Phyre^2

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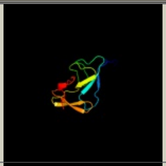
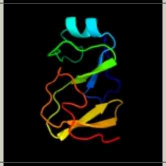
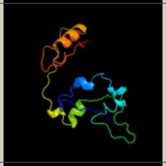
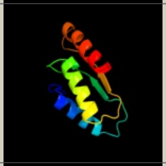
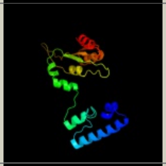
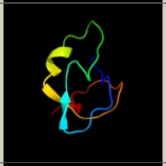
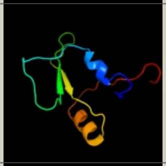
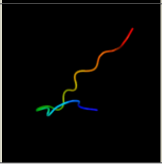
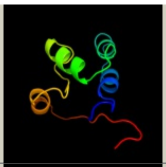
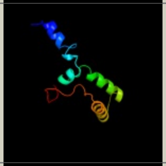
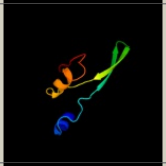
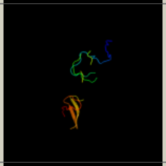
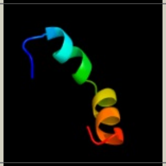
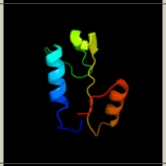
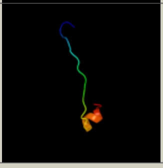
Description	P39829
Date	Thu Jan 5 12:00:53 GMT 2012
Unique Job ID	5823a77f3a0672ae

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lazB_	Alignment		100.0	98	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-galactarate dehydratase; **PDBTitle:** the crystal structure of the n-terminal domain of d-2 galactarate dehydratase from escherichia coli cft073
2	c3k3sG_	Alignment		99.9	36	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**altronate hydrolase; **PDBTitle:** crystal structure of altronate hydrolase (fragment 1-84) from shigella2 flexneri.
3	c1qd1A_	Alignment		72.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**formiminotransferase-cyclodeaminase; **PDBTitle:** the crystal structure of the formiminotransferase domain of2 formiminotransferase-cyclodeaminase.
4	c3degC_	Alignment		59.7	19	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
5	d2nu7b1	Alignment		54.9	9	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
6	c1tt9B_	Alignment		53.2	17	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**formimidoyltransferase-cyclodeaminase **PDBTitle:** structure of the bifunctional and golgi associated2 formiminotransferase cyclodeaminase octamer
7	c3cwcB_	Alignment		52.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative glycerate kinase 2; **PDBTitle:** crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
8	d2zdra1	Alignment		51.0	18	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
9	c3g8rA_	Alignment		48.7	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**probable spore coat polysaccharide biosynthesis protein e; **PDBTitle:** crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
10	c3b8hA_	Alignment		41.9	13	**PDB header:**biosynthetic protein/transferase **Chain:** A: **PDB Molecule:**elongation factor 2; **PDBTitle:** structure of the eef2-exoa(e546a)-nad+ complex
11	d2f69a2	Alignment		41.2	29	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases

12	c3tr5C_	Alignment		40.0	17	**PDB header:**translation **Chain:** C: **PDB Molecule:**peptide chain release factor 3; **PDBTitle:** structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii
13	d1csha_	Alignment		38.3	14	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
14	c3izq1_	Alignment		37.9	15	**PDB header:**ribosomal protein,hydrolase **Chain:** 1: **PDB Molecule:**elongation factor 1 alpha-like protein; **PDBTitle:** structure of the dom34-hbs1-gdpnp complex bound to a translating2 ribosome
15	c3frnA_	Alignment		34.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**flagellar protein flga; **PDBTitle:** crystal structure of flagellar protein flga from thermotoga maritima2 msb8
16	c2elfA_	Alignment		32.2	13	**PDB header:**translation **Chain:** A: **PDB Molecule:**protein translation elongation factor 1a; **PDBTitle:** crystal structure of the selb-like elongation factor ef-pyl2 from methanosarcina mazei
17	c3cnlA_	Alignment		31.8	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of gnp-bound ylqf from t. maritima
18	c3m7oB_	Alignment		30.8	11	**PDB header:**immune system **Chain:** B: **PDB Molecule:**lymphocyte antigen 86; **PDBTitle:** crystal structure of mouse md-1 in complex with phosphatidylcholine
19	c2ywfA_	Alignment		30.0	12	**PDB header:**translation **Chain:** A: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** crystal structure of gmppnp-bound lepa from aquifex aeolicus
20	d1puja_	Alignment		28.0	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
21	d1c8ba_	Alignment	not modelled	28.0	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**HybD-like **Family:**Germination protease
22	c1g7tA_	Alignment	not modelled	27.3	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if2/eif5b; **PDBTitle:** x-ray structure of translation initiation factor if2/eif5b2 complexed with gdpnp
23	d1vlia1	Alignment	not modelled	27.1	17	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
24	c3bicA_	Alignment	not modelled	25.8	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylmalonyl-coa mutase, mitochondrial precursor; **PDBTitle:** crystal structure of human methylmalonyl-coa mutase
25	c2j69D_	Alignment	not modelled	25.3	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**bacterial dynamin-like protein; **PDBTitle:** bacterial dynamin-like protein bdlp
26	c1vliA_	Alignment	not modelled	24.4	26	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
27	c1xqhE_	Alignment	not modelled	23.7	23	**PDB header:**transferase **Chain:** E: **PDB Molecule:**histone-lysine n-methyltransferase, h3 lysine-4 **PDBTitle:** crystal structure of a ternary complex of the2 methyltransferase set9 (also known as set7/9) with a p533 peptide and sah
						PDB header:chaperone

28	c3ka5A_	Alignment	not modelled	23.5	40	**Chain:** A: **PDB Molecule:**ribosome-associated protein y (psrp-1); **PDBTitle:** crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a
29	c3h6lA_	Alignment	not modelled	23.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setd2; **PDBTitle:** methyltransferase domain of human set domain-containing protein 2
30	c3k2tA_	Alignment	not modelled	22.7	40	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo2511 protein; **PDBTitle:** crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
31	c3f9xA_	Alignment	not modelled	22.4	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setd8; **PDBTitle:** structural insights into lysine multiple methylation by set2 domain methyltransferases, set8-y334f / h4-lys20me2 /3 adohcy
32	c1xuzA_	Alignment	not modelled	22.3	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
33	c1zo1I_	Alignment	not modelled	21.5	15	**PDB header:**translation/rna **Chain:** I: **PDB Molecule:**translation initiation factor 2; **PDBTitle:** if2, if1, and trna fitted to cryo-em data of e. coli 70s2 initiation complex
34	c2bm0A_	Alignment	not modelled	21.4	18	**PDB header:**elongation factor **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** ribosomal elongation factor g (ef-g) fusidic acid resistant2 mutant t84a
35	c3m5uA_	Alignment	not modelled	21.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** crystal structure of phosphoserine aminotransferase from2 campylobacter jejuni
36	c3opeA_	Alignment	not modelled	21.2	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable histone-lysine n-methyltransferase ash1l; **PDBTitle:** structural basis of auto-inhibitory mechanism of histone2 methyltransferase
37	c1x5bA_	Alignment	not modelled	21.0	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**signal transducing adaptor molecule 2; **PDBTitle:** the solution structure of the vhs domain of human signal2 transducing adaptor molecule 2
38	c2z64C_	Alignment	not modelled	21.0	14	**PDB header:**immune system **Chain:** C: **PDB Molecule:**lymphocyte antigen 96; **PDBTitle:** crystal structure of mouse tlr4 and mouse md-2 complex
39	d1h3ia2	Alignment	not modelled	20.9	20	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
40	c3bo5A_	Alignment	not modelled	20.7	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setmar; **PDBTitle:** crystal structure of methyltransferase domain of human histone-lysine2 n-methyltransferase setmar
41	c3ooiA_	Alignment	not modelled	20.3	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase, h3 lysine-36 and h4 **PDBTitle:** crystal structure of human histone-lysine n-methyltransferase nsd1 set2 domain in complex with s-adenosyl-l-methionine
42	d1umqa_	Alignment	not modelled	19.4	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
43	c1umqA_	Alignment	not modelled	19.4	10	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**photosynthetic apparatus regulatory protein; **PDBTitle:** solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
44	d1ml9a_	Alignment	not modelled	19.3	38	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
45	d1elka_	Alignment	not modelled	18.8	12	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
46	c2xexA_	Alignment	not modelled	18.5	17	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** crystal structure of staphylococcus aureus elongation factor2 g
47	d1mvha_	Alignment	not modelled	17.6	31	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
48	c1mvhA_	Alignment	not modelled	17.6	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cryptic loci regulator 4; **PDBTitle:** structure of the set domain histone lysine2 methyltransferase clr4
49	d1dvpa1	Alignment	not modelled	17.2	13	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
50	d1nuia2	Alignment	not modelled	16.8	56	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
						PDB header:transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase

51	c2r3aA_	Alignment	not modelled	16.2	23	suv39h2; **PDBTitle:** methyltransferase domain of human suppressor of variegation2 3-9 homolog 2
52	c1s0uA_	Alignment	not modelled	16.0	15	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 gamma subunit; **PDBTitle:** eif2gamma apo
53	d1eucb1	Alignment	not modelled	15.8	9	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
54	d2ctsa_	Alignment	not modelled	15.8	15	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
55	c2k4zA_	Alignment	not modelled	14.7	3	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dsrr; **PDBTitle:** solution nmr structure of allochromatium vinosum dsrr:2 northeast structural genomics consortium target op5
56	c3cb4D_	Alignment	not modelled	14.3	19	**PDB header:**translation **Chain:** D: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** the crystal structure of lepa
57	d1csca_	Alignment	not modelled	13.7	15	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
58	d1txna_	Alignment	not modelled	13.7	14	**Fold:**Coproporphyrinogen III oxidase **Superfamily:**Coproporphyrinogen III oxidase **Family:**Coproporphyrinogen III oxidase
59	c3s8pA_	Alignment	not modelled	13.6	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase suv420h1; **PDBTitle:** crystal structure of the set domain of human histone-lysine n-2 methyltransferase suv420h1 in complex with s-adenosyl-l-methionine
60	d1ucva_	Alignment	not modelled	12.7	23	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
61	c3by5A_	Alignment	not modelled	12.7	30	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cobalamin biosynthesis protein; **PDBTitle:** crystal structure of cobalamin biosynthesis protein chig from2 agrobacterium tumefaciens str. c58
62	d3by5a1	Alignment	not modelled	12.7	30	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
63	c2qptA_	Alignment	not modelled	12.3	16	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**eh domain-containing protein-2; **PDBTitle:** crystal structure of an ehd atpase involved in membrane remodelling
64	c3mu3A_	Alignment	not modelled	12.2	11	**PDB header:**immune system **Chain:** A: **PDB Molecule:**protein md-1; **PDBTitle:** crystal structure of chicken md-1 complexed with lipid iva
65	d1ynya1	Alignment	not modelled	12.0	22	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
66	d1wjta_	Alignment	not modelled	11.7	13	**Fold:**N-cbl like **Superfamily:**Conserved domain common to transcription factors TFIIS, elongin A, CRSP70 **Family:**Conserved domain common to transcription factors TFIIS, elongin A, CRSP70
67	d2olra1	Alignment	not modelled	11.7	15	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**PEP carboxykinase C-terminal domain
68	c3simA_	Alignment	not modelled	11.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein, family 18 chitinase; **PDBTitle:** crystallographic structure analysis of family 18 chitinase from crocus2 vernus
69	c3nioF_	Alignment	not modelled	11.4	23	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**guanidinobutyrase; **PDBTitle:** crystal structure of pseudomonas aeruginosa guanidinobutyrase
70	d1fx0a1	Alignment	not modelled	11.4	18	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
71	c2rdo7_	Alignment	not modelled	11.3	15	**PDB header:**ribosome **Chain:** 7: **PDB Molecule:**elongation factor g; **PDBTitle:** 50s subunit with ef-g(gdpnp) and rrf bound
72	c1e1cA_	Alignment	not modelled	11.2	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylmalonyl-coa mutase alpha chain; **PDBTitle:** methylmalonyl-coa mutase h244a mutant
73	d1to6a_	Alignment	not modelled	11.1	15	**Fold:**Glycerate kinase I **Superfamily:**Glycerate kinase I **Family:**Glycerate kinase I
74	c1skqB_	Alignment	not modelled	10.8	18	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor 1-alpha; **PDBTitle:** the crystal structure of sulfolobus solfataricus elongation2 factor 1-alpha in complex with magnesium and gdp
75	d1fuea_	Alignment	not modelled	10.8	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
76	d1v8qa_	Alignment	not modelled	10.7	37	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**Ribosomal L27 protein

77	c3fin0_	Alignment	not modelled	10.7	37	**PDB header:**ribosome **Chain:** 0: **PDB Molecule:**50s ribosomal protein l27; **PDBTitle:** t. thermophilus 70s ribosome in complex with mrna, trnas2 and ef-tu.gdp.kirromycin ternary complex, fitted to a 6.43 a cryo-em map. this file contains the 50s subunit.
78	c2hdnJ_	Alignment	not modelled	10.7	14	**PDB header:**translation **Chain:** J: **PDB Molecule:**elongation factor ef-tu; **PDBTitle:** trypsin-modified elongation factor tu in complex with2 tetracycline at 2.8 angstrom resolution
79	d1hr0w_	Alignment	not modelled	10.3	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
80	d1yv9a1	Alignment	not modelled	10.3	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**NagD-like
81	d1o0ya_	Alignment	not modelled	10.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
82	d2f23a2	Alignment	not modelled	10.0	14	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
83	c3b8iF_	Alignment	not modelled	9.9	18	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pa4872 oxaloacetate decarboxylase; **PDBTitle:** crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
84	d2py8a1	Alignment	not modelled	9.9	10	**Fold:**RbcX-like **Superfamily:**RbcX-like **Family:**RbcX-like
85	c2qpwA_	Alignment	not modelled	9.7	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**pr domain zinc finger protein 2; **PDBTitle:** methyltransferase domain of human pr domain-containing2 protein 2
86	d2h2ja2	Alignment	not modelled	9.6	5	**Fold:**beta-clip **Superfamily:**SET domain **Family:**RuBisCo LSMT catalytic domain
87	c2gedB_	Alignment	not modelled	9.4	18	**PDB header:**protein transport, signaling protein **Chain:** B: **PDB Molecule:**signal recognition particle receptor beta **PDBTitle:** signal recognition particle receptor beta-subunit in2 nucleotide-free dimerized form
88	c2f5jA_	Alignment	not modelled	9.4	26	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**mortality factor 4-like protein 1; **PDBTitle:** crystal structure of mrg domain from human mrg15
89	c3nipB_	Alignment	not modelled	9.3	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-guanidinopropionase; **PDBTitle:** crystal structure of pseudomonas aeruginosa guanidinopropionase2 complexed with 1,6-diaminohexane
90	c3mmpC_	Alignment	not modelled	9.2	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**elongation factor tu 2, elongation factor ts; **PDBTitle:** structure of the qb replicase, an rna-dependent rna polymerase2 consisting of viral and host proteins
91	d1vf5c1	Alignment	not modelled	9.1	36	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
92	c2w5zA_	Alignment	not modelled	8.8	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase hrx; **PDBTitle:** ternary complex of the mixed lineage leukaemia (mll1) set2 domain with the cofactor product s-adenosylhomocysteine3 and histone peptide.
93	d1z9ha1	Alignment	not modelled	8.6	10	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
94	c3eoeC_	Alignment	not modelled	8.5	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
95	c3izyP_	Alignment	not modelled	8.5	12	**PDB header:**rna, ribosomal protein **Chain:** P: **PDB Molecule:**translation initiation factor if-2, mitochondrial; **PDBTitle:** mammalian mitochondrial translation initiation factor 2
96	d1gq6a_	Alignment	not modelled	8.4	28	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
97	d1pkla3	Alignment	not modelled	8.1	12	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
98	d1xm3a_	Alignment	not modelled	8.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
99	d1wx0a1	Alignment	not modelled	8.0	60	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase