Phyre^2

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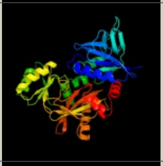
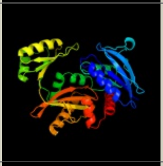
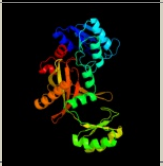
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3i12A_	Alignment		100.0	90	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-d-alanine ligase a; **PDBTitle:** the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
2	c1ehiB_	Alignment		100.0	36	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine:d-lactate ligase; **PDBTitle:** d-alanine:d-lactate ligase (lmddl2) of vancomycin-resistant2 leuconostoc mesenteroides
3	c3e5nA_	Alignment		100.0	64	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-d-alanine ligase a; **PDBTitle:** crystal strucutre of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
4	c2i80B_	Alignment		100.0	41	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine-d-alanine ligase; **PDBTitle:** allosteric inhibition of staphylococcus aureus d-alanine:d-alanine2 ligase revealed by crystallographic studies
5	c3tqtB_	Alignment		100.0	41	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** structure of the d-alanine-d-alanine ligase from coxiella burnetii
6	c1e4eB_	Alignment		100.0	37	**PDB header:**ligase **Chain:** B: **PDB Molecule:**vancomycin/teicoplanin a-type resistance protein vana; **PDBTitle:** d-alanyl-d-lacate ligase
7	c3se7A_	Alignment		100.0	39	**PDB header:**ligase **Chain:** A: **PDB Molecule:**vana; **PDBTitle:** ancient vana
8	c3k3pA_	Alignment		100.0	38	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of the apo form of d-alanine:d-alanine ligase (ddl)2 from streptococcus mutans
9	c2dlnA_	Alignment		100.0	36	**PDB header:**ligase(peptidoglycan synthesis) **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** vancomycin resistance: structure of d-alanine:d-alanine2 ligase at 2.3 angstroms resolution
10	c3lwbA_	Alignment		100.0	45	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of apo d-alanine:d-alanine ligase (ddl) from2 mycobacterium tuberculosis
11	c2zdqA_	Alignment		100.0	41	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of d-alanine:d-alanine ligase with atp2 and d-alanine:d-alanine from thermus thermophius hb8

12	c2pvpB_	Alignment		100.0	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine-d-alanine ligase; **PDBTitle:** crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
13	c3r23B_	Alignment		100.0	31	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
14	c1m6vE_	Alignment		100.0	17	**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
15	c3ouzA_	Alignment		100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
16	c3bg5C_	Alignment		100.0	18	**PDB header:**ligase **Chain:** C: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of staphylococcus aureus pyruvate2 carboxylase
17	c2dzdB_	Alignment		100.0	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase
18	c1ulzA_	Alignment		100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase n-terminal domain; **PDBTitle:** crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
19	c3g8cB_	Alignment		100.0	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal stucture of biotin carboxylase in complex with2 biotin, bicarbonate, adp and mg ion
20	c1kjjA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
21	c2vpqA_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
22	c1w96B_	Alignment	not modelled	100.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase; **PDBTitle:** crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
23	c3q2oB_	Alignment	not modelled	100.0	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
24	c2hjwA_	Alignment	not modelled	100.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** crystal structure of the bc domain of acc2
25	c3u9sE_	Alignment	not modelled	100.0	19	**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
26	c3n6rK_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
27	c2xd4A_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
						PDB header:ligase

28	c3gidB_	Alignment	not modelled	100.0	13	**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
29	c2gpwC_	Alignment	not modelled	100.0	17	**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.
30	c3lp8A_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine-glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
31	d1ehia2	Alignment	not modelled	100.0	37	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
32	c2yyaB_	Alignment	not modelled	100.0	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of gar synthetase from aquifex aeolicus
33	c3uvzB_	Alignment	not modelled	100.0	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
34	c1vkzA_	Alignment	not modelled	100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution
35	c3etjB_	Alignment	not modelled	100.0	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure e. coli purk in complex with mg, adp, and2 pi
36	c3orqA_	Alignment	not modelled	100.0	20	**PDB header:**ligase,biosynthetic protein **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide synthetase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
37	c3k5iB_	Alignment	not modelled	100.0	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosyl-aminoimidazole carboxylase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-3 aminoimadazole ribonucleotide
38	c2ip4A_	Alignment	not modelled	100.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
39	c2qk4A_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trifunctional purine biosynthetic protein adenosine-3; **PDBTitle:** human glycinamide ribonucleotide synthetase
40	c2ys6A_	Alignment	not modelled	100.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide synthetase; **PDBTitle:** crystal structure of gar synthetase from geobacillus kaustophilus
41	c2dwcB_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**433aa long hypothetical phosphoribosylglycinamide formyl **PDBTitle:** crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
42	c1gsoA_	Alignment	not modelled	100.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**protein (glycinamide ribonucleotide synthetase); **PDBTitle:** glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
43	d1e4ea2	Alignment	not modelled	100.0	37	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
44	d1iowa2	Alignment	not modelled	100.0	34	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
45	c2pn1A_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoylphosphate synthase large subunit; **PDBTitle:** crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from exiguobacterium sp. 255-15 at 2.00 a3 resolution
46	c2r85B_	Alignment	not modelled	100.0	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**purp protein pf1517; **PDBTitle:** crystal structure of purp from pyrococcus furiosus complexed with amp
47	c3df7A_	Alignment	not modelled	100.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative atp-grasp superfamily protein; **PDBTitle:** crystal structure of a putative atp-grasp superfamily2 protein from archaeoglobus fulgidus
48	c2z04A_	Alignment	not modelled	100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
49	c1uc8B_	Alignment	not modelled	100.0	17	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**lysine biosynthesis enzyme; **PDBTitle:** crystal structure of a lysine biosynthesis enzyme, lysx,2 from thermus thermophilus hb8
50	c1z2pX_	Alignment	not modelled	100.0	11	**PDB header:**transferase **Chain:** X: **PDB Molecule:**inositol 1,3,4-trisphosphate 5/6-kinase; **PDBTitle:** inositol 1,3,4-trisphosphate 5/6-kinase in complex with mg2+/amp-2 pcp/ins(1,3,4)p3
51	d1w96a3	Alignment	not modelled	100.0	15	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like

						Family:BC ATP-binding domain-like
52	d2r7ka2	Alignment	not modelled	100.0	17	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**PurP ATP-binding domain-like
53	d1a9xa5	Alignment	not modelled	100.0	14	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
54	d2r85a2	Alignment	not modelled	99.9	16	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**PurP ATP-binding domain-like
55	c3ln6A_	Alignment	not modelled	99.9	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutathione biosynthesis bifunctional protein gshab; **PDBTitle:** crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
56	c1i7nA_	Alignment	not modelled	99.9	13	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**synapsin ii; **PDBTitle:** crystal structure analysis of the c domain of synapsin ii2 from rat brain
57	d1vkza3	Alignment	not modelled	99.9	17	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
58	c2qb5B_	Alignment	not modelled	99.9	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**inositol-tetrakisphosphate 1-kinase; **PDBTitle:** crystal structure of human inositol 1,3,4-trisphosphate 5/6-kinase2 (itpk1) in complex with adp and mn2+
59	c2p0aA_	Alignment	not modelled	99.9	14	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**synapsin-3; **PDBTitle:** the crystal structure of human synapsin iii (syn3) in complex with2 amppnp
60	d3etja3	Alignment	not modelled	99.9	20	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
61	c1pk8D_	Alignment	not modelled	99.9	12	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**rat synapsin i; **PDBTitle:** crystal structure of rat synapsin i c domain complexed to2 ca.atp
62	d1kjqa3	Alignment	not modelled	99.9	21	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
63	d2j9ga3	Alignment	not modelled	99.9	17	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
64	d1ulza3	Alignment	not modelled	99.9	16	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
65	d1a9xa6	Alignment	not modelled	99.9	18	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
66	c2qf7A_	Alignment	not modelled	99.9	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase protein; **PDBTitle:** crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
67	c3ln7A_	Alignment	not modelled	99.9	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutathione biosynthesis bifunctional protein gshab; **PDBTitle:** crystal structure of a bifunctional glutathione synthetase from2 pasteurella multocida
68	d1gsoa3	Alignment	not modelled	99.9	12	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
69	d1uc8a2	Alignment	not modelled	99.9	16	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Lysine biosynthesis enzyme LysX ATP-binding domain
70	c1gshA_	Alignment	not modelled	99.9	12	**PDB header:**glutathione biosynthesis ligase **Chain:** A: **PDB Molecule:**glutathione biosynthetic ligase; **PDBTitle:** structure of escherichia coli glutathione synthetase at ph 7.5
71	d1pk8a2	Alignment	not modelled	99.9	12	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Synapsin C-terminal domain
72	c3t9aA_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**inositol pyrophosphate kinase; **PDBTitle:** crystal structure of the catalytic domain of human diphosphoinositol2 pentakisphosphate kinase 2 (ppip5k2) in complex with amppnp at ph 7.0
73	d1i7na2	Alignment	not modelled	99.9	13	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Synapsin C-terminal domain
74	d1e4ea1	Alignment	not modelled	99.8	36	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
75	d1ehia1	Alignment	not modelled	99.8	32	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
76	d1iowa1	Alignment	not modelled	99.7	36	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
77	c2r7mA_	Alignment	not modelled	99.6	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**5-formaminoimidazole-4-carboxamide-1-(beta)-d-

						PDBTitle: crystal structure of faicar synthetase (purp) from m.2 jannaschii complexed with amp
78	d1gsaa2	Alignment	not modelled	99.5	12	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
79	c2cqyA_	Alignment	not modelled	99.1	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**propionyl-coa carboxylase alpha chain, **PDBTitle:** solution structure of b domain from human propionyl-coa2 carboxylase alpha subunit
80	c2pbzC_	Alignment	not modelled	99.1	18	**PDB header:**ligase **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of an imp biosynthesis protein purp from2 thermococcus kodakaraensis
81	d1a9xa4	Alignment	not modelled	99.0	18	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
82	c1wr2A_	Alignment	not modelled	98.7	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1789; **PDBTitle:** crystal structure of ph1788 from pyrococcus horikoshii ot3
83	c2nu9E_	Alignment	not modelled	98.7	18	**PDB header:**ligase **Chain:** E: **PDB Molecule:**succinyl-coa synthetase beta chain; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
84	d1eucb2	Alignment	not modelled	98.6	18	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Succinyl-CoA synthetase, beta-chain, N-terminal domain
85	d1a9xa3	Alignment	not modelled	98.6	15	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
86	c1eucB_	Alignment	not modelled	98.6	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**succinyl-coa synthetase, beta chain; **PDBTitle:** crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase
87	d2nu7b2	Alignment	not modelled	98.5	16	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Succinyl-CoA synthetase, beta-chain, N-terminal domain
88	d2pbza2	Alignment	not modelled	98.5	19	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**PurP ATP-binding domain-like
89	c3tinA_	Alignment	not modelled	98.5	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ttl protein; **PDBTitle:** tubulin tyrosine ligase
90	d1kjqa2	Alignment	not modelled	98.4	19	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
91	d1ulza2	Alignment	not modelled	98.1	16	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
92	d2j9ga2	Alignment	not modelled	98.0	13	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
93	c3mwdA_	Alignment	not modelled	97.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp-citrate synthase; **PDBTitle:** truncated human atp-citrate lyase with citrate bound
94	d1w96a2	Alignment	not modelled	97.0	15	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
95	d2jfga1	Alignment	not modelled	96.8	12	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
96	c2xdoC_	Alignment	not modelled	96.3	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**tetx2 protein; **PDBTitle:** structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
97	d1gsoa2	Alignment	not modelled	96.0	16	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
98	c3i3lA_	Alignment	not modelled	95.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkylhalidase cmls; **PDBTitle:** crystal structure of cmls, a flavin-dependent halogenase
99	c3kljA_	Alignment	not modelled	95.4	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad(fad)-dependent dehydrogenase, nirb-family (n-terminal **PDBTitle:** crystal structure of nadh:rubredoxin oxidoreductase from clostridium2 acetobutylicum
100	c1ps9A_	Alignment	not modelled	95.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
101	d1e5qa1	Alignment	not modelled	94.8	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
102	c3ic5A_	Alignment	not modelled	94.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
103	c2hkoA_	Alignment	not modelled	94.4	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** crystal structure of lsd1
						PDB header:oxidoreductase

104	c1djnB_	Alignment	not modelled	94.3	25	**Chain:** B: **PDB Molecule:**trimethylamine dehydrogenase; **PDBTitle:** structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
105	c3k30B_	Alignment	not modelled	94.3	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histamine dehydrogenase; **PDBTitle:** histamine dehydrogenase from nocardiodes simplex
106	d1ps9a3	Alignment	not modelled	94.3	13	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
107	c2e1mA_	Alignment	not modelled	94.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-glutamate oxidase; **PDBTitle:** crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
108	c1e5lA_	Alignment	not modelled	94.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
109	c3rhaA_	Alignment	not modelled	94.2	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putrescine oxidase; **PDBTitle:** the crystal structure of oxidoreductase from arthrobacter aurescens
110	c3atrA_	Alignment	not modelled	94.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**conserved archaeal protein; **PDBTitle:** geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
111	c2xagA_	Alignment	not modelled	94.0	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
112	c2v1dA_	Alignment	not modelled	94.0	20	**PDB header:**oxidoreductase/repressor **Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1; **PDBTitle:** structural basis of lsd1-corest selectivity in histone h32 recognition
113	c3allA_	Alignment	not modelled	94.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; **PDBTitle:** crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
114	c2vdcI_	Alignment	not modelled	94.0	13	**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.
115	c2eq8E_	Alignment	not modelled	94.0	8	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
116	c1vdcA_	Alignment	not modelled	93.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dependent thioredoxin reductase; **PDBTitle:** structure of nadph dependent thioredoxin reductase
117	d1djqa3	Alignment	not modelled	93.9	25	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
118	c1c0iA_	Alignment	not modelled	93.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-amino acid oxidase; **PDBTitle:** crystal structure of d-amino acid oxidase in complex with2 two anthranylate molecules
119	d2dw4a2	Alignment	not modelled	93.9	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
120	c1f8sA_	Alignment	not modelled	93.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-amino acid oxidase; **PDBTitle:** crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.