Phyre^2

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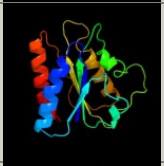
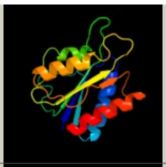
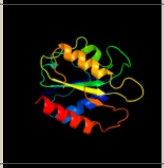
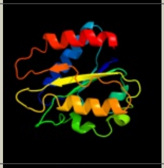
Description	P65367
Date	Thu Jan 5 12:10:13 GMT 2012
Unique Job ID	b0d7a94d4f841ae4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1j9zB_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-cytochrome p450 reductase; **PDBTitle:** cypor-w677g
2	c3hr4C_	Alignment		100.0	24	**PDB header:**oxidoreductase/metal binding protein **Chain:** C: **PDB Molecule:**nitric oxide synthase, inducible; **PDBTitle:** human inos reductase and calmodulin complex
3	c2bpoA_	Alignment		100.0	21	**PDB header:**reductase **Chain:** A: **PDB Molecule:**nadph-cytochrom p450 reductase; **PDBTitle:** crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
4	c1tllA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase, brain; **PDBTitle:** crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
5	d1b1ca_	Alignment		100.0	23	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
6	d1ja1a2	Alignment		100.0	23	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
7	d1tlla2	Alignment		100.0	26	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
8	d1ykga1	Alignment		100.0	28	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
9	c2hnbA_	Alignment		100.0	29	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**protein mioc; **PDBTitle:** solution structure of a bacterial holo-flavodoxin
10	d1bvyf_	Alignment		100.0	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
11	c1bvyF_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (cytochrome p450 bm-3); **PDBTitle:** complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3)

12	c3f6sI_	Alignment		100.0	16	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
13	d1f4pa_	Alignment		100.0	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
14	c2wc1A_	Alignment		100.0	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin; **PDBTitle:** three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a
15	d1yoba1	Alignment		100.0	24	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
16	d2fcra_	Alignment		100.0	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
17	d1czna_	Alignment		100.0	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
18	d1oboa_	Alignment		99.9	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
19	d1ag9a_	Alignment		99.9	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
20	d1fuea_	Alignment		99.9	27	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
21	c3hlyA_	Alignment	not modelled	99.9	12	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
22	d5nula_	Alignment	not modelled	99.9	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
23	d2fz5a1	Alignment	not modelled	99.9	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
24	d1rlja_	Alignment	not modelled	99.9	25	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavoprotein NrdI
25	c2x2oA_	Alignment	not modelled	99.9	17	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**nrdi protein; **PDBTitle:** the flavoprotein nrdi from bacillus cereus with the2 initially oxidized fmn cofactor in an intermediate3 radiation reduced state
26	d1e5da1	Alignment	not modelled	99.9	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
27	c1vmeB_	Alignment	not modelled	99.9	13	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
28	c3fniA_	Alignment	not modelled	99.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3; **PDBTitle:** crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target

						nsr431a
29	c3n39D_	Alignment	not modelled	99.8	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein nrdi; **PDBTitle:** ribonucleotide reductase dimanganese(ii)-nrdf from escherichia coli in2 complex with nrdi
30	d1vmea1	Alignment	not modelled	99.8	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
31	d1ycga1	Alignment	not modelled	99.8	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
32	c1ychD_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase
33	c2ohiB_	Alignment	not modelled	99.8	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
34	c2q9uB_	Alignment	not modelled	99.8	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
35	d2arka1	Alignment	not modelled	99.8	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
36	c1e5dA_	Alignment	not modelled	99.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
37	c3d7nA_	Alignment	not modelled	99.7	10	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin, wrba-like protein; **PDBTitle:** the crystal structure of the flavodoxin, wrba-like protein from2 agrobacterium tumefaciens
38	d2a5la1	Alignment	not modelled	99.6	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
39	d1ydga_	Alignment	not modelled	99.5	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
40	c3b6iB_	Alignment	not modelled	99.5	13	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**flavoprotein wrba; **PDBTitle:** wrba from escherichia coli, native structure
41	c3klbA_	Alignment	not modelled	99.5	16	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative flavoprotein; **PDBTitle:** crystal structure of putative flavoprotein in complex with fmn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
42	c2zkiH_	Alignment	not modelled	99.4	10	**PDB header:**transcription **Chain:** H: **PDB Molecule:**199aa long hypothetical trp repressor binding **PDBTitle:** crystal structure of hypothetical trp repressor binding2 protein from sulfolobus tokodaii (st0872)
43	c3edoA_	Alignment	not modelled	99.1	10	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative trp repressor binding protein; **PDBTitle:** crystal structure of flavoprotein in complex with fmn2 (yp_193882.1) from lactobacillus acidophilus ncfm at 1.203 a resolution
44	c3rpeA_	Alignment	not modelled	98.8	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**modulator of drug activity b; **PDBTitle:** 1.1 angstrom crystal structure of putative modulator of drug activity2 (mdab) from yersinia pestis co92.
45	d1t5ba_	Alignment	not modelled	98.8	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
46	c3k1yE_	Alignment	not modelled	98.8	14	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**oxidoreductase; **PDBTitle:** x-ray structure of oxidoreductase from corynebacterium2 diphtheriae. orthorombic crystal form, northeast structural3 genomics consortium target cdr100d
47	c2q62A_	Alignment	not modelled	98.7	17	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**arsh; **PDBTitle:** crystal structure of arsh from sinorhizobium meliloti
48	d1sqsa_	Alignment	not modelled	98.6	8	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
49	c3lcmB_	Alignment	not modelled	98.6	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
50	d1rtta_	Alignment	not modelled	98.6	7	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
51	c2hpvA_	Alignment	not modelled	98.6	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase; **PDBTitle:** crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
52	d2qwxa1	Alignment	not modelled	98.5	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
53	d1t0ia_	Alignment	not modelled	98.5	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase

54	d1qrda_	Alignment	not modelled	98.5	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
55	c3f2vA_	Alignment	not modelled	98.5	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**general stress protein 14; **PDBTitle:** crystal structure of the general stress protein 142 (tde0354) in complex with fmn from treponema denticola,3 northeast structural genomics consortium target tdr58.
56	c3p0rA_	Alignment	not modelled	98.5	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**azoreductase; **PDBTitle:** crystal structure of azoreductase from bacillus anthracis str. sterne
57	d1nni1_	Alignment	not modelled	98.4	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
58	d2z98a1	Alignment	not modelled	98.3	7	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
59	c2v9cA_	Alignment	not modelled	98.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase 1; **PDBTitle:** x-ray crystallographic structure of a pseudomonas2 aeruginosa azoreductase in complex with methyl red.
60	c2vzhA_	Alignment	not modelled	98.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-dependent fmn reductase; **PDBTitle:** structures of nadh:fmn oxidoreductase (emob)-fmn complex
61	c2fzvC_	Alignment	not modelled	98.2	14	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative arsenical resistance protein; **PDBTitle:** crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
62	c3fvwA_	Alignment	not modelled	98.2	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative nad(p)h-dependent fmn reductase; **PDBTitle:** crystal structure of the q8dwd8_strmu protein from2 streptococcus mutans. northeast structural genomics3 consortium target smr99.
63	d1dxqa_	Alignment	not modelled	98.2	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
64	d2fzva1	Alignment	not modelled	98.1	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
65	c2amjD_	Alignment	not modelled	98.1	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**modulator of drug activity b; **PDBTitle:** crystal structure of modulator of drug activity b from escherichia2 coli o157:h7
66	d1rlia_	Alignment	not modelled	98.1	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein YwqN
67	d1d4aa_	Alignment	not modelled	97.9	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
68	c1tvmA_	Alignment	not modelled	94.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, galactitol-specific iib component; **PDBTitle:** nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
69	c3czcA_	Alignment	not modelled	92.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
70	d1ccwa_	Alignment	not modelled	92.2	15	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
71	c3ha2B_	Alignment	not modelled	92.0	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-quinone reductase; **PDBTitle:** crystal structure of protein (nadph-quinone reductase) from2 p.pentosaceus, northeast structural genomics consortium target ptr24a
72	c3s40C_	Alignment	not modelled	89.9	9	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
73	d1t0ba_	Alignment	not modelled	88.7	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**ThuA-like
74	c3nbmA_	Alignment	not modelled	86.8	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, lactose-specific iibc components; **PDBTitle:** the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
75	c1vkrA_	Alignment	not modelled	86.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannitol-specific pts system enzyme iiabc components; **PDBTitle:** structure of iib domain of the mannitol-specific permease enzyme ii
76	d1vkra_	Alignment	not modelled	86.2	13	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
77	d1iiba_	Alignment	not modelled	82.3	15	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
78	d3eega2	Alignment	not modelled	82.1	11	**Fold:**CbiG N-terminal domain-like **Superfamily:**CbiG N-terminal domain-like

						Family: CbiG N-terminal domain-like
79	d1t1va_	Alignment	not modelled	81.9	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**SH3BGR (SH3-binding, glutamic acid-rich protein-like)
80	c3eeqB_	Alignment	not modelled	81.1	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative cobalamin biosynthesis protein g **PDBTitle:** crystal structure of a putative cobalamin biosynthesis2 protein g homolog from sulfolobus solfataricus
81	d1iowa1	Alignment	not modelled	81.0	17	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
82	d1b4ub_	Alignment	not modelled	80.2	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
83	c3ia7A_	Alignment	not modelled	75.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
84	c3qyfA_	Alignment	not modelled	75.8	18	**PDB header:**antiviral protein **Chain:** A: **PDB Molecule:**crispr-associated protein; **PDBTitle:** crystal structure of the crispr-associated protein sso1393 from2 sulfolobus solfataricus
85	d1u0ta_	Alignment	not modelled	75.2	17	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
86	c2o7jA_	Alignment	not modelled	73.6	9	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**oligopeptide abc transporter, periplasmic **PDBTitle:** the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose
87	c2l2qA_	Alignment	not modelled	72.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, cellobiose-specific iib component (cela); **PDBTitle:** solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
88	c3eywA_	Alignment	not modelled	72.3	7	**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
89	d1w85b2	Alignment	not modelled	70.2	17	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
90	c2y7eA_	Alignment	not modelled	68.3	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-keto-5-aminohexanoate cleavage enzyme; **PDBTitle:** crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
91	c3t66A_	Alignment	not modelled	67.9	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nickel abc transporter (nickel-binding protein); **PDBTitle:** crystal structure of nickel abc transporter from bacillus halodurans
92	c3dhnA_	Alignment	not modelled	67.5	15	**PDB header:**isomerase, lyase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
93	d1qf6a1	Alignment	not modelled	67.2	14	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
94	c3gpiA_	Alignment	not modelled	64.4	39	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** structure of putative nad-dependent epimerase/dehydratase2 from methylobacillus flagellatus
95	d1fmfa_	Alignment	not modelled	64.1	16	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
96	c1ztyA_	Alignment	not modelled	62.4	14	**PDB header:**sugar binding protein, signaling protein **Chain:** A: **PDB Molecule:**chitin oligosaccharide binding protein; **PDBTitle:** crystal structure of the chitin oligasaccharide binding2 protein
97	c2r60A_	Alignment	not modelled	62.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
98	c2qx0A_	Alignment	not modelled	60.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**7,8-dihydro-6-hydroxymethylpterin- **PDBTitle:** crystal structure of yersinia pestis hppk (ternary complex)
99	d2p1ra1	Alignment	not modelled	60.2	13	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
100	c3etjB_	Alignment	not modelled	59.8	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure e. coli purk in complex with mg, adp, and2 pi
101	d1ydha_	Alignment	not modelled	59.4	21	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
102	d1gpua3	Alignment	not modelled	59.2	27	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like

						Family: Transketolase C-terminal domain-like
103	d2r4qa1	Alignment	not modelled	58.7	13	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
104	c2dlnA_	Alignment	not modelled	57.4	17	**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
105	c3c1oA_	Alignment	not modelled	57.3	19	**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
106	c2q1wC_	Alignment	not modelled	55.7	19	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
107	c3rqtA_	Alignment	not modelled	54.7	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** 1.5 angstrom crystal structure of the complex of ligand binding2 component of abc-type import system from staphylococcus aureus with3 nickel and two histidines
108	d2c42a3	Alignment	not modelled	53.9	18	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
109	d1vr5a1	Alignment	not modelled	53.7	5	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
110	d1hdoa_	Alignment	not modelled	52.4	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
111	c3d8tB_	Alignment	not modelled	52.1	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** thermus thermophilus uroporphyrinogen iii synthase
112	c2q4oA_	Alignment	not modelled	51.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein at2g37210/t2n18.3; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
113	d2q4oa1	Alignment	not modelled	51.8	18	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
114	c2grvC_	Alignment	not modelled	51.6	24	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**lpqw; **PDBTitle:** crystal structure of lpqw
115	c2ct6A_	Alignment	not modelled	50.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sh3 domain-binding glutamic acid-rich-like **PDBTitle:** solution structure of the sh3 domain-binding glutamic acid-2 rich-like protein 2
116	d2r8oa3	Alignment	not modelled	48.7	29	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
117	c3lvuB_	Alignment	not modelled	48.6	10	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, periplasmic substrate-binding protein; **PDBTitle:** crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
118	c2q4dB_	Alignment	not modelled	47.9	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lysine decarboxylase-like protein at5g11950; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
119	c3no5C_	Alignment	not modelled	47.1	12	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
120	d1f0ka_	Alignment	not modelled	46.6	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG