Phyre^2

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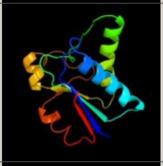
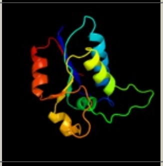
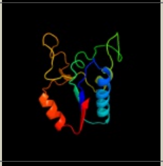
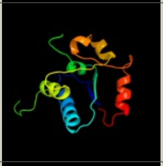
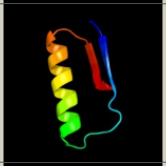
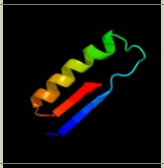
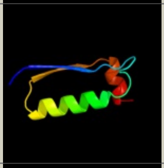
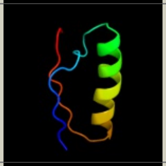
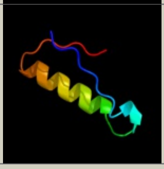
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2d1pb1	Alignment		100.0	100	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
2	d2hy5b1	Alignment		100.0	28	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
3	d2hy5a1	Alignment		99.9	21	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
4	d1jx7a_	Alignment		99.9	23	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
5	d2d1pa1	Alignment		99.9	23	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
6	c3mc3A_	Alignment		99.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dsre/dsrf-like family protein; **PDBTitle:** crystal structure of dsre/dsrf-like family protein (np_342589.1) from2 sulfolobus solfataricus at 1.49 a resolution
7	c2qs7D_	Alignment		99.6	8	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative oxidoreductase of the dsre/dsrf-like2 family (sso1126) from sulfolobus solfataricus p2 at 2.09 a resolution
8	d2hy5c1	Alignment		99.5	14	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrH-like
9	c3pnxF_	Alignment		99.5	14	**PDB header:**transferase **Chain:** F: **PDB Molecule:**putative sulfurtransferase dsre; **PDBTitle:** crystal structure of a putative sulfurtransferase dsre (swol_2425)2 from syntrophomonas wolfei str. goettingen at 1.92 a resolution
10	d2d1pc1	Alignment		99.1	19	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrH-like
11	d1x9aa_	Alignment		98.7	14	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrH-like

12	c2pd2A_	Alignment		98.2	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein st0148; **PDBTitle:** crystal structure of (st0148) conserved hypothetical from sulfolobus2 tokodaii strain7
13	d1l1sa_	Alignment		98.2	16	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
14	c2fb6A_	Alignment		98.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** structure of conserved protein of unknown function bt1422 from2 bacteroides thetaiotaomicron
15	c2r60A_	Alignment		85.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
16	c3ia7A_	Alignment		82.7	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
17	d1qrda_	Alignment		78.3	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
18	c2ejbA_	Alignment		61.6	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
19	c3oy2A_	Alignment		53.7	20	**PDB header:**viral protein,transferase **Chain:** A: **PDB Molecule:**glycosyltransferase b736l; **PDBTitle:** crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
20	d2afhe1	Alignment		41.5	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
21	c2pz0B_	Alignment	not modelled	40.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
22	d1qgoa_	Alignment	not modelled	38.6	16	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Cobalt chelatase CbiK
23	c1gshA_	Alignment	not modelled	37.2	13	**PDB header:**glutathione biosynthesis ligase **Chain:** A: **PDB Molecule:**glutathione biosynthetic ligase; **PDBTitle:** structure of escherichia coli glutathione synthetase at ph 7.5
24	d1gsaa1	Alignment	not modelled	36.5	14	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Prokaryotic glutathione synthetase, N-terminal domain
25	c3okaA_	Alignment	not modelled	35.6	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol **PDBTitle:** crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)
26	d1f0ka_	Alignment	not modelled	33.2	21	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
27	d1efva1	Alignment	not modelled	32.1	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
28	c3idfA_	Alignment	not modelled	31.2	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**usp-like protein; **PDBTitle:** the crystal structure of a usp-like protein from wolinella2 succinogenes to 2.0a

29	d1t5ba_	Alignment	not modelled	29.7	7	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
30	d1gpja2	Alignment	not modelled	28.5	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
31	d2bisa1	Alignment	not modelled	28.4	19	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
32	c3l12A_	Alignment	not modelled	26.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (yp_165505.1) from silicibacter pomeroyi dss-3 at3 1.60 a resolution
33	c2l18A_	Alignment	not modelled	26.1	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** an arsenate reductase in the phosphate binding state
34	c2bekB_	Alignment	not modelled	25.7	14	**PDB header:**chromosome segregation **Chain:** B: **PDB Molecule:**segregation protein; **PDBTitle:** structure of the bacterial chromosome segregation protein2 soj
35	c1t9gR_	Alignment	not modelled	25.1	13	**PDB header:**oxidoreductase, electron transport **Chain:** R: **PDB Molecule:**electron transfer flavoprotein alpha-subunit, **PDBTitle:** structure of the human mcad:etf complex
36	c2zkiH_	Alignment	not modelled	23.4	8	**PDB header:**transcription **Chain:** H: **PDB Molecule:**199aa long hypothetical trp repressor binding **PDBTitle:** crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
37	d1ycga1	Alignment	not modelled	22.0	8	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
38	c3no3A_	Alignment	not modelled	21.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerophosphodiester phosphodiesterase; **PDBTitle:** crystal structure of a glycerophosphodiester phosphodiesterase2 (bdi_0402) from parabacteroides distasonis atcc 8503 at 1.89 a3 resolution
39	d2gm3a1	Alignment	not modelled	21.3	5	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
40	c3etjB_	Alignment	not modelled	21.1	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure e. coli purk in complex with mg, adp, and2 pi
41	d1ydga_	Alignment	not modelled	21.0	23	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
42	c2i5bC_	Alignment	not modelled	20.6	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphomethylpyrimidine kinase; **PDBTitle:** the crystal structure of an adp complex of bacillus2 subtilis pyridoxal kinase provides evidence for the3 parralel emergence of enzyme activity during evolution
43	d4pfka_	Alignment	not modelled	20.1	19	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
44	d1q77a_	Alignment	not modelled	20.1	8	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
45	d1o1za_	Alignment	not modelled	20.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
46	c2x6rA_	Alignment	not modelled	19.9	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**trehalose-synthase tret; **PDBTitle:** crystal structure of trehalose synthase tret from p.2 horikoshi produced by soaking in trehalose
47	d2nlya1	Alignment	not modelled	19.4	17	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**Divergent polysaccharide deacetylase
48	c3lcmB_	Alignment	not modelled	19.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
49	c3i10A_	Alignment	not modelled	18.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (np_812074.1) from bacteroides thetaiotaomicron3 vpi-5482 at 1.35 a resolution
50	c3d4oA_	Alignment	not modelled	18.7	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit a; **PDBTitle:** crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
51	c3ouzA_	Alignment	not modelled	18.6	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
52	c3mz2A_	Alignment	not modelled	17.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of a glycerophosphoryl diester phosphodiesterase2 (bdi_3922) from parabacteroides distasonis

						atcc 8503 at 1.55 a3 resolution
53	c3qjgD_	Alignment	not modelled	17.3	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**epidermin biosynthesis protein epid; **PDBTitle:** epidermin biosynthesis protein epid from staphylococcus aureus
54	c1hyqA_	Alignment	not modelled	17.3	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division inhibitor (mind-1); **PDBTitle:** mind bacterial cell division regulator from a. fulgidus
55	d1hyqa_	Alignment	not modelled	17.3	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
56	c2rirA_	Alignment	not modelled	17.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase, a chain; **PDBTitle:** crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
57	c2dzdB_	Alignment	not modelled	16.5	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase
58	c3crnA_	Alignment	not modelled	16.4	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver domain protein, chey-like; **PDBTitle:** crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
59	d1vdca2	Alignment	not modelled	15.9	8	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
60	d1rzua_	Alignment	not modelled	15.7	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
61	c3c1oA_	Alignment	not modelled	14.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**eugenol synthase; **PDBTitle:** the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
62	c3i42A_	Alignment	not modelled	14.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**response regulator receiver domain protein (chey- **PDBTitle:** structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus
63	d3lada2	Alignment	not modelled	14.7	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
64	c2x0dA_	Alignment	not modelled	14.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**wsaf; **PDBTitle:** apo structure of wsaf
65	c1gpjA_	Alignment	not modelled	14.6	16	**PDB header:**reductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** glutamyl-trna reductase from methanopyrus kandleri
66	d1rtta_	Alignment	not modelled	14.4	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
67	c3mt0A_	Alignment	not modelled	14.4	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pa1789; **PDBTitle:** the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
68	c1ulzA_	Alignment	not modelled	14.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase n-terminal domain; **PDBTitle:** crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
69	c2otdC_	Alignment	not modelled	14.0	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**glycerophosphodiester phosphodiesterase; **PDBTitle:** the crystal structure of the glycerophosphodiester phosphodiesterase2 from shigella flexneri 2a
70	c3g5rA_	Alignment	not modelled	13.9	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylenetetrahydrofolate--trna-(uracil-5-)- **PDBTitle:** crystal structure of thermus thermophilus trmfo in complex with2 tetrahydrofolate
71	d2qwxa1	Alignment	not modelled	13.8	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
72	d1ebda2	Alignment	not modelled	13.0	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
73	d1ojta2	Alignment	not modelled	12.8	32	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
74	c2qsjB_	Alignment	not modelled	12.6	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**dna-binding response regulator, luxr family; **PDBTitle:** crystal structure of a luxr family dna-binding response2 regulator from silicibacter pomeroyi
75	c3ab8B_	Alignment	not modelled	12.6	24	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein ttha0350; **PDBTitle:** crystal structure of the hypothetical tandem-type universal stress2 protein ttha0350 complexed with atps.
76	d1ihua1	Alignment	not modelled	12.5	6	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
						PDB header:structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative glycerophosphodiester

77	c2o55A_	Alignment	not modelled	12.5	8	phosphodiesterase; **PDBTitle:** crystal structure of a putative glycerophosphodiester2 phosphodiesterase from galdieria sulphuraria
78	d1vmea1	Alignment	not modelled	12.4	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
79	c3fozB_	Alignment	not modelled	12.2	9	**PDB header:**transferase/rna **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate transferase; **PDBTitle:** structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
80	d1q8ka2	Alignment	not modelled	12.0	29	**Fold:**Ferredoxin-like **Superfamily:**eIF-2-alpha, C-terminal domain **Family:**eIF-2-alpha, C-terminal domain
81	c3a11D_	Alignment	not modelled	11.8	12	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b, delta **PDBTitle:** crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
82	c2gejA_	Alignment	not modelled	11.7	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol mannosyltransferase (pima); **PDBTitle:** crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
83	d1cp2a_	Alignment	not modelled	11.6	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
84	d1efpa1	Alignment	not modelled	10.9	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
85	c2gi4A_	Alignment	not modelled	10.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible phosphotyrosine protein phosphatase; **PDBTitle:** solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
86	c2p76H_	Alignment	not modelled	10.7	10	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of a glycerophosphodiester phosphodiesterase from2 staphylococcus aureus
87	d2iw1a1	Alignment	not modelled	10.5	18	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
88	d1ydya1	Alignment	not modelled	10.4	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
89	c1ydyA_	Alignment	not modelled	10.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of periplasmic glycerophosphodiester2 phosphodiesterase from escherichia coli
90	c3ks6A_	Alignment	not modelled	10.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (17743486) from agrobacterium tumefaciens3 str. c58 (dupont) at 1.80 a resolution
91	c3g8cB_	Alignment	not modelled	9.9	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal stucture of biotin carboxylase in complex with2 biotin, bicarbonate, adp and mg ion
92	c3dzcA_	Alignment	not modelled	9.9	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
93	d1fmfa_	Alignment	not modelled	9.7	14	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
94	c3ch0A_	Alignment	not modelled	9.7	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerophosphodiester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphoryl diester phosphodiesterase2 (yp_677622.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
95	d1l7da2	Alignment	not modelled	9.7	15	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**L-alanine dehydrogenase-like
96	d1wzua1	Alignment	not modelled	9.6	21	**Fold:**NadA-like **Superfamily:**NadA-like **Family:**NadA-like
97	c2qzsA_	Alignment	not modelled	9.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogen synthase; **PDBTitle:** crystal structure of wild-type e.coli gs in complex with adp2 and glucose(wtgsb)
98	c3eywA_	Alignment	not modelled	9.4	4	**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
99	d1dxla2	Alignment	not modelled	9.4	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains