Phyre^2

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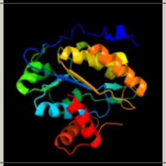
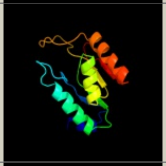
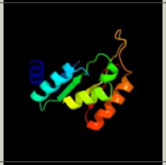
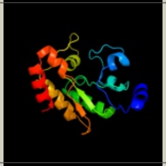
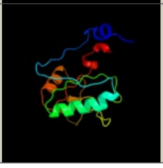
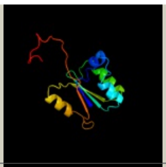
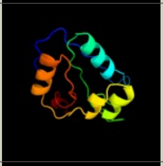
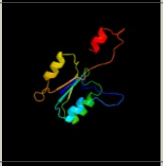
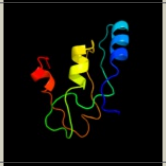
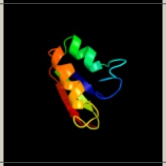
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vkma_	Alignment		100.0	38	**Fold:**Indigoidine synthase A-like **Superfamily:**Indigoidine synthase A-like **Family:**Indigoidine synthase A-like
2	c1otpA_	Alignment		93.4	21	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
3	c2j0fC_	Alignment		93.1	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
4	c1brwB_	Alignment		93.1	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
5	c2dsjA_	Alignment		92.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
6	c3h5qA_	Alignment		91.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
7	c1zfjA_	Alignment		91.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
8	d1s2wa_	Alignment		90.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
9	d1zfja1	Alignment		86.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
10	d1muma_	Alignment		83.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
11	c1khdD_	Alignment		83.0	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.93 resolution (current name, pectobacterium carotovorum)

12	c2fr1A_	Alignment		81.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**erythromycin synthase, eryai; **PDBTitle:** the first ketoreductase of the erythromycin synthase2 (crystal form 2)
13	d2elca2	Alignment		80.4	27	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
14	c1v8gB_	Alignment		79.7	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8
15	c1o17A_	Alignment		78.1	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyl-transferase (trpd)
16	c2vz8B_	Alignment		77.7	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fatty acid synthase; **PDBTitle:** crystal structure of mammalian fatty acid synthase
17	c3mjsA_	Alignment		76.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**amphb; **PDBTitle:** structure of a-type ketoreductases from modular polyketide synthase
18	d1jvna1	Alignment		74.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
19	c2z5lA_	Alignment		73.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tylactone synthase starter module and modules 1 **PDBTitle:** the first ketoreductase of the tylosin pks
20	d1r7ha_	Alignment		68.3	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
21	c2hjpA_	Alignment	not modelled	67.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
22	c1vquB_	Alignment	not modelled	65.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase 2; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase 22 (17130499) from nostoc sp. at 1.85 a resolution
23	c3fmfA_	Alignment	not modelled	65.8	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
24	c3n2oA_	Alignment	not modelled	64.6	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**biosynthetic arginine decarboxylase; **PDBTitle:** x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
25	c3khsB_	Alignment	not modelled	64.2	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
26	c3lyhB_	Alignment	not modelled	63.3	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cobalamin (vitamin b12) biosynthesis cbix protein; **PDBTitle:** crystal structure of putative cobalamin (vitamin b12) biosynthesis2 cbix protein (yp_958415.1) from marinobacter aquaeolei vt8 at 1.60 a3 resolution
27	d1mzha_	Alignment	not modelled	63.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase

28	c3qp9C_	Alignment	not modelled	59.7	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**type i polyketide synthase pikaii; **PDBTitle:** the structure of a c2-type ketoreductase from a modular polyketide2 synthase
29	d1uoua2	Alignment	not modelled	59.4	23	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
30	c3nzpA_	Alignment	not modelled	59.3	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**arginine decarboxylase; **PDBTitle:** crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
31	c1zlpA_	Alignment	not modelled	59.2	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**petal death protein; **PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
32	d1m3ua_	Alignment	not modelled	58.1	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
33	c3ih1A_	Alignment	not modelled	57.6	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
34	c3ffsC_	Alignment	not modelled	54.6	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
35	d1brwa2	Alignment	not modelled	54.3	27	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
36	c1ypfB_	Alignment	not modelled	51.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gmp reductase; **PDBTitle:** crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
37	c3ggsA_	Alignment	not modelled	49.3	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** human purine nucleoside phosphorylase double mutant e201q,n243d2 complexed with 2-fluoro-2'-deoxyadenosine
38	d1t9ba1	Alignment	not modelled	47.9	28	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
39	d1f0ka_	Alignment	not modelled	47.7	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
40	c1yadD_	Alignment	not modelled	47.6	24	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein teni; **PDBTitle:** structure of teni from bacillus subtilis
41	d2ihta1	Alignment	not modelled	47.1	24	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
42	c3cf4G_	Alignment	not modelled	45.1	15	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**acetyl-coa decarboxylase/synthase epsilon subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
43	c2bibA_	Alignment	not modelled	45.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**teichoic acid phosphorylcholine esterase/ choline binding **PDBTitle:** crystal structure of the complete modular teichioic acid2 phosphorylcholine esterase pce (cbpe) from streptococcus3 pneumoniae
44	d1xm3a_	Alignment	not modelled	45.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
45	d1khda2	Alignment	not modelled	44.9	21	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
46	c1jvnB_	Alignment	not modelled	43.8	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional histidine biosynthesis protein hishf; **PDBTitle:** crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
47	c3mioA_	Alignment	not modelled	42.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3,4-dihydroxy-2-butanone 4-phosphate synthase; **PDBTitle:** crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00
48	d3bgsa1	Alignment	not modelled	41.1	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
49	d1ujqa_	Alignment	not modelled	40.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
50	d3pnpa_	Alignment	not modelled	39.7	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases

						Family: Purine and uridine phosphorylases
51	d1zpda1	Alignment	not modelled	39.2	5	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
52	c3guzB_	Alignment	not modelled	37.8	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** structural and substrate-binding studies of pantothenate2 synthenate (ps)provide insights into homotropic inhibition3 by pantoate in ps's
53	c2qr6A_	Alignment	not modelled	37.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**imp dehydrogenase/gmp reductase; **PDBTitle:** crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution
54	c2agkA_	Alignment	not modelled	37.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) **PDBTitle:** structure of s. cerevisiae his6 protein
55	d1h5ya_	Alignment	not modelled	36.1	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
56	c1jd7A_	Alignment	not modelled	35.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
57	d1wdia_	Alignment	not modelled	34.9	27	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
58	c2qmoA_	Alignment	not modelled	34.5	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
59	d1n57a_	Alignment	not modelled	34.4	33	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
60	d2ae2a_	Alignment	not modelled	34.2	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
61	d1v77a_	Alignment	not modelled	33.9	10	**Fold:**7-stranded beta/alpha barrel **Superfamily:**PHP domain-like **Family:**RNase P subunit p30
62	c2yvqA_	Alignment	not modelled	33.5	58	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase; **PDBTitle:** crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
63	c3eooL_	Alignment	not modelled	33.4	17	**PDB header:**lyase **Chain:** L: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
64	c2xvzA_	Alignment	not modelled	32.8	11	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**chelatase, putative; **PDBTitle:** cobalt chelatase cbik (periplasmatic) from desulvobrio2 vulgaris hildenborough (co-crystallized with cobalt)
65	c3rggD_	Alignment	not modelled	32.6	23	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
66	c3chvA_	Alignment	not modelled	32.0	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**prokaryotic domain of unknown function (duf849) with a tim **PDBTitle:** crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
67	c3n6rK_	Alignment	not modelled	31.5	22	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
68	c3nxkE_	Alignment	not modelled	31.2	22	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**cytoplasmic l-asparaginase; **PDBTitle:** crystal structure of probable cytoplasmic l-asparaginase from2 campylobacter jejuni
69	c3e02A_	Alignment	not modelled	29.8	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf849; **PDBTitle:** crystal structure of a duf849 family protein (bxe_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
70	d1u11a_	Alignment	not modelled	29.6	10	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
71	c3b40A_	Alignment	not modelled	29.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable dipeptidase; **PDBTitle:** crystal structure of the probable dipeptidase pvdm from2 pseudomonas aeruginosa
72	d1ebda3	Alignment	not modelled	28.5	16	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
73	c2a7rD_	Alignment	not modelled	27.2	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**gmp reductase 2; **PDBTitle:** crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
74	c3nzqB_	Alignment	not modelled	27.2	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**biosynthetic arginine decarboxylase; **PDBTitle:** crystal structure of biosynthetic arginine decarboxylase

						adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
75	c2fw9A_	Alignment	not modelled	26.5	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
76	c2vedA_	Alignment	not modelled	25.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**membrane protein capa1, protein tyrosine kinase; **PDBTitle:** crystal structure of the chimerical mutant capabk55m2 protein
77	d2tpta2	Alignment	not modelled	25.2	21	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
78	d1g2oa_	Alignment	not modelled	24.6	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
79	d2ji7a1	Alignment	not modelled	24.5	23	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
80	c3e49A_	Alignment	not modelled	24.0	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf849 with a tim barrel fold; **PDBTitle:** crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bxe_c0966) from burkholderia xenovorans lb4003 at 1.75 a resolution
81	d1ovma1	Alignment	not modelled	23.2	6	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
82	d1q6za1	Alignment	not modelled	22.9	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
83	c3majA_	Alignment	not modelled	22.8	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna processing chain a; **PDBTitle:** crystal structure of putative dna processing protein dpra from2 rhodopseudomonas palustris cga009
84	d1wmaa1	Alignment	not modelled	22.6	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
85	c1a31A_	Alignment	not modelled	22.6	14	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**protein (topoisomerase i); **PDBTitle:** human reconstituted dna topoisomerase i in covalent complex2 with a 22 base pair dna duplex
86	c3ceuA_	Alignment	not modelled	22.6	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamine phosphate pyrophosphorylase; **PDBTitle:** crystal structure of thiamine phosphate pyrophosphorylase2 (bt_0647) from bacteroides thetaiotaomicron. northeast3 structural genomics consortium target btr268
87	d2adra2	Alignment	not modelled	22.4	28	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
88	d1v58a2	Alignment	not modelled	22.3	22	**Fold:**Cystatin-like **Superfamily:**DsbC/DsbG N-terminal domain-like **Family:**DsbC/DsbG N-terminal domain-like
89	d3grsa3	Alignment	not modelled	22.3	20	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
90	c3oixA_	Alignment	not modelled	22.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative dihydroorotate dehydrogenase; dihydroorotate **PDBTitle:** crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
91	d1vrda1	Alignment	not modelled	22.1	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
92	c1mg7B_	Alignment	not modelled	21.9	21	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**early switch protein xol-1 2.2k splice form; **PDBTitle:** crystal structure of xol-1
93	d1k4ia_	Alignment	not modelled	21.8	23	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
94	d1pkla2	Alignment	not modelled	21.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
95	c3o2sB_	Alignment	not modelled	21.6	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72 complex
96	c3o2qB_	Alignment	not modelled	21.5	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
97	d1ozha1	Alignment	not modelled	21.3	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
						Fold: Metallo-hydrolase/oxidoreductase

98	d1wraa1	Alignment	not modelled	21.0	13	**Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Pce catalytic domain-like
99	d2dasa1	Alignment	not modelled	20.9	32	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**TRASH domain
100	d1j6ua1	Alignment	not modelled	20.8	12	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
101	c2dasA_	Alignment	not modelled	20.6	32	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**zinc finger mym-type protein 5; **PDBTitle:** solution structure of trash domain of zinc finger mym-type2 protein 5
102	c3labA_	Alignment	not modelled	20.5	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative kdpg (2-keto-3-deoxy-6-phosphogluconate) **PDBTitle:** crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
103	c3lu2B_	Alignment	not modelled	20.4	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2462 protein; **PDBTitle:** structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
104	d1o17a2	Alignment	not modelled	20.4	18	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
105	d1aoga3	Alignment	not modelled	20.3	18	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
106	c3tovB_	Alignment	not modelled	20.1	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase family 9; **PDBTitle:** the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
107	d1tksa_	Alignment	not modelled	20.1	21	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB