










Phyre2

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 Description RVBD1559_(ilvA)_1763434_1764723
 Date Fri Aug 2 13:30:15 BST 2019
 Unique Job ID fed3745d694bca63

Detailed template information

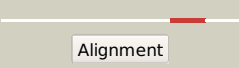
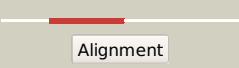
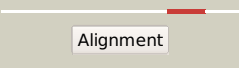
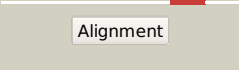
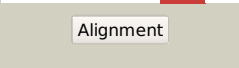
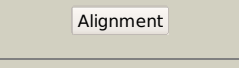
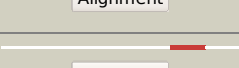
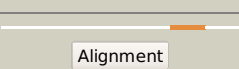
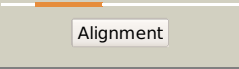
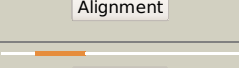
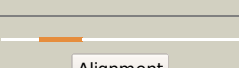
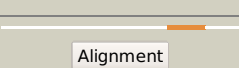
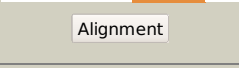
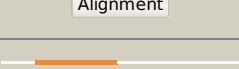

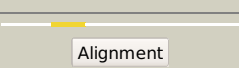
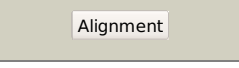



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1tdjA_	 Alignment		100.0	35	PDB header: allostery Chain: A; PDB Molecule: biosynthetic threonine deaminase; PDBTitle: threonine deaminase (biosynthetic) from e. coli
2	c3iauA_	 Alignment		100.0	38	PDB header: lyase Chain: A; PDB Molecule: threonine deaminase; PDBTitle: the structure of the processed form of threonine deaminase isoform 22 from solanum lycopersicum
3	c2gn0A_	 Alignment		100.0	36	PDB header: lyase Chain: A; PDB Molecule: threonine dehydratase catabolic; PDBTitle: crystal structure of dimeric biodegradative threonine deaminase (tdcb)2 from salmonella typhimurium at 1.7 a resolution (triclinic form with3 one complete subunit built in alternate conformation)
4	c3l6cA_	 Alignment		100.0	30	PDB header: isomerase Chain: A; PDB Molecule: serine racemase; PDBTitle: x-ray crystal structure of rat serine racemase in complex with2 malonate a potent inhibitor
5	d1v71a1	 Alignment		100.0	30	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
6	c5cvcB_	 Alignment		100.0	31	PDB header: isomerase Chain: B; PDB Molecule: serine racemase; PDBTitle: structure of maize serine racemase
7	c5ybwA_	 Alignment		100.0	28	PDB header: isomerase Chain: A; PDB Molecule: aspartate racemase; PDBTitle: crystal structure of pyridoxal 5'-phosphate-dependent aspartate2 racemase
8	d1pwha_	 Alignment		100.0	28	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
9	c3r0zA_	 Alignment		100.0	21	PDB header: lyase Chain: A; PDB Molecule: d-serine dehydratase; PDBTitle: crystal structure of apo d-serine deaminase from salmonella2 typhimurium
10	d1ve5a1	 Alignment		100.0	38	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
11	c6hulB_	 Alignment		100.0	19	PDB header: lyase Chain: B; PDB Molecule: tryptophan synthase beta chain 1; PDBTitle: sulfolobus solfataricus tryptophan synthase ab complex

12	d1tdja1	Alignment		100.0	40	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
13	d1p5ja_	Alignment		100.0	29	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
14	c1p5jA_	Alignment		100.0	29	PDB header: lyase Chain: A: PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure analysis of human serine dehydratase
15	c4d9gA_	Alignment		100.0	26	PDB header: lyase Chain: A: PDB Molecule: putative diaminopropionate ammonia-lyase; PDBTitle: crystal structure of selenomethionine incorporated holo2 diaminopropionate ammonia lyase from escherichia coli
16	c2rkbE_	Alignment		100.0	29	PDB header: lyase Chain: E: PDB Molecule: serine dehydratase-like; PDBTitle: serine dehydratase like-1 from human cancer cells
17	c5c3uA_	Alignment		100.0	25	PDB header: lyase Chain: A: PDB Molecule: l-serine ammonia-lyase; PDBTitle: crystal structure of a fungal l-serine ammonia-lyase from rhizomucor2 miehei
18	c5ygrA_	Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: diaminopropionate ammonia lyase; PDBTitle: crystal structure of plp bound diaminopropionate ammonia lyase from2 salmonella typhimurium
19	c4qysA_	Alignment		100.0	19	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain 2; PDBTitle: trpb2 enzymes
20	c4l3vB_	Alignment		100.0	19	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structure of delta516-525 human cystathionine beta-synthase
21	c3pc3A_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: A: PDB Molecule: cg1753, isoform a; PDBTitle: full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
22	c5ohxB_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of active cystathionine b-synthase from apis mellifera
23	d1jbqa_	Alignment	not modelled	100.0	20	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
24	c1jbqD_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: D: PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of human cystathionine beta-synthase: a unique pyridoxal 5'-2 phosphate dependent hemeprotein
25	c1x1qA_	Alignment	not modelled	100.0	25	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
26	d1ve1a1	Alignment	not modelled	100.0	23	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
27	d1qopb_	Alignment	not modelled	100.0	24	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
28	c6c2qA_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structures of cystathionine beta-synthase from

