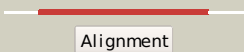

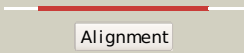
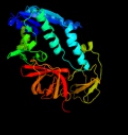
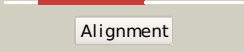

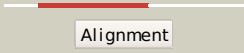



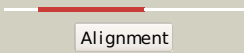

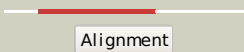

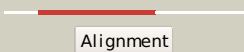

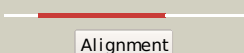



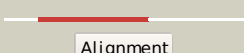










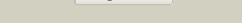



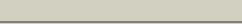
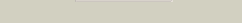
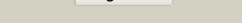
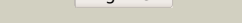
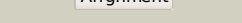
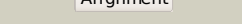
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hmaA_	 Alignment		100.0	60	PDB header: transferase Chain: A: PDB Molecule: probable trna (5-methylaminomethyl-2-thiouridylate)- PDBTitle: the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae
2	c2derA_	 Alignment		100.0	100	PDB header: transferase/rna Chain: A: PDB Molecule: trna-specific 2-thiouridylase mnma; PDBTitle: cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
3	c2vxoB_	 Alignment		100.0	21	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
4	c3q4gA_	 Alignment		99.9	25	PDB header: ligase Chain: A: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nad synthetase from vibrio cholerae
5	c2e21A_	 Alignment		99.9	17	PDB header: ligase Chain: A: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
6	c2nz2A_	 Alignment		99.9	18	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
7	d1wy5a1	 Alignment		99.9	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
8	c3a2kB_	 Alignment		99.9	17	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils complexed with trna
9	c3k32D_	 Alignment		99.9	18	PDB header: transferase Chain: D: PDB Molecule: uncharacterized protein mj0690; PDBTitle: the crystal structure of predicted subunit of trna2 methyltransferase from methanocaldococcus jannaschii dsm
10	c3fiuD_	 Alignment		99.9	24	PDB header: ligase Chain: D: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nmh synthetase from francisella tularensis
11	c2ywcC_	 Alignment		99.9	26	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp

12	c2c5sA_	Alignment		99.9	25	PDB header: rna-binding protein Chain: A: PDB Molecule: probable thiamine biosynthesis protein thii; PDBTitle: crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
13	d1gpmA1	Alignment		99.9	26	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
14	c1vl2C_	Alignment		99.9	20	PDB header: ligase Chain: C: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
15	d2c5sa1	Alignment		99.9	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ThiI-like
16	d1kqpa_	Alignment		99.9	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
17	c1gpmD_	Alignment		99.9	28	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
18	c3tqiB_	Alignment		99.9	28	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
19	c2dplA_	Alignment		99.9	28	PDB header: ligase Chain: A: PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit b; PDBTitle: crystal structure of the gmp synthase from pyrococcus horikoshii ot3
20	d1wxia1	Alignment		99.9	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
21	c1kh2D_	Alignment	not modelled	99.9	15	PDB header: ligase Chain: D: PDB Molecule: argininosuccinate synthetase; PDBTitle: crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
22	c3dplA_	Alignment	not modelled	99.9	24	PDB header: ligase Chain: A: PDB Molecule: nad+ synthetase; PDBTitle: crystal structure of nad+ synthetase from burkholderia pseudomallei
23	c1ni5A_	Alignment	not modelled	99.9	17	PDB header: cell cycle Chain: A: PDB Molecule: putative cell cycle protein mesj; PDBTitle: structure of the mesj pp-atpase from escherichia coli
24	c2e18B_	Alignment	not modelled	99.9	29	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of project ph0182 from pyrococcus horikoshii ot3
25	d1ni5a1	Alignment	not modelled	99.9	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
26	c3p52B_	Alignment	not modelled	99.9	22	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion
27	d1vl2a1	Alignment	not modelled	99.9	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
28	d1j20a1	Alignment	not modelled	99.9	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
						Fold: Adenine nucleotide alpha hydrolase-like

29	d1k92a1	Alignment	not modelled	99.9	11	Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
30	c3bl5E_	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: E: PDB Molecule: queuosine biosynthesis protein quec; PDBTitle: crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
31	c3uowB_	Alignment	not modelled	99.8	21	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
32	d1xnga1	Alignment	not modelled	99.8	26	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
33	c1k97A_	Alignment	not modelled	99.8	14	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
34	d2pg3a1	Alignment	not modelled	99.8	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
35	d1vbka1	Alignment	not modelled	99.8	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
36	c3n05B_	Alignment	not modelled	99.7	23	PDB header: ligase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
37	d1sura_	Alignment	not modelled	99.6	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
38	d1ru8a_	Alignment	not modelled	99.5	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
39	c2o8vA_	Alignment	not modelled	99.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: paps reductase in a covalent complex with thioredoxin c35a
40	c1vbka_	Alignment	not modelled	99.4	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1313; PDBTitle: crystal structure of ph1313 from pyrococcus horikoshii ot3
41	c3ilvA_	Alignment	not modelled	99.4	15	PDB header: ligase Chain: A: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
42	c3dlaD_	Alignment	not modelled	99.3	16	PDB header: ligase Chain: D: PDB Molecule: glutamine-dependent nad(+) synthetase; PDBTitle: x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
43	c2goyC_	Alignment	not modelled	99.3	13	PDB header: oxidoreductase Chain: C: PDB Molecule: adenosine phosphosulfate reductase; PDBTitle: crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
44	c1zunA_	Alignment	not modelled	99.3	13	PDB header: transferase Chain: A: PDB Molecule: sulfate adenyllyltransferase subunit 2; PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
45	d1zuna1	Alignment	not modelled	99.3	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
46	c2oq2B_	Alignment	not modelled	99.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
47	c1ct9D_	Alignment	not modelled	98.9	18	PDB header: ligase Chain: D: PDB Molecule: asparagine synthetase b; PDBTitle: crystal structure of asparagine synthetase b from2 escherichia coli
48	d1ct9a1	Alignment	not modelled	98.9	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
49	d1q15a1	Alignment	not modelled	98.8	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
50	d1jgtal	Alignment	not modelled	98.7	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
51	c1q15A_	Alignment	not modelled	98.6	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: cara; PDBTitle: carbapenam synthetase
52	d2d13a1	Alignment	not modelled	98.5	26	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
53	c3g59A_	Alignment	not modelled	98.5	13	PDB header: transferase Chain: A: PDB Molecule: fmn adenyllyltransferase; PDBTitle: crystal structure of candida glabrata fmn2 adenyllyltransferase in complex with atp
54	c1m1zB_	Alignment	not modelled	98.5	20	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactam synthetase; PDBTitle: beta-lactam synthetase apo enzyme
						PDB header: transferase

55	c2wsiA_	Alignment	not modelled	98.2	14	Chain: A: PDB Molecule: fad synthetase; PDBTitle: crystal structure of yeast fad synthetase (fad1) in complex2 with fad
56	c3o1lB_	Alignment	not modelled	96.2	14	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
57	c3n0vD_	Alignment	not modelled	96.0	18	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
58	c3louB_	Alignment	not modelled	94.3	16	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
59	c1m6vE_	Alignment	not modelled	93.1	15	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
60	c2ys6A_	Alignment	not modelled	93.0	17	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of gar synthetase from geobacillus kaustophilus
61	c1kk3A_	Alignment	not modelled	92.4	22	PDB header: translation Chain: A: PDB Molecule: eif2gamma; PDBTitle: structure of the wild-type large gamma subunit of2 initiation factor eif2 from pyrococcus abyssi complexed3 with gdp-mg2+
62	c1skqB_	Alignment	not modelled	92.3	19	PDB header: translation Chain: B: PDB Molecule: elongation factor 1-alpha; PDBTitle: the crystal structure of sulfolobus solfataricus elongation2 factor 1-alpha in complex with magnesium and gdp
63	c3obiC_	Alignment	not modelled	91.6	16	PDB header: hydrolase Chain: C: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
64	c3e1yG_	Alignment	not modelled	90.4	9	PDB header: translation Chain: G: PDB Molecule: eukaryotic peptide chain release factor gtp-binding subunit PDBTitle: crystal structure of human erf1/erf3 complex
65	d1d2ea2	Alignment	not modelled	89.8	16	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain Family: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
66	c2yyaB_	Alignment	not modelled	86.4	16	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus
67	c2bvnB_	Alignment	not modelled	86.3	21	PDB header: elongation factor Chain: B: PDB Molecule: elongation factor tu; PDBTitle: e. coli ef-tu:gdpnp in complex with the antibiotic2 enacyloxin iia
68	c3zquA_	Alignment	not modelled	84.9	21	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: structure of a probable aromatic acid decarboxylase
69	c3nrbD_	Alignment	not modelled	84.6	18	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru_2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
70	c3k5iB_	Alignment	not modelled	84.0	17	PDB header: lyase Chain: B: PDB Molecule: phosphoribosyl-aminimidazole carboxylase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-3 aminimidazole ribonucleotide
71	c3mcfF_	Alignment	not modelled	82.7	21	PDB header: oxidoreductase Chain: F: PDB Molecule: dipicolinate synthase, b chain; PDBTitle: crystal structure of the dipicolinate synthase chain b from2 bacillus cereus. northeast structural genomics consortium3 target bcr215.
72	c2gn9B_	Alignment	not modelled	81.8	8	PDB header: lyase Chain: B: PDB Molecule: udp-glcnac c6 dehydratase; PDBTitle: crystal structure of udp-glcnac inverting 4,6-dehydratase in complex2 with nadp and udp-glc
73	c3mmpC_	Alignment	not modelled	81.7	17	PDB header: transferase Chain: C: PDB Molecule: elongation factor tu 2, elongation factor ts; PDBTitle: structure of the qb replicase, an rna-dependent rna polymerase2 consisting of viral and host proteins
74	c2xd4A_	Alignment	not modelled	80.1	13	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycylamide2 ribonucleotide synthetase
75	c3lqkA_	Alignment	not modelled	77.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit b; PDBTitle: crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
76	c3fojA_	Alignment	not modelled	77.6	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of ssp1007 from staphylococcus2 saprophyticus subsp. saprophyticus. northeast structural3 genomics target syr101a.
77	c3p9xB_	Alignment	not modelled	77.2	15	PDB header: transferase Chain: B: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
						PDB header: structural genomics, unknown function

78	c1wv9B_	Alignment	not modelled	76.3	25	Chain: B: PDB Molecule: rhodanese homolog tt1651; PDBTitle: crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
79	c3agqA_	Alignment	not modelled	75.0	15	PDB header: translation,transferase Chain: A: PDB Molecule: elongation factor ts, elongation factor tu 1, linker, q PDBTitle: structure of viral polymerase form ii
80	dlfca2_	Alignment	not modelled	73.7	21	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain Family: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
81	c3enkB_	Alignment	not modelled	73.3	18	PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei
82	c2ejbA_	Alignment	not modelled	73.3	19	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
83	c1s0uA_	Alignment	not modelled	72.7	18	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 2 gamma subunit; PDBTitle: eif2gamma apo
84	dlqzua_	Alignment	not modelled	71.9	26	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
85	dlmeoa_	Alignment	not modelled	70.1	22	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
86	dlqtwa_	Alignment	not modelled	69.3	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Endonuclease IV
87	c2x7vA_	Alignment	not modelled	68.4	18	PDB header: hydrolase Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
88	c3g5jA_	Alignment	not modelled	67.8	24	PDB header: nucleotide binding protein Chain: A: PDB Molecule: putative atp/gtp binding protein; PDBTitle: crystal structure of n-terminal domain of putative atp/gtp binding2 protein from clostridium difficile 630
89	dlkk1a2_	Alignment	not modelled	65.5	36	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain Family: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
90	d2c78a2_	Alignment	not modelled	65.4	25	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain Family: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
91	c1mvlA_	Alignment	not modelled	65.2	19	PDB header: lyase Chain: A: PDB Molecule: ppc decarboxylase athal3a; PDBTitle: ppc decarboxylase mutant c175s
92	dlmvlA_	Alignment	not modelled	65.2	19	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
93	dlp3y1_	Alignment	not modelled	65.2	18	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
94	c2dzdB_	Alignment	not modelled	64.9	17	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase
95	c3mcaA_	Alignment	not modelled	63.9	12	PDB header: translation regulation/hydrolase Chain: A: PDB Molecule: elongation factor 1 alpha-like protein; PDBTitle: structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
96	c2hdnJ_	Alignment	not modelled	62.9	21	PDB header: translation Chain: J: PDB Molecule: elongation factor ef-tu; PDBTitle: trypsin-modified elongation factor tu in complex with2 tetracycline at 2.8 angstrom resolution
97	dlnbwa1_	Alignment	not modelled	61.7	28	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Swiveling domain of dehydratase reactivase alpha subunit Family: Swiveling domain of dehydratase reactivase alpha subunit
98	c3e20A_	Alignment	not modelled	60.6	16	PDB header: translation Chain: A: PDB Molecule: eukaryotic peptide chain release factor gtp-binding PDBTitle: crystal structure of s.pombe erf1/erf3 complex
99	c3ilmD_	Alignment	not modelled	60.4	26	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr3790 protein; PDBTitle: crystal structure of the alr3790 protein from anabaena sp. northeast2 structural genomics consortium target nsr437h
100	dlyt8a4_	Alignment	not modelled	59.8	31	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
101	dlxgka_	Alignment	not modelled	58.8	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
102	dlg5qa_	Alignment	not modelled	58.1	19	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD

						Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
103	d1qyca_	 Alignment	not modelled	57.8	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
104	d1sb8a_	 Alignment	not modelled	56.9	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
105	d1j8yf2	 Alignment	not modelled	56.4	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
106	c1qzuB_	 Alignment	not modelled	56.1	25	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein mds018; PDBTitle: crystal structure of human phosphopantothenoylcysteine decarboxylase
107	c3qjgD_	 Alignment	not modelled	55.5	20	PDB header: oxidoreductase Chain: D: PDB Molecule: epidermin biosynthesis protein epid; PDBTitle: epidermin biosynthesis protein epid from staphylococcus aureus
108	d1jnya2	 Alignment	not modelled	54.8	15	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: EF-Tu/eEF-1alpha/elf2-gamma C-terminal domain Family: EF-Tu/eEF-1alpha/elf2-gamma C-terminal domain
109	c2jtqA_	 Alignment	not modelled	54.7	23	PDB header: transferase Chain: A: PDB Molecule: phage shock protein e; PDBTitle: rhodanese from e.coli
110	c3nbmA_	 Alignment	not modelled	51.7	16	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.
111	d1gy8a_	 Alignment	not modelled	50.4	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
112	c2k0zA_	 Alignment	not modelled	50.0	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein hp1203; PDBTitle: solution nmr structure of protein hp1203 from helicobacter pylori2 26695. northeast structural genomics consortium (nesg) target3 pt1/ontario center for structural proteomics target hp1203
113	c2rh8A_	 Alignment	not modelled	49.1	20	PDB header: oxidoreductase Chain: A: PDB Molecule: anthocyanidin reductase; PDBTitle: structure of apo anthocyanidin reductase from vitis vinifera
114	c2kerA_	 Alignment	not modelled	48.7	23	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: alpha-amylase inhibitor z-2685; PDBTitle: alpha-amylase inhibitor parvulustat (z-2685) from2 streptomyces parvulus
115	c1t2aC_	 Alignment	not modelled	48.3	29	PDB header: structural genomics,lyase Chain: C: PDB Molecule: gdp-mannose 4,6 dehydratase; PDBTitle: crystal structure of human gdp-d-mannose 4,6-dehydratase
116	d1t2aa_	 Alignment	not modelled	48.3	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
117	c3lp8A_	 Alignment	not modelled	48.2	14	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
118	d1pjqa3	 Alignment	not modelled	48.2	47	Fold: Siroheme synthase middle domains-like Superfamily: Siroheme synthase middle domains-like Family: Siroheme synthase middle domains-like
119	d1rz3a_	 Alignment	not modelled	48.1	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
120	c3opyE_	 Alignment	not modelled	47.3	25	PDB header: transferase Chain: E: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state