**diaminopimelic acid dehydrogenase; **PDBTitle:** c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
40	c2ixaA_	Alignment	not modelled	95.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
41	c3f4lF_	Alignment	not modelled	95.7	12	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative oxidoreductase yhhx; **PDBTitle:** crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647
42	c3nt5B_	Alignment	not modelled	95.7	15	**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
43	c3c1aB_	Alignment	not modelled	95.7	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution
44	c3uuwB_	Alignment	not modelled	95.7	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.
45	c3gfgB_	Alignment	not modelled	95.6	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized oxidoreductase yvaa; **PDBTitle:** structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
46	c2ip4A_	Alignment	not modelled	95.6	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
47	d1f06a1	Alignment	not modelled	95.5	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
48	d1a9xa3	Alignment	not modelled	95.5	11	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
49	c2yv2A_	Alignment	not modelled	95.4	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**succinyl-coa synthetase alpha chain; **PDBTitle:** crystal structure of succinyl-coa synthetase alpha chain from2 aeropyrum pernix k1
50	c3bioB_	Alignment	not modelled	95.4	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase (gfo/idh/moca family member) from2 porphyromonas gingivalis w83
51	c1h6dL_	Alignment	not modelled	95.3	14	**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
52	c1ofgF_	Alignment	not modelled	95.3	14	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** glucose-fructose oxidoreductase
53	c3moiA_	Alignment	not modelled	95.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
						Fold:NAD(P)-binding Rossmann-fold domains

54	d2d59a1	Alignment	not modelled	95.2	13	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
55	c1e5lA_	Alignment	not modelled	95.2	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
56	d1y81a1	Alignment	not modelled	95.2	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
57	c3do5A_	Alignment	not modelled	95.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution
58	c1oi7A_	Alignment	not modelled	95.0	15	**PDB header:**synthetase **Chain:** A: **PDB Molecule:**succinyl-coa synthetase alpha chain; **PDBTitle:** the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus
59	c2qk4A_	Alignment	not modelled	95.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trifunctional purine biosynthetic protein adenosine-3; **PDBTitle:** human glycinamide ribonucleotide synthetase
60	c1drwA_	Alignment	not modelled	95.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** escherichia coli dhpr/nhdh complex
61	c2p2sA_	Alignment	not modelled	94.9	13	**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
62	d1ryda1	Alignment	not modelled	94.8	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
63	c2nvwB_	Alignment	not modelled	94.8	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal sctucture of transcriptional regulator gal80p from2 kluyveromyes lactis
64	c2dc1A_	Alignment	not modelled	94.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-aspartate dehydrogenase; **PDBTitle:** crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
65	c3v5nA_	Alignment	not modelled	94.7	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** the crystal structure of oxidoreductase from sinorhizobium meliloti
66	d1lc0a1	Alignment	not modelled	94.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
67	c1evjC_	Alignment	not modelled	94.4	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
68	c3a14B_	Alignment	not modelled	94.4	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of dxr from thermotoga maritima, in complex with2 nadph
69	c2dzdB_	Alignment	not modelled	94.3	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase
70	c3btuD_	Alignment	not modelled	94.3	16	**PDB header:**transcription **Chain:** D: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
71	c3dtyA_	Alignment	not modelled	94.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from pseudomonas2 syringae
72	d1gsoa2	Alignment	not modelled	94.3	15	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
73	c2vpqA_	Alignment	not modelled	94.2	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
74	d1yl7a1	Alignment	not modelled	94.2	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
75	c3ouzA_	Alignment	not modelled	94.1	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
76	c3ic5A_	Alignment	not modelled	94.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
77	c2z2vA_	Alignment	not modelled	94.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1688; **PDBTitle:** crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
78	c3lp8A_	Alignment	not modelled	94.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine-glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
						PDB header:transferase **Chain:** B: **PDB Molecule:**433aa long hypothetical

79	c2dwcB_	Alignment	not modelled	93.9	14	phosphoribosylglycinamide formyl **PDBTitle:** crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
80	c3ndjA_	Alignment	not modelled	93.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
81	c1tltB_	Alignment	not modelled	93.7	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase (virulence factor mvim homolog); **PDBTitle:** crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
82	c1kjjA_	Alignment	not modelled	93.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
83	c2axqA_	Alignment	not modelled	93.6	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
84	d2czca2	Alignment	not modelled	93.6	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
85	c2ys6A_	Alignment	not modelled	93.5	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide synthetase; **PDBTitle:** crystal structure of gar synthetase from geobacillus kaustophilus
86	c1m6vE_	Alignment	not modelled	93.5	10	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
87	c2yyaB_	Alignment	not modelled	93.4	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of gar synthetase from aquifex aeolicus
88	c2ph5A_	Alignment	not modelled	93.3	11	**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
89	d2jfga1	Alignment	not modelled	93.1	14	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
90	c2xd4A_	Alignment	not modelled	93.1	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
91	c1xeaD_	Alignment	not modelled	93.0	12	**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
92	d1pjqa1	Alignment	not modelled	93.0	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
93	d1e5qa1	Alignment	not modelled	92.9	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
94	d1iuka_	Alignment	not modelled	92.9	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
95	d1h6da1	Alignment	not modelled	92.9	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
96	c2jcyA_	Alignment	not modelled	92.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium3 tuberculosis
97	c3ip3D_	Alignment	not modelled	92.7	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, putative; **PDBTitle:** structure of putative oxidoreductase (tm_0425) from2 thermotoga maritima
98	d2csua1	Alignment	not modelled	92.5	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
99	c3ijpA_	Alignment	not modelled	92.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution
100	c2duwA_	Alignment	not modelled	92.3	16	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**putative coa-binding protein; **PDBTitle:** solution structure of putative coa-binding protein of2 klebsiella pneumoniae
101	d1cf2o1	Alignment	not modelled	92.3	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
102	c2gpwC_	Alignment	not modelled	92.2	11	**PDB header:**ligase **Chain:** C: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.
						PDB header:ligase **Chain:** A: **PDB Molecule:**protein (glycinamide ribonucleotide

103	c1gsoA_	Alignment	not modelled	92.1	20	synthetase); **PDBTitle:** glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
104	c3mtjA_	Alignment	not modelled	91.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
105	d1ebfa1	Alignment	not modelled	91.9	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
106	d1diha1	Alignment	not modelled	91.6	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
107	c3g8cB_	Alignment	not modelled	91.6	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal stucture of biotin carboxylase in complex with2 biotin, bicarbonate, adp and mg ion
108	c1ulzA_	Alignment	not modelled	91.4	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase n-terminal domain; **PDBTitle:** crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
109	c3ktdC_	Alignment	not modelled	91.2	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
110	c3gidB_	Alignment	not modelled	91.1	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** the biotin carboxylase (bc) domain of human acetyl-coa2 carboxylase 2 (acc2) in complex with soraphen a
111	c1j5pA_	Alignment	not modelled	91.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate dehydrogenase; **PDBTitle:** crystal structure of aspartate dehydrogenase (tm1643) from thermotoga2 maritima at 1.9 a resolution
112	c3uw3A_	Alignment	not modelled	90.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of an aspartate-semialdehyde dehydrogenase from2 burkholderia thailandensis
113	c2ozpA_	Alignment	not modelled	90.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**n-acetyl-gamma-glutamyl-phosphate reductase; **PDBTitle:** crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (ttha1904) from thermus thermophilus
114	c2csuB_	Alignment	not modelled	90.7	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**457aa long hypothetical protein; **PDBTitle:** crystal structure of ph0766 from pyrococcus horikoshii ot3
115	c1ebuA_	Alignment	not modelled	90.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** homoserine dehydrogenase complex with nad analogue and l-2 homoserine
116	c1mb4B_	Alignment	not modelled	90.6	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase2 from vibrio cholerae with nadp and s-methyl-l-cysteine3 sulfoxide
117	c3u9sE_	Alignment	not modelled	90.5	17	**PDB header:**ligase **Chain:** E: **PDB Molecule:**methylcrotonyl-coa carboxylase, alpha-subunit; **PDBTitle:** crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
118	c2qx7A_	Alignment	not modelled	90.5	13	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**eugenol synthase 1; **PDBTitle:** structure of eugenol synthase from ocimum basilicum
119	d1pqua1	Alignment	not modelled	90.5	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
120	c1t4bB_	Alignment	not modelled	90.3	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** 1.6 angstrom structure of esherichia coli aspartate-2 semialdehyde dehydrogenase.