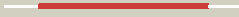
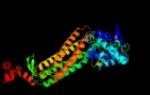
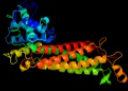
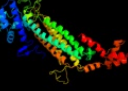
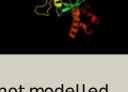
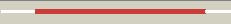
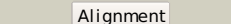
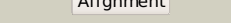
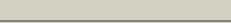
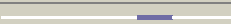
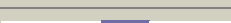
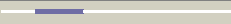
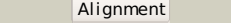
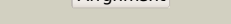
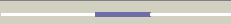
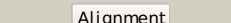
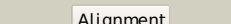


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dljswa_	 Alignment		100.0	100	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
2	dlj3ua_	 Alignment		100.0	50	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
3	dlvdka_	 Alignment		100.0	42	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
4	c1yfmA_	 Alignment		100.0	38	PDB header: lyase Chain: A: PDB Molecule: fumarase; PDBTitle: recombinant yeast fumarase
5	d1yfma_	 Alignment		100.0	38	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
6	d1fuoa_	 Alignment		100.0	40	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
7	c3no9C_	 Alignment		100.0	40	PDB header: lyase Chain: C: PDB Molecule: fumarate hydratase class ii; PDBTitle: crystal structure of apo fumarate hydratase from mycobacterium2 tuberculosis
8	c3ocfB_	 Alignment		100.0	52	PDB header: lyase Chain: B: PDB Molecule: fumarate lyase:delta crystallin; PDBTitle: crystal structure of fumarate lyase:delta crystallin from brucella2 melitensis in native form
9	c3e04C_	 Alignment		100.0	40	PDB header: lyase Chain: C: PDB Molecule: fumarate hydratase; PDBTitle: crystal structure of human fumarate hydratase
10	dljswc_	 Alignment		100.0	100	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
11	c3gtdB_	 Alignment		100.0	37	PDB header: lyase Chain: B: PDB Molecule: fumarate hydratase class ii; PDBTitle: 2.4 angstrom crystal structure of fumarate hydratase from rickettsia2 prowazekii

12	c3r6yG_	Alignment		100.0	52	PDB header: lyase Chain: G: PDB Molecule: aspartase; PDBTitle: crystal structure of chymotrypsin-treated aspartase from bacillus sp.2 ym55-1
13	c2pfmA_	Alignment		100.0	19	PDB header: lyase Chain: A: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase (purb) from bacillus2 anthracis
14	d1re5a_	Alignment		100.0	21	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
15	d1c3ca_	Alignment		100.0	19	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
16	d1q5na_	Alignment		100.0	18	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
17	d1tj7a_	Alignment		100.0	19	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
18	c2e9fC_	Alignment		100.0	21	PDB header: lyase Chain: C: PDB Molecule: argininosuccinate lyase; PDBTitle: crystal structure of t.th.hb8 argininosuccinate lyase complexed with2 l-arginine
19	d1i0aa_	Alignment		100.0	18	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
20	d1hy0a_	Alignment		100.0	19	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
21	d1k62a_	Alignment	not modelled	100.0	18	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
22	d1tjva_	Alignment	not modelled	100.0	19	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
23	c3c8tA_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: fumarate lyase; PDBTitle: crystal structure of fumarate lyase from mesorhizobium sp. bnc1
24	c2vd6B_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: B: PDB Molecule: adenylosuccinate lyase; PDBTitle: human adenylosuccinate lyase in complex with its substrate n6-(1,2-dicarboxyethyl)-amp, and its products amp and3 fumarate.
25	d1dofa_	Alignment	not modelled	100.0	17	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
26	c1visA_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: A: PDB Molecule: adenylosuccinate lyase; PDBTitle: structural genomics of caenorhabditis elegans: adenylosuccinate lyase
27	c3bhgA_	Alignment	not modelled	100.0	12	PDB header: lyase Chain: A: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase from legionella2 pneumophila
28	c2ptsA_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: A: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of wild type escherichia coli adenylosuccinate lyase

