Phyre^2

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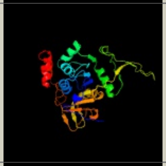
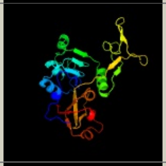
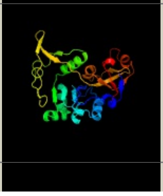
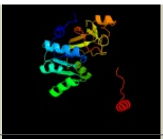
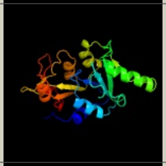
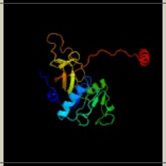
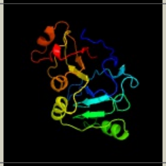
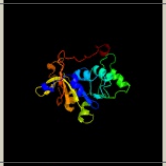
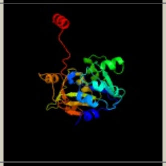
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6co9A_	Alignment		100.0	76	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable coa-transferase alpha subunit; **PDBTitle:** crystal structure of rhodococcus jostii rha1 ipdab cochea-coa complex
2	d1poia_	Alignment		100.0	27	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
3	c5mzyA_	Alignment		100.0	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glutaconate coa-transferase family, subunit a; **PDBTitle:** crystal structure of the decarboxylase aiba/aibb in complex with a2 possible transition state analog
4	d2ahua2	Alignment		100.0	21	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
5	d1ooya2	Alignment		100.0	23	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
6	c3rrlC_	Alignment		100.0	25	**PDB header:**transferase **Chain:** C: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase subunit a; **PDBTitle:** complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695
7	c3cdkA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase **PDBTitle:** crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis
8	c2ahvC_	Alignment		100.0	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative enzyme ydif; **PDBTitle:** crystal structure of acyl-coa transferase from e. coli o157:h7 (ydif)-2 thioester complex with coa- 1
9	d1k6da_	Alignment		100.0	25	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
10	c4kgbB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase; **PDBTitle:** structure of succinyl-coa: 3-ketoacid coa transferase from drosophila2 melanogaster
11	c1ooyA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase, **PDBTitle:** succinyl-coa:3-ketoacid coa transferase from pig heart

12	c2hj0A_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative citrate lyase, alfa subunit; **PDBTitle:** crystal structure of the putative alfa subunit of citrate lyase in2 complex with citrate from streptococcus mutans, northeast structural3 genomics target smr12 .
13	c3qlkB_	Alignment		100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**coenzyme a transferase; **PDBTitle:** crystal structure of ripa from yersinia pestis
14	c1xr4B_	Alignment		99.9	23	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**putative citrate lyase alpha chain/citrate-acp transferase; **PDBTitle:** x-ray crystal structure of putative citrate lyase alpha chain/citrate-2 acp transferase [salmonella typhimurium]
15	c4eu4A_	Alignment		99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**succinyl-coa:acetate coenzyme a transferase; **PDBTitle:** succinyl-coa: acetate coa-transferase (aarch6) in complex with coa2 (hexagonal lattice)
16	c3gk7A_	Alignment		99.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coa-transferase from2 clostridium aminobutyricum
17	c5vitP_	Alignment		99.9	18	**PDB header:**transferase **Chain:** P: **PDB Molecule:**mdca; **PDBTitle:** crystal structure of a pseudomonas malonate decarboxylase hetero-2 tetramer in complex with malonate
18	c2g39A_	Alignment		99.9	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**acetyl-coa hydrolase; **PDBTitle:** crystal structure of coenzyme a transferase from pseudomonas2 aeruginosa
19	c2oasA_	Alignment		99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coenzyme a transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coenzyme a transferase (atoa)2 in complex with coa from shewanella oneidensis, northeast structural3 genomics target sor119.
20	c2nvvF_	Alignment		99.9	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**acetyl-coa hydrolase/transferase family protein; **PDBTitle:** crystal structure of the putative acetyl-coa hydrolase/transferase2 pg1013 from porphyromonas gingivalis, northeast structural genomics3 target pgr16.
21	c3d3uA_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coa-transferase (abft-2) from2 porphyromonas gingivalis. northeast structural genomics consortium3 target pgr26
22	c3eh7A_	Alignment	not modelled	99.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** the structure of a putative 4-hydroxybutyrate coa-transferase from2 porphyromonas gingivalis w83
23	d2g39a1	Alignment	not modelled	99.7	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
24	d1xr4a1	Alignment	not modelled	99.7	22	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
25	c6eepA_	Alignment	not modelled	97.9	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase from legionella2 pneumophila
26	c5uf2A_	Alignment	not modelled	97.6	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose 5 phosphate isomerase a from neisseria2 gonorrhoeae
27	c1m0sA_	Alignment	not modelled	97.6	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** northeast structural genomics consortium (nesg id ir21)
28	c3l7oB_	Alignment	not modelled	97.6	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
						Fold: NagB/RpiA/CoA transferase-like

29	d1m0sa1	Alignment	not modelled	97.5	18	**Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
30	c5dbnD_	Alignment	not modelled	97.5	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetate coa-transferase subunit beta; **PDBTitle:** crystal structure of atoda complex
31	c2f8mB_	Alignment	not modelled	97.5	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** ribose 5-phosphate isomerase from plasmodium falciparum
32	c6j1kA_	Alignment	not modelled	97.5	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from ochrobactrum2 sp. csl1
33	c4gmkB_	Alignment	not modelled	97.4	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose 5-phosphate isomerase from the probiotic2 bacterium lactobacillus salivarius ucc118
34	c3kwmC_	Alignment	not modelled	97.3	25	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-isomerase a
35	c1lk5C_	Alignment	not modelled	97.3	23	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-ribose-5-phosphate isomerase; **PDBTitle:** structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
36	c3hheA_	Alignment	not modelled	97.3	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
37	c1lkzB_	Alignment	not modelled	97.2	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase a; **PDBTitle:** crystal structure of d-ribose-5-phosphate isomerase (rpia) from2 escherichia coli.
38	d2g39a2	Alignment	not modelled	96.9	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
39	c1uj6A_	Alignment	not modelled	96.7	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
40	d1xr4a2	Alignment	not modelled	96.2	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
41	c2pjmA_	Alignment	not modelled	96.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
42	d1uj4a1	Alignment	not modelled	95.9	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
43	d1lk5a1	Alignment	not modelled	95.0	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
44	c4nmlA_	Alignment	not modelled	95.0	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribulose 5-phosphate isomerase; **PDBTitle:** 2.60 angstrom resolution crystal structure of putative ribose 5-2 phosphate isomerase from toxoplasma gondii me49 in complex with dl-3 malic acid
45	c5n02B_	Alignment	not modelled	94.9	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutaconate coa-transferase family, subunit b; **PDBTitle:** crystal structure of the decarboxylase aiba/aibb c56s variant
46	c3cdkD_	Alignment	not modelled	93.8	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase **PDBTitle:** crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis
47	c4x84C_	Alignment	not modelled	93.7	24	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa
48	c3u7jA_	Alignment	not modelled	92.7	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
49	c1xtzA_	Alignment	not modelled	88.5	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
50	d1ooya1	Alignment	not modelled	63.2	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
51	d1o8bb1	Alignment	not modelled	62.5	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
52	c3rrlD_	Alignment	not modelled	59.3	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase subunit b; **PDBTitle:** complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695
53	c6conF_	Alignment	not modelled	53.4	12	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**coa-transferase subunit beta; **PDBTitle:** crystal structure of mycobacterium tuberculosis ipdab
54	c4oqqA_	Alignment	not modelled	49.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**deoxyribonucleoside regulator; **PDBTitle:** structure of the effector-binding domain of

						deoxyribonucleoside2 regulator deor from bacillus subtilis
55	d1poib_	Alignment	not modelled	47.1	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
56	c3nzeB_	Alignment	not modelled	43.8	27	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator, sugar-binding family; **PDBTitle:** the crystal structure of a domain of a possible sugar-binding2 transcriptional regulator from arthrobacter aurescens tc1.
57	d2r5fa1	Alignment	not modelled	41.0	24	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
58	c3n2zB_	Alignment	not modelled	41.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lysosomal pro-x carboxypeptidase; **PDBTitle:** the structure of human prolylcarboxypeptidase at 2.80 angstroms2 resolution
59	d2ahua1	Alignment	not modelled	39.2	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
60	c6co6B_	Alignment	not modelled	38.7	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable coa-transferase beta subunit; **PDBTitle:** crystal structure of rhodococcus jostii rha1 ipdab
61	d1gdha2	Alignment	not modelled	37.6	10	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
62	c4r9nA_	Alignment	not modelled	37.2	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lmo0547 protein; **PDBTitle:** deor family transcriptional regulator from listeria monocytogenes.
63	d2gnpa1	Alignment	not modelled	37.0	14	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
64	c1dbgA_	Alignment	not modelled	35.8	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**chondroitinase b; **PDBTitle:** crystal structure of chondroitinase b
65	d1ofla_	Alignment	not modelled	29.2	24	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Chondroitinase B
66	d1t5oa_	Alignment	not modelled	28.4	14	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
67	c5mvrA_	Alignment	not modelled	27.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna threonylcarbamoyladenosine biosynthesis protein tsae; **PDBTitle:** crystal structure of bacillus subtilus ydib
68	d1udxa3	Alignment	not modelled	25.8	26	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
69	d3efba1	Alignment	not modelled	23.7	22	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
70	d1t9ka_	Alignment	not modelled	21.0	17	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
71	d1o8ba1	Alignment	not modelled	20.9	11	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
72	c2yvkA_	Alignment	not modelled	18.8	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
73	c5dboA_	Alignment	not modelled	18.7	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor eif-2b-like protein; **PDBTitle:** crystal structure of the tetrameric eif2b-beta2-delta2 complex from c.2 thermophilum
74	c6qg0G_	Alignment	not modelled	18.2	20	**PDB header:**translation **Chain:** G: **PDB Molecule:**translation initiation factor eif-2b subunit delta; **PDBTitle:** structure of eif2b-eif2 (phosphorylated at ser51) complex (model 1)
75	c4rhjE_	Alignment	not modelled	18.1	24	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**arginase; **PDBTitle:** crystal structure of wild-type t. brucei arginase-like protein in a2 reduced form
76	c6i3mF_	Alignment	not modelled	18.1	10	**PDB header:**translation **Chain:** F: **PDB Molecule:**translation initiation factor eif-2b subunit beta; **PDBTitle:** eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
77	d1p32a_	Alignment	not modelled	16.6	7	**Fold:**Mitochondrial glycoprotein MAM33-like **Superfamily:**Mitochondrial glycoprotein MAM33-like **Family:**Mitochondrial glycoprotein MAM33-like
78	c3kv1A_	Alignment	not modelled	16.3	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional repressor; **PDBTitle:** crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
79	c5z9tB_	Alignment	not modelled	15.7	29	**PDB header:**lyase **Chain:** B: **PDB Molecule:**alginate lyase alyf-ou02; **PDBTitle:** a new pl6 alginate lyase complex with trisaccharide
						PDB header:translation

80	c5b04B_	Alignment	not modelled	15.4	25	**Chain:** B: **PDB Molecule:**translation initiation factor eif-2b subunit alpha; **PDBTitle:** crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
81	c3gucB_	Alignment	not modelled	14.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ubiquitin-like modifier-activating enzyme 5; **PDBTitle:** human ubiquitin-activating enzyme 5 in complex with amppnp
82	c2w48D_	Alignment	not modelled	13.8	24	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
83	d1iq8a1	Alignment	not modelled	13.7	4	**Fold:**TIM beta/alpha-barrel **Superfamily:**tRNA-guanine transglycosylase **Family:**tRNA-guanine transglycosylase
84	c4zeoH_	Alignment	not modelled	13.2	19	**PDB header:**translation **Chain:** H: **PDB Molecule:**translation initiation factor eif-2b-like protein; **PDBTitle:** crystal structure of eif2b delta from chaetomium thermophilum
85	c4zemB_	Alignment	not modelled	13.0	9	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation initiation factor eif2b-like protein, **PDBTitle:** crystal structure of eif2b beta from chaetomium thermophilum
86	d1ru4a_	Alignment	not modelled	13.0	21	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectate transeliminase
87	c3dhiA_	Alignment	not modelled	12.6	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**toluene 4-monooxygenase hydroxylase alpha subunit; **PDBTitle:** crystal structure of reduced toluene 4-monoxygenase hydroxylase2 complexed with effector protein
88	d1jw9b_	Alignment	not modelled	12.5	23	**Fold:**Activating enzymes of the ubiquitin-like proteins **Superfamily:**Activating enzymes of the ubiquitin-like proteins **Family:**Molybdenum cofactor biosynthesis protein MoeB
89	c6fpeE_	Alignment	not modelled	12.4	21	**PDB header:**rna binding protein **Chain:** E: **PDB Molecule:**atpase yjee, predicted to have essential role in cell wall **PDBTitle:** bacterial protein complex
90	c1vjtA_	Alignment	not modelled	12.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
91	d2a0ma1	Alignment	not modelled	12.0	18	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
92	c4ljkA_	Alignment	not modelled	11.8	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna processing chain a (dpra); **PDBTitle:** structural insights into the unique single-stranded dna binding mode2 of dna processing protein a from helicobacter pylori
93	c6i3mD_	Alignment	not modelled	11.7	22	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit delta; **PDBTitle:** eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
94	d1kqfa1	Alignment	not modelled	11.4	17	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
95	c6i7tB_	Alignment	not modelled	11.3	14	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation initiation factor eif-2b subunit alpha; **PDBTitle:** eif2b:eif2 complex
96	c2ri0B_	Alignment	not modelled	11.3	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** crystal structure of glucosamine 6-phosphate deaminase (nagb) from s.2 mutans
97	c3n7uD_	Alignment	not modelled	11.2	7	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide
98	c4go1A_	Alignment	not modelled	10.9	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lsrr; **PDBTitle:** crystal structure of full length transcription repressor lsrr from e.2 coli.
99	c3a11D_	Alignment	not modelled	10.8	10	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b, delta subunit; **PDBTitle:** crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1