					saccharomyces2 cerevisiae: the structure of the plp-l-serine intermediate
29	c4aecB	Alignment	not modelled	100.0	19 PDB header: lyase Chain: B: PDB Molecule: cysteine synthase, mitochondrial; PDBTitle: crystal structure of the arabidopsis thaliana o-acetylserine-(thiol)-2 lyase c
30	c2pqmA	Alignment	not modelled	100.0	18 PDB header: lyase Chain: A: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution
31	d1v8za1	Alignment	not modelled	100.0	26 Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
32	d1z7wa1	Alignment	not modelled	100.0	19 Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
33	d2bhsa1	Alignment	not modelled	100.0	23 Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
34	c3vbeA	Alignment	not modelled	100.0	21 PDB header: transferase Chain: A: PDB Molecule: beta-cyanoalanine synthase; PDBTitle: crystal structure of beta-cyanoalanine synthase in soybean
35	c5i7wA	Alignment	not modelled	100.0	26 PDB header: transferase Chain: A: PDB Molecule: cysteine synthase a; PDBTitle: crystal structure of a cysteine synthase from brucella suis
36	c3x43F	Alignment	not modelled	100.0	22 PDB header: transferase Chain: F: PDB Molecule: o-ureido-l-serine synthase; PDBTitle: crystal structure of o-ureido-l-serine synthase
37	c5kinD	Alignment	not modelled	100.0	24 PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
38	c5tchH	Alignment	not modelled	100.0	27 PDB header: lyase Chain: H: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
39	c4lmaA	Alignment	not modelled	100.0	19 PDB header: transferase Chain: A: PDB Molecule: cysteine synthase; PDBTitle: crystal structure analysis of o-acetylserine sulfhydrylase cysk1 from2 microcystis aeruginosa 7806
40	c5d87A	Alignment	not modelled	100.0	19 PDB header: biosynthetic protein Chain: A: PDB Molecule: probable siderophore biosynthesis protein sbna y152f/s185g2 variant
41	c2d1fA	Alignment	not modelled	100.0	26 PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: structure of mycobacterium tuberculosis threonine synthase
42	d1y7la1	Alignment	not modelled	100.0	20 Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
43	d1wkva1	Alignment	not modelled	100.0	22 Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
44	c3dwgA	Alignment	not modelled	100.0	21 PDB header: transferase Chain: A: PDB Molecule: cysteine synthase b; PDBTitle: crystal structure of a sulfur carrier protein complex found in the2 cysteine biosynthetic pathway of mycobacterium tuberculosis
45	c4ql4A	Alignment	not modelled	100.0	23 PDB header: lyase Chain: A: PDB Molecule: o-acetylserine lyase; PDBTitle: crystal structure of o-acetylserine sulfhydrylase from bacillus2 anthracis
46	c2zsjB	Alignment	not modelled	100.0	25 PDB header: lyase Chain: B: PDB Molecule: threonine synthase; PDBTitle: crystal structure of threonine synthase from aquifex aeolicus vf5
47	c4negA	Alignment	not modelled	100.0	26 PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: the crystal structure of tryptophan synthase subunit beta from2 bacillus anthracis str. 'ames ancestor'
48	d1o58a	Alignment	not modelled	100.0	23 Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
49	d1fcja	Alignment	not modelled	100.0	19 Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
50	c4airB	Alignment	not modelled	100.0	24 PDB header: transferase Chain: B: PDB Molecule: cysteine synthase; PDBTitle: leishmania major cysteine synthase
51	d1v7ca	Alignment	not modelled	100.0	27 Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes PDB header: transferase

52	c2q3bA	Alignment	not modelled	100.0	22	Chain: A: PDB Molecule: cysteine synthase a; PDBTitle: 1.8 a resolution crystal structure of o-acetylserine sulfhydrylase2 (oass) holoenzyme from mycobacterium tuberculosis
53	c5xenB	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of a hydrogen sulfide-producing enzyme (fn1220) from2 fusobacterium nucleatum in complex with l-serine-plp schiff base
54	c5b1iC	Alignment	not modelled	100.0	19	PDB header: lyase Chain: C: PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structure of k42a mutant of cystathionine beta-synthase from2 lactobacillus plantarum in a complex with l-methionine
55	c5xa2B	Alignment	not modelled	100.0	22	PDB header: transferase Chain: B: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of o-acetylserine sulfhydrylase from planctomyces2 limnophila
56	d1e5xa	Alignment	not modelled	100.0	18	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
57	c6cgqA	Alignment	not modelled	100.0	24	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: threonine synthase from bacillus subtilis atcc 6633 with plp and plp-2 ala
58	c2eguA	Alignment	not modelled	100.0	28	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of o-acetylserine sulfhydrylase from geobacillus2 kaustophilus hta426
59	c4i1xA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of cysteine synthase from helicobacter pylori 26695
60	c2o2jA	Alignment	not modelled	100.0	30	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: mycobacterium tuberculosis tryptophan synthase beta chain dimer2 (apoforn)
61	c4d8tC	Alignment	not modelled	100.0	19	PDB header: lyase Chain: C: PDB Molecule: d-cysteine desulfhydrase; PDBTitle: crystal structure of d-cysteine desulfhydrase from salmonella2 typhimurium at 2.2 a resolution
62	d1j0aa	Alignment	not modelled	100.0	22	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
63	d1f2da	Alignment	not modelled	100.0	21	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
64	c5b54D	Alignment	not modelled	100.0	19	PDB header: transferase Chain: D: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of hydrogen sulfide-producing enzyme (fn1055) from2 fusobacterium nucleatum: lysine-dimethylated form
65	d1tyza	Alignment	not modelled	100.0	20	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
66	c4f4fB	Alignment	not modelled	100.0	13	PDB header: lyase Chain: B: PDB Molecule: threonine synthase; PDBTitle: x-ray crystal structure of plp bound threonine synthase from brucella2 melitensis
67	c3v7nA	Alignment	not modelled	100.0	15	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: crystal structure of threonine synthase (thrc) from burkholderia2 thailandensis
68	d1vb3a1	Alignment	not modelled	100.0	12	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
69	d1ki7a	Alignment	not modelled	100.0	13	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
70	d1tdja2	Alignment	not modelled	99.4	20	Fold: Ferredoxin-like Superfamily: ACT-like Family: Allosteric threonine deaminase C-terminal domain
71	d1tdja3	Alignment	not modelled	98.2	30	Fold: Ferredoxin-like Superfamily: ACT-like Family: Allosteric threonine deaminase C-terminal domain
72	c3ibwA	Alignment	not modelled	98.0	12	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase; PDBTitle: crystal structure of the act domain from gtp pyrophosphokinase of2 chlorobium tepidum. northeast structural genomics consortium target3 ctr148a
73	c5uscB	Alignment	not modelled	97.4	14	PDB header: hydrolase Chain: B: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase tyra from bacillus2 anthracis in complex with nad and l-tyrosine
74	d1phza1	Alignment	not modelled	96.9	18	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
75	d1u8sa2	Alignment	not modelled	96.9	11	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor

76	d2qmwa2	Alignment	not modelled	96.9	16	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
77	c4lubA	Alignment	not modelled	96.9	20	PDB header: lyase Chain: A: PDB Molecule: putative prephenate dehydratase; PDBTitle: x-ray structure of prephenate dehydratase from streptococcus mutans
78	d2f06a1	Alignment	not modelled	96.6	16	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
79	c2qmxB	Alignment	not modelled	96.5	20	PDB header: ligase Chain: B: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum t1s
80	c2qmwa	Alignment	not modelled	96.4	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
81	c3luyA	Alignment	not modelled	96.3	17	PDB header: isomerase Chain: A: PDB Molecule: probable chorismate mutase; PDBTitle: putative chorismate mutase from bifidobacterium adolescentis
82	c3mwbA	Alignment	not modelled	96.3	18	PDB header: lyase Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
83	d1zpa1	Alignment	not modelled	96.0	12	Fold: Ferredoxin-like Superfamily: ACT-like Family: SP0238-like
84	c2lvwA	Alignment	not modelled	95.7	6	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme 1 small subunit; PDBTitle: solution nmr studies of the dimeric regulatory subunit ilvn of the2 e.coli acetoxyacid synthase i (ahas i)
85	c3n0vD	Alignment	not modelled	95.7	12	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
86	c2nyIB	Alignment	not modelled	95.6	7	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: unknown protein; PDBTitle: crystal structure of an unknown protein from galdieria sulphuraria
87	d1sc6a3	Alignment	not modelled	95.6	15	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
88	c1u8sB	Alignment	not modelled	95.6	10	PDB header: transcription Chain: B: PDB Molecule: glycine cleavage system transcriptional PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor
89	c5jk5A	Alignment	not modelled	95.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: phenylalanine hydroxylase from dictyostelium - bh2 complex
90	c2f06B	Alignment	not modelled	95.2	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0572 from bacteroides thetaiotaomicron
91	d2f06a2	Alignment	not modelled	95.0	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
92	c3nrbD	Alignment	not modelled	94.7	12	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
93	c3o11B	Alignment	not modelled	94.6	16	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
94	c6dzsD	Alignment	not modelled	94.6	13	PDB header: oxidoreductase Chain: D: PDB Molecule: homoserine dehydrogenase; PDBTitle: mycobacterial homoserine dehydrogenase thra in complex with nadp
95	d1u8sa1	Alignment	not modelled	94.1	12	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
96	d1vgya3	Alignment	not modelled	94.1	12	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
97	c2f1fA	Alignment	not modelled	93.8	17	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme iii small subunit; PDBTitle: crystal structure of the regulatory subunit of acetoxyacid2 synthase isozyme iii from e. coli
98	c2mdaB	Alignment	not modelled	93.1	23	PDB header: oxidoreductase Chain: B: PDB Molecule: tyrosine 3-monooxygenase; PDBTitle: the solution structure of the regulatory domain of tyrosine2 hydroxylase
99	c2pnmA	Alignment	not modelled	92.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (phenylalanine-4-hydroxylase); PDBTitle: structure of phenylalanine hydroxylase dephosphorylated
100	c3louB	Alignment	not modelled	92.8	6	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

101	c3obiC	 Alignment	not modelled	92.2	9	PDB header: hydrolase Chain: C: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodospseudomonas palustris cga009 at 1.95 a resolution
102	c3eywA	 Alignment	not modelled	92.0	15	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
103	c1y7pB	 Alignment	not modelled	92.0	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein af1403; PDBTitle: 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
104	c5denA	 Alignment	not modelled	91.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: the first structure of a full-length mammalian phenylalanine2 hydroxylase reveals the architecture of an auto-inhibited tetramer
105	c2pc6C	 Alignment	not modelled	90.9	13	PDB header: lyase Chain: C: PDB Molecule: probable acetolactate synthase isozyme iii (small subunit); PDBTitle: crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
106	c2fgcA	 Alignment	not modelled	90.9	9	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase, small subunit; PDBTitle: crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
107	d2fgca2	 Alignment	not modelled	90.7	9	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
108	c3w7bB	 Alignment	not modelled	90.1	15	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
109	c3mtjA	 Alignment	not modelled	89.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
110	d1t57a	 Alignment	not modelled	88.8	16	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
111	d2f1fa1	 Alignment	not modelled	88.1	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
112	d1vp8a	 Alignment	not modelled	85.7	22	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
113	c3iupB	 Alignment	not modelled	84.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadph:quinone oxidoreductase; PDBTitle: crystal structure of putative nadph:quinone oxidoreductase2 (yp_296108.1) from ralstonia eutropha jmp134 at 1.70 a resolution
114	d2pc6a2	 Alignment	not modelled	84.3	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
115	c3l76B	 Alignment	not modelled	82.8	13	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of aspartate kinase from synechocystis
116	d1bg6a2	 Alignment	not modelled	82.3	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
117	c4lhdB	 Alignment	not modelled	82.2	16	PDB header: oxidoreductase Chain: B: PDB Molecule: glycine dehydrogenase [decarboxylating]; PDBTitle: crystal structure of synechocystis sp. pcc 6803 glycine decarboxylase2 (p-protein), holo form with pyridoxal-5'-phosphate and glycine,3 closed flexible loop
118	d1o8ca2	 Alignment	not modelled	80.3	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
119	d1m14a2	 Alignment	not modelled	79.9	17	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
120	c3k7yA	 Alignment	not modelled	79.6	11	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: aspartate aminotransferase of plasmodium falciparum