29	c2qgaC	 Alignment	not modelled	100.0	17	PDB header: lyase Chain: C: PDB Molecule: adenylosuccinate lyase; PDBTitle: plasmodium vivax adenylosuccinate lyase pv003765 with amp bound
30	c2fenA	 Alignment	not modelled	100.0	15	PDB header: isomerase Chain: A: PDB Molecule: 3-carboxy-cis,cis-muconate lactonizing enzyme; PDBTitle: 3-carboxy-cis,cis-muconate lactonizing enzyme from agrobacterium2 radiobacter s2
31	d1f1oa	 Alignment	not modelled	100.0	15	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
32	c2xgvA	 Alignment	not modelled	31.8	13	PDB header: viral protein Chain: A: PDB Molecule: psiv capsid n-terminal domain; PDBTitle: structure of the n-terminal domain of capsid protein from2 rabbit endogenous lentivirus (relik)
33	d2ce7a1	 Alignment	not modelled	27.0	18	Fold: FtsH protease domain-like Superfamily: FtsH protease domain-like Family: FtsH protease domain-like
34	d2di4a1	 Alignment	not modelled	26.1	19	Fold: FtsH protease domain-like Superfamily: FtsH protease domain-like Family: FtsH protease domain-like
35	c2di4B	 Alignment	not modelled	21.1	21	PDB header: hydrolase Chain: B: PDB Molecule: cell division protein ftsH homolog; PDBTitle: crystal structure of the ftsH protease domain
36	c3lq9B	 Alignment	not modelled	20.9	26	PDB header: signaling protein Chain: B: PDB Molecule: dna-damage-inducible transcript 4 protein; PDBTitle: crystal strucure of human redd1, a hypoxia-induced regulator2 of mtor
37	d1lbua1	 Alignment	not modelled	20.3	26	Fold: PGBD-like Superfamily: PGBD-like Family: Peptidoglycan binding domain, PGBD
38	d2dy1a3	 Alignment	not modelled	19.5	15	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
39	c2ctoA	 Alignment	not modelled	15.4	42	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: novel protein; PDBTitle: solution structure of the hmg box like domain from human2 hypothetical protein flj14904
40	c3fbtB	 Alignment	not modelled	14.8	17	PDB header: oxidoreductase, lyase Chain: B: PDB Molecule: chorismate mutase and shikimate 5-dehydrogenase PDBTitle: crystal structure of a chorismate mutase/shikimate 5-2 dehydrogenase fusion protein from clostridium3 acetobutylicum
41	c3bbnC	 Alignment	not modelled	14.3	50	PDB header: ribosome Chain: C: PDB Molecule: ribosomal protein s3; PDBTitle: homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
42	c1dipA	 Alignment	not modelled	13.8	22	PDB header: acetylation Chain: A: PDB Molecule: delta-sleep-inducing peptide immunoreactive PDBTitle: the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
43	c3hzaA	 Alignment	not modelled	12.5	11	PDB header: transferase Chain: A: PDB Molecule: monofunctional glycosyltransferase; PDBTitle: s. aureus monofunctional glycosyltransferase (mtga)in complex with2 moenomycin
44	d2bv3a3	 Alignment	not modelled	12.5	20	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Translational machinery components
45	d1h8ba	 Alignment	not modelled	11.9	13	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins
46	d1nvt2	 Alignment	not modelled	11.7	13	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
47	c3m1eA	 Alignment	not modelled	11.6	16	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of benm_dbd
48	d1vi2a2	 Alignment	not modelled	11.4	14	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
49	d1u5ta1	 Alignment	not modelled	11.3	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
50	c2fgyA	 Alignment	not modelled	11.0	9	PDB header: lyase Chain: A: PDB Molecule: carboxysome shell polypeptide; PDBTitle: beta carbonic anhydrase from the carboxysomal shell of2 halothiobacillus neapolitanus (csoaca)
51	d1q3ma	 Alignment	not modelled	10.5	23	Fold: GLA-domain Superfamily: GLA-domain Family: GLA-domain
52	c3bkhA	 Alignment	not modelled	10.3	22	PDB header: hydrolase Chain: A: PDB Molecule: lytic transglycosylase; PDBTitle: crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
53	c2ev9B	 Alignment	not modelled	9.9	29	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from thermus2 thermophilus hb8 in complex with nadp(h) and shikimate
		Alignment				Fold: Thioredoxin fold

