Phyre^2

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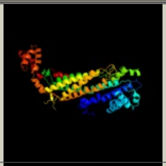
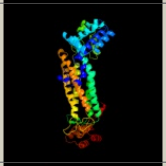
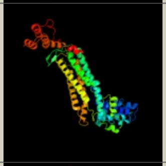
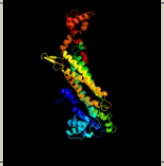
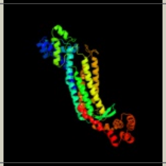
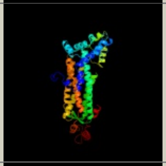
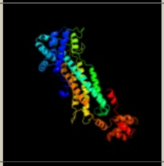
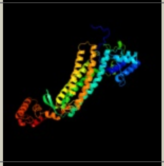
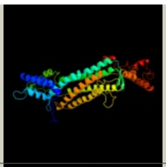
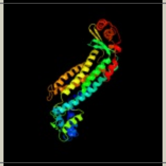
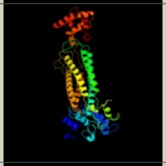
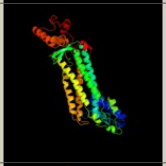
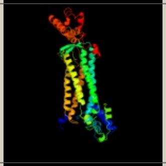
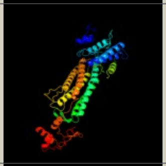
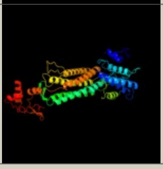
Description	P0AB89
Date	Thu Jan 5 11:14:54 GMT 2012
Unique Job ID	0cda2a1aeccc442b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ptsA_	Alignment		100.0	95	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** crystal structure of wild type escherichia coli adenylosuccinate lyase
2	c3bhgA_	Alignment		100.0	55	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** crystal structure of adenylosuccinate lyase from legionella2 pneumophila
3	c2qgaC_	Alignment		100.0	46	**PDB header:**lyase **Chain:** C: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** plasmodium vivax adenylosuccinate lyase pv003765 with amp bound
4	c2vd6B_	Alignment		100.0	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** human adenylosuccinate lyase in complex with its substrate2 n6-(1,2-dicarboxyethyl)-amp, and its products amp and3 fumarate.
5	c2pfmA_	Alignment		100.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** crystal structure of adenylosuccinate lyase (purb) from bacillus2 anthracis
6	d1c3ca_	Alignment		100.0	21	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
7	c1yisA_	Alignment		100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** structural genomics of caenorhabditis elegans: adenylosuccinate lyase
8	d1re5a_	Alignment		100.0	21	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
9	d1i0aa_	Alignment		100.0	18	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
10	d1tj7a_	Alignment		100.0	17	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
11	d1q5na_	Alignment		100.0	18	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase

12	d1hy0a_	Alignment		100.0	17	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
13	d1dofa_	Alignment		100.0	24	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
14	d1k62a_	Alignment		100.0	18	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
15	d1j3ua_	Alignment		100.0	15	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
16	c2e9fC_	Alignment		100.0	18	**PDB header:**lyase **Chain:** C: **PDB Molecule:**argininosuccinate lyase; **PDBTitle:** crystal structure of t.th.hb8 argininosuccinate lyase complexed with2 l-arginine
17	d1tjva_	Alignment		100.0	17	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
18	c3c8tA_	Alignment		100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fumarate lyase; **PDBTitle:** crystal structure of fumarate lyase from mesorhizobium sp. bnc1
19	c1yfmA_	Alignment		100.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fumarase; **PDBTitle:** recombinant yeast fumarase
20	d1yfma_	Alignment		100.0	16	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
21	d1fuoa_	Alignment	not modelled	100.0	17	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
22	d1vdka_	Alignment	not modelled	100.0	18	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
23	d1jswa_	Alignment	not modelled	100.0	15	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
24	c3no9C_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fumarate hydratase class ii; **PDBTitle:** crystal structure of apo fumarate hydratase from mycobacterium2 tuberculosis
25	c3ocfB_	Alignment	not modelled	100.0	16	**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
26	d1jswc_	Alignment	not modelled	100.0	14	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
27	c3e04C_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fumarate hydratase; **PDBTitle:** crystal structure of human fumarate hydratase
28	c2fenA_	Alignment	not modelled	100.0	21	**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
						PDB header:lyase

29	c3gtdB_	Alignment	not modelled	100.0	15	**Chain:** B: **PDB Molecule:**fumarate hydratase class ii; **PDBTitle:** 2.4 angstrom crystal structure of fumarate hydratase from rickettsia2 prowazekii
30	d1f1oa_	Alignment	not modelled	100.0	24	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
31	c3r6yG_	Alignment	not modelled	100.0	14	**PDB header:**lyase **Chain:** G: **PDB Molecule:**aspartase; **PDBTitle:** crystal structure of chymotrypsin-treated aspartase from bacillus sp.2 ym55-1
32	c2ctoA_	Alignment	not modelled	28.3	50	**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
33	d1rp4a_	Alignment	not modelled	18.4	11	**Fold:**ERO1-like **Superfamily:**ERO1-like **Family:**ERO1-like
34	c3ahrA_	Alignment	not modelled	15.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ero1-like protein alpha; **PDBTitle:** inactive human ero1
35	c2xgvA_	Alignment	not modelled	15.0	23	**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)
36	c1wjvA_	Alignment	not modelled	14.2	56	**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
37	c2ev9B_	Alignment	not modelled	13.1	43	**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
38	c3fbtB_	Alignment	not modelled	12.7	33	**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
39	c3bbnC_	Alignment	not modelled	12.7	57	**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.
40	d1nvta2	Alignment	not modelled	12.2	29	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Shikimate dehydrogenase-like
41	d2cb2a1	Alignment	not modelled	11.3	33	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**SOR-like
42	d1v5pa_	Alignment	not modelled	10.7	50	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
43	d1vi2a2	Alignment	not modelled	10.4	14	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Shikimate dehydrogenase-like
44	d1g3pa2	Alignment	not modelled	9.6	33	**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
45	d1npya2	Alignment	not modelled	9.3	23	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Shikimate dehydrogenase-like
46	c3egqB_	Alignment	not modelled	9.3	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tetr family transcriptional regulator; **PDBTitle:** crystal structure of a tetr-family transcriptional regulator (af_1817)2 from archaeoglobus fulgidus at 2.55 a resolution
47	d1p77a2	Alignment	not modelled	9.1	20	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Shikimate dehydrogenase-like
48	c3dikA_	Alignment	not modelled	8.9	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**capsid protein p24; **PDBTitle:** pseudo-atomic model of the hiv-1 ca hexameric lattice
49	c1nvtA_	Alignment	not modelled	8.8	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate 5'-dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase (aroe or2 mj1084) in complex with nadp+
50	c3pwzA_	Alignment	not modelled	8.7	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase 3; **PDBTitle:** crystal structure of an ael1 enzyme from pseudomonas putida
51	c1p74B_	Alignment	not modelled	8.3	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase (aroe) from2 haemophilus influenzae
52	c1dipA_	Alignment	not modelled	7.9	14	**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
53	d2qalc1	Alignment	not modelled	7.7	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)
54	c3u62A_	Alignment	not modelled	7.6	57	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from thermotoga maritima

55	d1lbua1	Alignment	not modelled	7.6	23	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**Peptidoglycan binding domain, PGBD
56	c3pgjB_	Alignment	not modelled	7.5	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate
57	c3tozA_	Alignment	not modelled	7.4	27	**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.
58	c2hk8B_	Alignment	not modelled	7.4	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
59	d1wjva1	Alignment	not modelled	7.4	63	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**C2HC finger
60	d1nyta2	Alignment	not modelled	7.4	29	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Shikimate dehydrogenase-like
61	c1ekuA_	Alignment	not modelled	7.3	31	**PDB header:**immune system **Chain:** A: **PDB Molecule:**interferon gamma; **PDBTitle:** crystal structure of a biologically active single chain2 mutant of human ifn-gamma
62	c2eggA_	Alignment	not modelled	7.3	57	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate 5-dehydrogenase (aroe) from2 geobacillus kaustophilus
63	d1prtb1	Alignment	not modelled	7.1	42	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
64	c2choA_	Alignment	not modelled	6.5	83	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucosaminidase; **PDBTitle:** bacteroides thetaiotaomicron hexosaminidase with o-2 glcnacase activity
65	d1u5ta1	Alignment	not modelled	6.5	3	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
66	c3o8qB_	Alignment	not modelled	6.5	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase i alpha; **PDBTitle:** 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
67	c2zmeA_	Alignment	not modelled	6.4	4	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
68	c3oakC_	Alignment	not modelled	6.4	21	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** crystal structure of a spn1 (iws1)-spt6 complex
69	c1npyA_	Alignment	not modelled	6.4	43	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical shikimate 5-dehydrogenase-like **PDBTitle:** structure of shikimate 5-dehydrogenase-like protein hi0607
70	c1jmtB_	Alignment	not modelled	6.4	29	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**splicing factor u2af 65 kda subunit; **PDBTitle:** x-ray structure of a core u2af65/u2af35 heterodimer
71	c2dinA_	Alignment	not modelled	6.2	32	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cell division cycle 5-like protein; **PDBTitle:** solution structure of the myb_dna-binding domain of human2 cell division cycle 5-like protein
72	d2ibge1	Alignment	not modelled	6.2	11	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**Hedgehog (development protein), N-terminal signaling domain
73	d2uubc1	Alignment	not modelled	6.1	50	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
74	c3no7A_	Alignment	not modelled	6.0	23	**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
75	c1nytC_	Alignment	not modelled	6.0	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** shikimate dehydrogenase aroe complexed with nadp+
76	c3cuqA_	Alignment	not modelled	5.9	4	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
77	c2nloA_	Alignment	not modelled	5.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum
78	d1jfla2	Alignment	not modelled	5.7	12	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
79	c2dchX_	Alignment	not modelled	5.7	36	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**putative homing endonuclease; **PDBTitle:** crystal structure of archaeal intron-encoded homing endonuclease i-2 tsp061i
80	c1vi2B_	Alignment	not modelled	5.6	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase 2; **PDBTitle:** crystal structure of shikimate-5-dehydrogenase with nad

81	d1cg2a2	Alignment	not modelled	5.6	22	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
82	c2qv5A_	Alignment	not modelled	5.6	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
83	c1iijA_	Alignment	not modelled	5.5	50	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**erbb-2 receptor protein-tyrosine kinase; **PDBTitle:** solution structure of the neu/erbb-2 membrane spanning2 segment
84	c3hsbB_	Alignment	not modelled	5.5	43	**PDB header:**rna binding protein/rna **Chain:** B: **PDB Molecule:**protein hfq; **PDBTitle:** crystal structure of ymah (hfq) from bacillus subtilis in complex with2 an rna aptamer
85	d2i9xa1	Alignment	not modelled	5.2	43	**Fold:**SpoVG-like **Superfamily:**SpoVG-like **Family:**SpoVG-like
86	c2i9zB_	Alignment	not modelled	5.2	43	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative septation protein spovg; **PDBTitle:** structural genomics, the crystal structure of full-length spovg from2 staphylococcus epidermidis atcc 12228
87	c1s1iC_	Alignment	not modelled	5.2	15	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**60s ribosomal protein l3; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
88	c2jq1A_	Alignment	not modelled	5.1	33	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**phylloseptin-3; **PDBTitle:** phylloseptin-3