





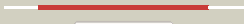















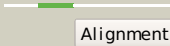
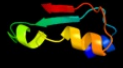
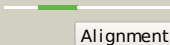

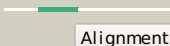

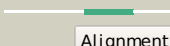




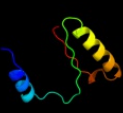

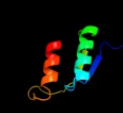




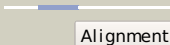

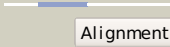
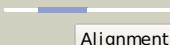
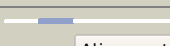






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yoeA	 Alignment		100.0	99	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein ybek; PDBTitle: crystal structure of a the e. coli pyrimidine nucleoside hydrolase2 ybek with bound ribose
2	d2masa	 Alignment		100.0	36	Fold: Nucleoside hydrolase Superfamily: Nucleoside hydrolase Family: Nucleoside hydrolase
3	c3b9xA	 Alignment		100.0	39	PDB header: hydrolase Chain: A: PDB Molecule: pyrimidine-specific ribonucleoside hydrolase rihb; PDBTitle: crystal structure of the e. coli pyrimidine nucleoside hydrolase yeik2 in complex with inosine
4	d1q8fa	 Alignment		100.0	39	Fold: Nucleoside hydrolase Superfamily: Nucleoside hydrolase Family: Nucleoside hydrolase
5	d1ezra	 Alignment		100.0	36	Fold: Nucleoside hydrolase Superfamily: Nucleoside hydrolase Family: Nucleoside hydrolase
6	c3fz0C	 Alignment		100.0	32	PDB header: hydrolase Chain: C: PDB Molecule: nucleoside hydrolase, putative; PDBTitle: inosine-guanosine nucleoside hydrolase (ig-nh)
7	c2c40B	 Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: inosine-uridine preferring nucleoside hydrolase family PDBTitle: crystal structure of inosine-uridine preferring nucleoside2 hydrolase from bacillus anthracis at 2.2a resolution
8	d1kica	 Alignment		100.0	24	Fold: Nucleoside hydrolase Superfamily: Nucleoside hydrolase Family: Nucleoside hydrolase
9	c2yhga	 Alignment		99.5	16	PDB header: hydrolase Chain: A: PDB Molecule: cellulose-binding protein; PDBTitle: ab initio phasing of a nucleoside hydrolase-related hypothetical2 protein from saccharophagus degradans that is associated with3 carbohydrate metabolism
10	d1gpm1	 Alignment		80.0	9	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
11	d7reqa2	 Alignment		64.1	19	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain

12	d1ccwa_	 Alignment		58.6	15	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
13	c2dplA_	 Alignment		52.7	16	PDB header: ligase Chain: A: PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit b; PDBTitle: crystal structure of the gmp synthase from pyrococcus horikoshii ot3
14	d2c5sa1	 Alignment		44.1	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
15	c2zyiB_	 Alignment		40.9	24	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
16	c1y80A_	 Alignment		37.2	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iiii)-binding protein from2 moorella thermoacetica
17	d1o5za2	 Alignment		32.0	16	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: Folylpolyglutamate synthetase
18	c3p52B_	 Alignment		31.9	21	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
19	c3tqiB_	 Alignment		31.1	11	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
20	d1o7ja_	 Alignment		28.6	23	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
21	c3r79B_	 Alignment	not modelled	28.5	14	PDB header: structure genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from agrobacterium2 tumefaciens
22	d1o94c_	 Alignment	not modelled	23.8	28	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
23	c3p2kA_	 Alignment	not modelled	22.5	11	PDB header: transferase Chain: A: PDB Molecule: 16s rrna methylase; PDBTitle: structure of an antibiotic related methyltransferase
24	d1nnsa_	 Alignment	not modelled	21.7	13	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
25	c2vosA_	 Alignment	not modelled	20.5	28	PDB header: ligase Chain: A: PDB Molecule: folylpolyglutamate synthase protein folc; PDBTitle: mycobacterium tuberculosis folylpolyglutamate synthase2 complexed with adp
26	c3fiuD_	 Alignment	not modelled	19.3	24	PDB header: ligase Chain: D: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nmh synthetase from francisella tularensis
27	d1wsaa_	 Alignment	not modelled	18.4	18	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
28	d4pgaa_	 Alignment	not modelled	18.0	19	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
29	d1j20a1	 Alignment	not modelled	18.0	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like

						Family:N-type ATP pyrophosphatases
30	c2derA	Alignment	not modelled	17.6	14	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
31	c3ezxA	Alignment	not modelled	17.3	19	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
32	c2hmaA	Alignment	not modelled	17.2	15	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 trnu from streptococcus pneumoniae
33	c3sz8D	Alignment	not modelled	17.1	12	PDB header: transferase Chain: D: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase 2; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
34	c1w78A	Alignment	not modelled	17.1	17	PDB header: synthase Chain: A: PDB Molecule: folc bifunctional protein; PDBTitle: e.coli folc in complex with dhpp and adp
35	d1lw7a1	Alignment	not modelled	15.6	8	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenyllyltransferase
36	c2d6fA	Alignment	not modelled	15.5	22	PDB header: ligase/rna Chain: A: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
37	d2ocda1	Alignment	not modelled	15.1	18	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
38	c1gpmD	Alignment	not modelled	15.1	9	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
39	d1tcaa	Alignment	not modelled	15.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
40	c3cseA	Alignment	not modelled	14.9	33	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: candida glabrata dihydrofolate reductase complexed with2 nadph and 2,4-diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-3-ynyl)-6-ethylpyrimidine (ucp120b)
41	d2gc6a2	Alignment	not modelled	14.4	17	Fold: Ribokinaselike Superfamily: MurD-like peptide ligases, catalytic domain Family: Folylpolyglutamate synthetase
42	d1ik6a2	Alignment	not modelled	14.2	32	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
43	d2vk9a1	Alignment	not modelled	13.6	15	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Glycosylating toxin catalytic domain-like
44	d1agxa	Alignment	not modelled	11.6	12	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
45	d3bula2	Alignment	not modelled	11.5	16	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
46	c1yunB	Alignment	not modelled	10.8	33	PDB header: transferase Chain: B: PDB Molecule: probable nicotinate-nucleotide PDBTitle: crystal structure of nicotinic acid mononucleotide2 adenyllyltransferase from pseudomonas aeruginosa
47	d3cx5a2	Alignment	not modelled	9.7	15	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: MPP-like
48	d1xnga1	Alignment	not modelled	9.2	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
49	c1wnfA	Alignment	not modelled	8.9	18	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of ph0066 from pyrococcus horikoshii
50	d1umdb2	Alignment	not modelled	8.6	16	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
51	c1o5zA	Alignment	not modelled	8.5	18	PDB header: ligase Chain: A: PDB Molecule: folylpolyglutamate synthase/dihydrofolate synthase; PDBTitle: crystal structure of folylpolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution
52	c3rg9A	Alignment	not modelled	8.4	30	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase; PDBTitle: trypanosoma brucei dihydrofolate reductase (tdhfr) in complex with2 wr99210
53	d2bfdb2	Alignment	not modelled	8.3	32	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
						PDB header: plp-binding protein

54	c1w8gA_	Alignment	not modelled	8.1	15	Chain: A: PDB Molecule: hypothetical upf0001 protein yggs; PDBTitle: crystal structure of e. coli k-12 yggs
55	c3si9B_	Alignment	not modelled	7.8	14	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
56	c1lw7A_	Alignment	not modelled	7.5	8	PDB header: transferase Chain: A: PDB Molecule: transcriptional regulator nadr; PDBTitle: nadr protein from haemophilus influenzae
57	c3dlaD_	Alignment	not modelled	7.4	21	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
58	c3ghfA_	Alignment	not modelled	7.3	9	PDB header: cell cycle Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the septum site-determining protein2 minc from salmonella typhimurium
59	d1qs0b2	Alignment	not modelled	7.3	21	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
60	d2bvla1	Alignment	not modelled	7.3	23	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Glycosylating toxin catalytic domain-like
61	c3uowB_	Alignment	not modelled	6.9	15	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
62	d1kqpa_	Alignment	not modelled	6.9	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
63	d1efvb_	Alignment	not modelled	6.9	31	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
64	c1jpkA_	Alignment	not modelled	6.8	15	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
65	c3nxE_	Alignment	not modelled	6.8	21	PDB header: hydrolase Chain: E: PDB Molecule: cytoplasmic l-asparaginase; PDBTitle: crystal structure of probable cytoplasmic l-asparaginase from2 campylobacter jejuni
66	d1xrsb1	Alignment	not modelled	6.8	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
67	d2d6fa2	Alignment	not modelled	6.8	21	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
68	d1fmfa_	Alignment	not modelled	6.7	15	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
69	d2ozlb2	Alignment	not modelled	6.7	21	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
70	c2wltA_	Alignment	not modelled	6.6	16	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: the crystal structure of helicobacter pylori l-asparaginase2 at 1.4 a resolution
71	c1xtyD_	Alignment	not modelled	6.5	25	PDB header: hydrolase Chain: D: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of sulfobolus solfataricus peptidyl-trna2 hydrolase
72	d1ct5a_	Alignment	not modelled	6.5	10	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: "Hypothetical" protein ybl036c
73	d1q7sa_	Alignment	not modelled	6.3	27	Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
74	d1urha2	Alignment	not modelled	6.1	25	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
75	c2dy3B_	Alignment	not modelled	6.0	16	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from corynebacterium glutamicum
76	d1kama_	Alignment	not modelled	6.0	33	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Adenylyltransferase
77	d5mdha1	Alignment	not modelled	6.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
78	c3jz0B_	Alignment	not modelled	6.0	24	PDB header: transferase/antibiotic Chain: B: PDB Molecule: lincosamide nucleotidyltransferase; PDBTitle: linb complexed with clindamycin and ampcpp
79	c1kh2D_	Alignment	not modelled	5.9	24	PDB header: ligase Chain: D: PDB Molecule: argininosuccinate synthetase; PDBTitle: crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
80	c2d3kA_	Alignment	not modelled	5.9	36	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: structural study on project id ph1539 from pyrococcus2

					horikoshii ot3
81	d1ffgb_	Alignment	not modelled	5.9	31 Fold: Ferredoxin-like Superfamily: CheY-binding domain of CheA Family: CheY-binding domain of CheA
82	c2zv3E_	Alignment	not modelled	5.8	33 PDB header: hydrolase Chain: E: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of project mj0051 from methanocaldococcus2 jannaschii dsm 2661
83	c2gc6A_	Alignment	not modelled	5.8	17 PDB header: ligase Chain: A: PDB Molecule: folylpolyglutamate synthase; PDBTitle: s73a mutant of l. casei fpgs
84	c3f0uX_	Alignment	not modelled	5.8	19 PDB header: oxidoreductase Chain: X: PDB Molecule: trimethoprim-sensitive dihydrofolate reductase; PDBTitle: staphylococcus aureus f98y mutant dihydrofolate reductase2 complexed with nadph and 2,4-diamino-5-[3-(3-methoxy-5-3 phenylphenyl)but-1-ynyl]-6-methylpyrimidine
85	d1vbka1	Alignment	not modelled	5.7	15 Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
86	d3erja1	Alignment	not modelled	5.7	33 Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
87	c1xrsB_	Alignment	not modelled	5.6	12 PDB header: isomerase Chain: B: PDB Molecule: d-lysine 5,6-aminomutase beta subunit; PDBTitle: crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
88	c2ywcC_	Alignment	not modelled	5.6	20 PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
89	d2nu7b1	Alignment	not modelled	5.6	11 Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
90	d1u5sb1	Alignment	not modelled	5.6	18 Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
91	d1hioa_	Alignment	not modelled	5.6	18 Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
92	c1a0oH_	Alignment	not modelled	5.5	31 PDB header: chemotaxis Chain: H: PDB Molecule: chea; PDBTitle: chey-binding domain of chea in complex with chey
93	d2pg3a1	Alignment	not modelled	5.5	19 Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
94	c3ilxA_	Alignment	not modelled	5.5	15 PDB header: isomerase Chain: A: PDB Molecule: predicted amino acid aldolase or racemase; PDBTitle: crystal structure of an ala racemase-like protein (i11761) from2 idiomarina loihiensis at 1.50 a resolution
95	d1t1ra2	Alignment	not modelled	5.4	17 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
96	d2b3ya2	Alignment	not modelled	5.4	23 Fold: Aconitase iron-sulfur domain Superfamily: Aconitase iron-sulfur domain Family: Aconitase iron-sulfur domain
97	d1s8na_	Alignment	not modelled	5.3	3 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
98	d1kmva_	Alignment	not modelled	5.3	43 Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
99	d1qf5a_	Alignment	not modelled	5.2	19 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like