54	d2fug21	Alignment	not modelled	9.9	21	Superfamily: Thioredoxin-like Family: NQO2-like
55	d1q8ha	Alignment	not modelled	9.6	19	Fold: GLA-domain Superfamily: GLA-domain Family: GLA-domain
56	c1q8hA	Alignment	not modelled	9.6	19	PDB header: metal binding protein Chain: A: PDB Molecule: osteocalcin; PDBTitle: crystal structure of porcine osteocalcin
57	d1m9dc	Alignment	not modelled	9.2	15	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
58	c3tozA	Alignment	not modelled	9.2	33	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
59	d2b0ja1	Alignment	not modelled	9.1	16	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HMD dimerization domain-like
60	c1nvtA	Alignment	not modelled	8.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5'-dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroe or2 mj1084) in complex with nadp+
61	d1npya2	Alignment	not modelled	8.8	23	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
62	c2hk8B	Alignment	not modelled	8.3	13	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
63	c3iz5U	Alignment	not modelled	8.1	19	PDB header: ribosome Chain: U: PDB Molecule: 60s ribosomal protein l21 (l21e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of tritium aestivum translating 80s ribosome
64	d2qalc1	Alignment	not modelled	8.0	38	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
65	d1p77a2	Alignment	not modelled	7.5	14	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
66	c3pwzA	Alignment	not modelled	7.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase 3; PDBTitle: crystal structure of an ael1 enzyme from pseudomonas putida
67	d1pbya1	Alignment	not modelled	7.2	23	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
68	d1nyta2	Alignment	not modelled	6.8	15	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
69	c1p74B	Alignment	not modelled	6.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroe) from2 haemophilus influenzae
70	c1wjvA	Alignment	not modelled	6.7	44	PDB header: dna binding protein Chain: A: PDB Molecule: cell growth regulating nucleolar protein lyar; PDBTitle: solution structure of the n-terminal zinc finger domain of2 mouse cell growth regulating nucleolar protein lyar
71	d1jmxal	Alignment	not modelled	6.6	10	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
72	c3izcU	Alignment	not modelled	6.6	26	PDB header: ribosome Chain: U: PDB Molecule: 60s ribosomal protein rpl21 (l21e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
73	c2zmeA	Alignment	not modelled	6.4	8	PDB header: protein transport Chain: A: PDB Molecule: vacuolar-sorting protein snf8; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
74	d2pxrc1	Alignment	not modelled	6.3	15	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
75	c2eggA	Alignment	not modelled	6.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from2 geobacillus kaustophilus
76	c1u5tA	Alignment	not modelled	6.3	16	PDB header: transport protein Chain: A: PDB Molecule: appears to be functionally related to snf7; PDBTitle: structure of the escrt-ii endosomal trafficking complex
77	d2nr7a1	Alignment	not modelled	6.1	26	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: NMB1012-like
78	c1npyA	Alignment	not modelled	6.1	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical shikimate 5-dehydrogenase-like PDBTitle: structure of shikimate 5-dehydrogenase-like protein hi0607
79	c3u62A	Alignment	not modelled	6.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from thermotoga maritima

80	d2uubc1	Alignment	not modelled	5.9	33	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
81	c3ff5B_	Alignment	not modelled	5.9	35	PDB header: protein transport Chain: B: PDB Molecule: peroxisomal biogenesis factor 14; PDBTitle: crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
82	c3no7A_	Alignment	not modelled	5.9	16	PDB header: dna binding protein Chain: A: PDB Molecule: putative plasmid related protein; PDBTitle: crystal structure of the centromere-binding protein parb from plasmid2 pcxc100
83	c3cuqA_	Alignment	not modelled	5.9	9	PDB header: protein transport Chain: A: PDB Molecule: vacuolar-sorting protein snf8; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
84	c3a8yD_	Alignment	not modelled	5.8	14	PDB header: hydrolase Chain: D: PDB Molecule: bag family molecular chaperone regulator 5; PDBTitle: crystal structure of the complex between the bag5 bd5 and2 hsp70 nbd
85	c2nloA_	Alignment	not modelled	5.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum
86	d2oqoa1	Alignment	not modelled	5.8	13	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: PBP transglycosylase domain-like
87	d2ga1a1	Alignment	not modelled	5.7	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Alr1493-like
88	c1b9nA_	Alignment	not modelled	5.7	17	PDB header: transcription Chain: A: PDB Molecule: protein (mode); PDBTitle: regulator from escherichia coli
89	c1lbuA_	Alignment	not modelled	5.6	23	PDB header: hydrolase Chain: A: PDB Molecule: muramoyl-pentapeptide carboxypeptidase; PDBTitle: hydrolase metallo (zn) dd-peptidase
90	d1g3pa2	Alignment	not modelled	5.5	27	Fold: N-terminal domains of the minor coat protein g3p Superfamily: N-terminal domains of the minor coat protein g3p Family: N-terminal domains of the minor coat protein g3p
91	d2olua1	Alignment	not modelled	5.2	11	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: PBP transglycosylase domain-like
92	c3nojA_	Alignment	not modelled	5.2	13	PDB header: lyase Chain: A: PDB Molecule: 4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate PDBTitle: the structure of hmg/cha aldolase from the protocatechuate degradation2 pathway of pseudomonas putida
93	d2d28c1	Alignment	not modelled	5.1	20	Fold: Alpha-lytic protease prodomain-like Superfamily: EspE N-terminal domain-like Family: GSPII protein E N-terminal domain-like
94	d1k6ya1	Alignment	not modelled	5.1	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase
95	d1wjfa_	Alignment	not modelled	5.1	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase