Phyre2

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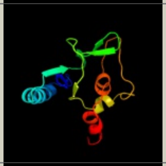
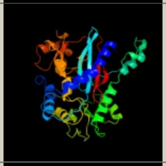
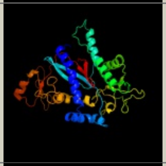
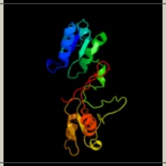
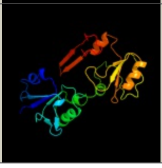
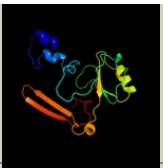
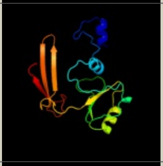
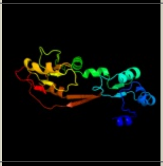
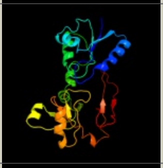
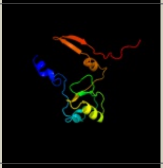
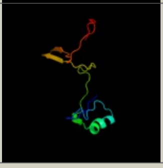
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ioaA_	Alignment		100.0	28	**PDB header:**ligase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional glutathionylspermidine **PDBTitle:** e. coli bifunctional glutathionylspermidine2 synthetase/amidase incomplex with mg2+ and adp and3 phosphinate inhibitor
2	c2vpmB_	Alignment		100.0	29	**PDB header:**ligase **Chain:** B: **PDB Molecule:**trypanothione synthetase; **PDBTitle:** trypanothione synthetase
3	d2io8a3	Alignment		100.0	33	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Glutathionylspermidine synthase ATP-binding domain-like
4	c3n6xA_	Alignment		100.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative glutathionylspermidine synthase; **PDBTitle:** crystal structure of a putative glutathionylspermidine synthase2 (mfla_0391) from methylobacillus flagellatus kt at 2.35 a resolution
5	d2io8a1	Alignment		99.8	20	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Glutathionylspermidine synthase substrate-binding domain-like
6	c2hgsA_	Alignment		99.5	15	**PDB header:**amine/carboxylate ligase **Chain:** A: **PDB Molecule:**protein (glutathione synthetase); **PDBTitle:** human glutathione synthetase
7	c3kalB_	Alignment		99.5	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**homoglutathione synthetase; **PDBTitle:** structure of homoglutathione synthetase from glycine max in2 closed conformation with homoglutathione, adp, a sulfate3 ion, and three magnesium ions bound
8	c1m0tB_	Alignment		99.3	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**glutathione synthetase; **PDBTitle:** yeast glutathione synthase
9	c2wyoC_	Alignment		99.3	17	**PDB header:**ligase **Chain:** C: **PDB Molecule:**glutathione synthetase; **PDBTitle:** trypanosoma brucei glutathione synthetase
10	c1gshA_	Alignment		99.1	14	**PDB header:**glutathione biosynthesis ligase **Chain:** A: **PDB Molecule:**glutathione biosynthetic ligase; **PDBTitle:** structure of escherichia coli glutathione synthetase at ph 7.5
11	c2p0aA_	Alignment		98.5	13	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**synapsin-3; **PDBTitle:** the crystal structure of human synapsin iii (syn3) in complex with2 amppnp

12	c1i7nA_	Alignment		98.3	13	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**synapsin ii; **PDBTitle:** crystal structure analysis of the c domain of synapsin ii2 from rat brain
13	c1pk8D_	Alignment		98.2	13	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**rat synapsin i; **PDBTitle:** crystal structure of rat synapsin i c domain complexed to2 ca.atp
14	c1uc8B_	Alignment		98.2	13	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**lysine biosynthesis enzyme; **PDBTitle:** crystal structure of a lysine biosynthesis enzyme, lysx,2 from thermus thermophilus hb8
15	d2hgsa4	Alignment		98.0	16	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Eukaryotic glutathione synthetase ATP-binding domain
16	c2qb5B_	Alignment		98.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**inositol-tetrakisphosphate 1-kinase; **PDBTitle:** crystal structure of human inositol 1,3,4-trisphosphate 5/6-kinase2 (itpk1) in complex with adp and mn2+
17	d1pk8a2	Alignment		97.9	8	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Synapsin C-terminal domain
18	c2dlnA_	Alignment		97.6	12	**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
19	c3ln6A_	Alignment		97.4	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutathione biosynthesis bifunctional protein gshab; **PDBTitle:** crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
20	c3ln7A_	Alignment		97.4	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutathione biosynthesis bifunctional protein gshab; **PDBTitle:** crystal structure of a bifunctional glutathione synthetase from2 pasteurella multocida
21	d1i7na2	Alignment	not modelled	97.3	10	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Synapsin C-terminal domain
22	c3t9aA_	Alignment	not modelled	97.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**inositol pyrophosphate kinase; **PDBTitle:** crystal structure of the catalytic domain of human diphosphoinositol2 pentakisphosphate kinase 2 (ppip5k2) in complex with amppnp at ph 7.0
23	c1kjjA_	Alignment	not modelled	97.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
24	c2yyaB_	Alignment	not modelled	97.1	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of gar synthetase from aquifex aeolicus
25	c2xd4A_	Alignment	not modelled	97.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
26	c3tqtB_	Alignment	not modelled	97.0	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** structure of the d-alanine-d-alanine ligase from coxiella burnetii
27	c3i12A_	Alignment	not modelled	97.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-d-alanine ligase a; **PDBTitle:** the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
						Fold:ATP-grasp

28	d1gsaa2	Alignment	not modelled	96.8	18	**Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
29	d1m0wa2	Alignment	not modelled	96.7	17	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Eukaryotic glutathione synthetase ATP-binding domain
30	c1e4eB_	Alignment	not modelled	96.7	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**vancomycin/teicoplanin a-type resistance protein vana; **PDBTitle:** d-alanyl-d-lacate ligase
31	c2pvpB_	Alignment	not modelled	96.7	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine-d-alanine ligase; **PDBTitle:** crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
32	c3lp8A_	Alignment	not modelled	96.4	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine-glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
33	c3lwbA_	Alignment	not modelled	96.3	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of apo d-alanine:d-alanine ligase (ddl) from2 mycobacterium tuberculosis
34	c3bg5C_	Alignment	not modelled	96.1	16	**PDB header:**ligase **Chain:** C: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of staphylococcus aureus pyruvate2 carboxylase
35	c2hjwA_	Alignment	not modelled	95.9	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** crystal structure of the bc domain of acc2
36	d1gsaa1	Alignment	not modelled	95.8	9	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Prokaryotic glutathione synthetase, N-terminal domain
37	c2ip4A_	Alignment	not modelled	95.8	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
38	c2zdqA_	Alignment	not modelled	95.7	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of d-alanine:d-alanine ligase with atp2 and d-alanine:d-alanine from thermus thermophius hb8
39	c1vkzA_	Alignment	not modelled	95.5	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution
40	c1z2pX_	Alignment	not modelled	95.5	15	**PDB header:**transferase **Chain:** X: **PDB Molecule:**inositol 1,3,4-trisphosphate 5/6-kinase; **PDBTitle:** inositol 1,3,4-trisphosphate 5/6-kinase in complex with mg2+/amp-2 pcp/ins(1,3,4)p3
41	c3tinA_	Alignment	not modelled	95.4	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ttl protein; **PDBTitle:** tubulin tyrosine ligase
42	c2dzdB_	Alignment	not modelled	95.2	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase
43	c1ehiB_	Alignment	not modelled	95.2	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine:d-lactate ligase; **PDBTitle:** d-alanine:d-lactate ligase (lmddl2) of vancomycin-resistant2 leuconostoc mesenteroides
44	c1w96B_	Alignment	not modelled	95.1	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase; **PDBTitle:** crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
45	c3g8cB_	Alignment	not modelled	95.0	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal stucture of biotin carboxylase in complex with2 biotin, bicarbonate, adp and mg ion
46	c3ouzA_	Alignment	not modelled	94.9	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
47	c2cqyA_	Alignment	not modelled	94.8	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**propionyl-coa carboxylase alpha chain, **PDBTitle:** solution structure of b domain from human propionyl-coa2 carboxylase alpha subunit
48	d1uc8a2	Alignment	not modelled	94.4	15	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Lysine biosynthesis enzyme LysX ATP-binding domain
49	c3df7A_	Alignment	not modelled	94.4	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative atp-grasp superfamily protein; **PDBTitle:** crystal structure of a putative atp-grasp superfamily2 protein from archaeoglobus fulgidus
50	c1ulzA_	Alignment	not modelled	94.3	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase n-terminal domain; **PDBTitle:** crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
51	c2vpqA_	Alignment	not modelled	94.0	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
52	c3orqA_	Alignment	not modelled	93.9	9	**PDB header:**ligase,biosynthetic protein **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide synthetase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
53	c3gidB_	Alignment	not modelled	93.9	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** the biotin carboxylase (bc) domain of human acetyl-coa2 carboxylase 2 (acc2) in complex with soraphen a

54	c3uvzB_	Alignment	not modelled	93.8	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
55	c3k5iB_	Alignment	not modelled	93.7	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosyl-aminoimidazole carboxylase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-3 aminoimadazole ribonucleotide
56	d1w96a3	Alignment	not modelled	92.9	10	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
57	d1e4ea2	Alignment	not modelled	91.8	23	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
58	c2i80B_	Alignment	not modelled	91.1	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine-d-alanine ligase; **PDBTitle:** allosteric inhibition of staphylococcus aureus d-alanine:d-alanine2 ligase revealed by crystallographic studies
59	c3se7A_	Alignment	not modelled	90.9	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**vana; **PDBTitle:** ancient vana
60	d1a9xa5	Alignment	not modelled	90.8	12	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
61	d1gsoa3	Alignment	not modelled	90.4	32	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
62	c2ys6A_	Alignment	not modelled	90.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide synthetase; **PDBTitle:** crystal structure of gar synthetase from geobacillus kaustophilus
63	d2r85a2	Alignment	not modelled	89.4	10	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**PurP ATP-binding domain-like
64	d1ehia2	Alignment	not modelled	88.8	33	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
65	c3e5nA_	Alignment	not modelled	88.8	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-d-alanine ligase a; **PDBTitle:** crystal strucutre of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
66	d2r7ka2	Alignment	not modelled	88.7	15	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**PurP ATP-binding domain-like
67	d1vkza3	Alignment	not modelled	87.8	14	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
68	d1iowa2	Alignment	not modelled	87.7	36	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
69	c3k3pA_	Alignment	not modelled	86.8	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of the apo form of d-alanine:d-alanine ligase (ddl)2 from streptococcus mutans
70	c1m6vE_	Alignment	not modelled	85.5	14	**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
71	c3q2oB_	Alignment	not modelled	83.7	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
72	c3r23B_	Alignment	not modelled	83.4	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
73	d1kjqa3	Alignment	not modelled	79.0	15	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
74	c1gsoA_	Alignment	not modelled	75.7	32	**PDB header:**ligase **Chain:** A: **PDB Molecule:**protein (glycinamide ribonucleotide synthetase); **PDBTitle:** glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
75	c2z04A_	Alignment	not modelled	75.5	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
76	c3u9sE_	Alignment	not modelled	74.4	18	**PDB header:**ligase **Chain:** E: **PDB Molecule:**methylcrotonyl-coa carboxylase, alpha-subunit; **PDBTitle:** crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
77	d3etja3	Alignment	not modelled	73.9	7	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
78	d1ulza3	Alignment	not modelled	72.6	10	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like

						Family:BC ATP-binding domain-like
79	c2r85B_	Alignment	not modelled	72.0	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**purp protein pf1517; **PDBTitle:** crystal structure of purp from pyrococcus furiosus complexed with amp
80	c3n6rK_	Alignment	not modelled	70.9	23	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
81	c2pn1A_	Alignment	not modelled	70.1	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoylphosphate synthase large subunit; **PDBTitle:** crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from exiguobacterium sp. 255-15 at 2.00 a3 resolution
82	c2dwcB_	Alignment	not modelled	67.0	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**433aa long hypothetical phosphoribosylglycinamide formyl **PDBTitle:** crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
83	c2qk4A_	Alignment	not modelled	63.0	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trifunctional purine biosynthetic protein adenosine-3; **PDBTitle:** human glycinamide ribonucleotide synthetase
84	c3etjB_	Alignment	not modelled	59.0	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure e. coli purk in complex with mg, adp, and2 pi
85	c2gpwC_	Alignment	not modelled	56.7	14	**PDB header:**ligase **Chain:** C: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.
86	d2j9ga3	Alignment	not modelled	55.5	9	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
87	d1a9xa6	Alignment	not modelled	47.5	15	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
88	c3k1tA_	Alignment	not modelled	44.2	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase gsha; **PDBTitle:** crystal structure of putative gamma-glutamylcysteine synthetase2 (yp_546622.1) from methylobacillus flagellatus kt at 1.90 a3 resolution
89	c3l4eA_	Alignment	not modelled	27.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized peptidase lmo0363; **PDBTitle:** 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
90	c3oetF_	Alignment	not modelled	23.7	25	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** d-erythronate-4-phosphate dehydrogenase complexed with nad
91	c3d3kD_	Alignment	not modelled	22.1	7	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
92	d1v65a_	Alignment	not modelled	20.5	14	**Fold:**KRAB domain (Kruppel-associated box) **Superfamily:**KRAB domain (Kruppel-associated box) **Family:**KRAB domain (Kruppel-associated box)
93	c2o4cB_	Alignment	not modelled	20.3	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
94	d2q22a1	Alignment	not modelled	18.1	11	**Fold:**Ava3019-like **Superfamily:**Ava3019-like **Family:**Ava3019-like
95	c3e90C_	Alignment	not modelled	17.6	33	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ns2b cofactor; **PDBTitle:** west nile virus ns2b-ns3protease in complexed with2 inhibitor naph-kkr-h
96	d2oo3a1	Alignment	not modelled	17.4	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**LPG1296-like
97	c2ijoA_	Alignment	not modelled	16.4	33	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**polyprotein; **PDBTitle:** crystal structure of the west nile virus ns2b-ns3 protease2 complexed with bovine pancreatic trypsin inhibitor
98	c1f13A_	Alignment	not modelled	15.5	14	**PDB header:**coagulation factor **Chain:** A: **PDB Molecule:**cellular coagulation factor xiii zymogen; **PDBTitle:** recombinant human cellular coagulation factor xiii
99	c2r7mA_	Alignment	not modelled	14.0	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**5-formaminoimidazole-4-carboxamide-1-(beta)-d- **PDBTitle:** crystal structure of faicar synthetase (purp) from m.2 jannaschii complexed with amp