Phyre^2

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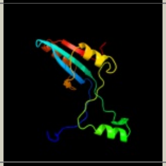
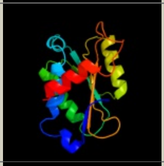
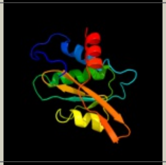
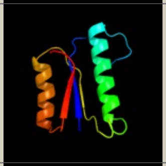
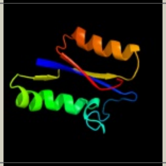
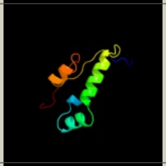
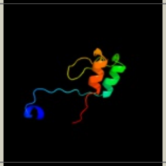
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1fuiB_	Alignment		100.0	100	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-fucose isomerase; **PDBTitle:** l-fucose isomerase from escherichia coli
2	c3a9rA_	Alignment		100.0	65	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-arabinose isomerase; **PDBTitle:** x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol
3	d1fuia1	Alignment		100.0	100	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**FucI/AraA C-terminal domain-like **Family:**L-fucose isomerase, C-terminal domain
4	d1fuia2	Alignment		100.0	100	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**L-fucose isomerase, N-terminal and second domains
5	d2ajta2	Alignment		100.0	11	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**AraA N-terminal and middle domain-like
6	c2hxgB_	Alignment		100.0	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-arabinose isomerase; **PDBTitle:** crystal structure of mn2+ bound ecai
7	d2ajta1	Alignment		83.6	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**FucI/AraA C-terminal domain-like **Family:**AraA C-terminal domain-like
8	d1kfia1	Alignment		83.0	15	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
9	d3pmga1	Alignment		82.4	15	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
10	d1mkza_	Alignment		78.6	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
11	d1xi8a3	Alignment		77.0	18	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like

12	c3lftA_	Alignment		73.4	13	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the abc domain in complex with l-trp from2 streptococcus pneumonia to 1.35a
13	d2ieaa3	Alignment		72.1	16	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
14	c3qfeB_	Alignment		70.8	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative dihydrodipicolinate synthase family protein; **PDBTitle:** crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis
15	c2p10D_	Alignment		69.2	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mll9387 protein; **PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
16	c2pjkA_	Alignment		68.8	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**178aa long hypothetical molybdenum cofactor **PDBTitle:** structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
17	d2p10a1	Alignment		67.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Mll9387-like
18	d1r9da_	Alignment		66.2	19	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
19	c3m9yB_	Alignment		63.6	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from methicillin2 resistant staphylococcus aureus at 1.9 angstrom resolution
20	d2f7wa1	Alignment		63.5	20	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
21	c3gjzB_	Alignment	not modelled	63.2	15	**PDB header:**immune system **Chain:** B: **PDB Molecule:**microcin immunity protein mccf; **PDBTitle:** crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
22	d1uuya_	Alignment	not modelled	61.9	12	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
23	d2a5la1	Alignment	not modelled	61.3	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
24	d2bfda1	Alignment	not modelled	61.2	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
25	d1zl0a2	Alignment	not modelled	61.0	11	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
26	c2wc1A_	Alignment	not modelled	60.1	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin; **PDBTitle:** three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a
27	c3s5oA_	Alignment	not modelled	58.6	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase, mitochondrial; **PDBTitle:** crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
28	d1yoba1	Alignment	not modelled	58.4	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related

29	d1y5ea1	Alignment	not modelled	56.6	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
30	d1w3ia_	Alignment	not modelled	56.5	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
31	c2vlbC_	Alignment	not modelled	55.2	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**arylmalonate decarboxylase; **PDBTitle:** structure of unliganded arylmalonate decarboxylase
32	d2g2ca1	Alignment	not modelled	54.9	23	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
33	c3snrA_	Alignment	not modelled	53.2	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
34	d1xxxa1	Alignment	not modelled	52.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
35	c2rfgB_	Alignment	not modelled	51.6	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
36	d1di6a_	Alignment	not modelled	50.8	21	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
37	c3ip5A_	Alignment	not modelled	50.8	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter, substrate binding protein (amino acid); **PDBTitle:** structure of atu2422-gaba receptor in complex with alanine
38	c3h6hB_	Alignment	not modelled	49.4	11	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**glutamate receptor, ionotropic kainate 2; **PDBTitle:** crystal structure of the glur6 amino terminal domain dimer assembly2 mpd form
39	d1m6ja_	Alignment	not modelled	49.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
40	c2zkiH_	Alignment	not modelled	48.3	15	**PDB header:**transcription **Chain:** H: **PDB Molecule:**199aa long hypothetical trp repressor binding **PDBTitle:** crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
41	c1yyaA_	Alignment	not modelled	46.8	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of tt0473, putative triosephosphate isomerase from2 thermus thermophilus hb8
42	d2p12a1	Alignment	not modelled	46.2	26	**Fold:**FomD barrel-like **Superfamily:**FomD-like **Family:**FomD-like
43	c2dp3A_	Alignment	not modelled	45.1	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of a double mutant (c202a/a198v) of triosephosphate2 isomerase from giardia lamblia
44	c2y8nC_	Alignment	not modelled	44.9	20	**PDB header:**lyase **Chain:** C: **PDB Molecule:**4-hydroxyphenylacetate decarboxylase large subunit; **PDBTitle:** crystal structure of glycyl radical enzyme
45	d1b9ba_	Alignment	not modelled	44.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
46	d1o5xa_	Alignment	not modelled	43.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
47	d1dkia_	Alignment	not modelled	42.2	24	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
48	c3ksmA_	Alignment	not modelled	42.2	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc-type sugar transport system, periplasmic component; **PDBTitle:** crystal structure of abc-type sugar transport system, periplasmic2 component from hahella chejuensis
49	d1r2ra_	Alignment	not modelled	41.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
50	c3q4nA_	Alignment	not modelled	40.4	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj0754; **PDBTitle:** crystal structure of hypothetical protein mj0754 from methanococcus2 jannaschii dsm 2661
51	d1aw1a_	Alignment	not modelled	40.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
52	d1pvja_	Alignment	not modelled	40.1	23	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
53	c3bb7A_	Alignment	not modelled	39.9	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interpain a; **PDBTitle:** structure of prevotella intermedia prointerpain a fragment 39-3592 (mutant c154a)
54	c2r8wB_	Alignment	not modelled	39.3	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**agr_c_1641p; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58

55	d1n55a_	Alignment	not modelled	39.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
56	c3gr7A_	Alignment	not modelled	38.6	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
57	d1suxa_	Alignment	not modelled	38.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
58	c3i45A_	Alignment	not modelled	37.7	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**twin-arginine translocation pathway signal protein; **PDBTitle:** crystal structure of putative twin-arginine translocation pathway2 signal protein from rhodospirillum rubrum atcc 11170
59	c2qh8A_	Alignment	not modelled	37.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of conserved domain protein from vibrio2 cholerae o1 biovar eltor str. n16961
60	d1neya_	Alignment	not modelled	37.1	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
61	c2qvcC_	Alignment	not modelled	36.9	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**sugar abc transporter, periplasmic sugar-binding **PDBTitle:** crystal structure of a periplasmic sugar abc transporter2 from thermotoga maritima
62	d1qo0a_	Alignment	not modelled	36.9	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
63	c3td9A_	Alignment	not modelled	36.5	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**branched chain amino acid abc transporter, periplasmic **PDBTitle:** crystal structure of a leucine binding protein livk (tm1135) from2 thermotoga maritima msb8 at 1.90 a resolution
64	c3bbaB_	Alignment	not modelled	36.3	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**interpain a; **PDBTitle:** structure of active wild-type prevotella intermedia interpain a2 cysteine protease
65	d1tjya_	Alignment	not modelled	36.2	13	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
66	d1trea_	Alignment	not modelled	35.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
67	d1ycga1	Alignment	not modelled	35.4	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
68	c3b4uB_	Alignment	not modelled	35.1	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
69	c3krsB_	Alignment	not modelled	34.7	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** structure of triosephosphate isomerase from cryptosporidium parvum at2 1.55a resolution
70	d2auna2	Alignment	not modelled	33.9	11	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
71	c3kxqB_	Alignment	not modelled	33.5	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from bartonella2 henselae at 1.6a resolution
72	d2ftsa3	Alignment	not modelled	33.4	9	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
73	c3na8A_	Alignment	not modelled	32.9	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
74	c3qi7A_	Alignment	not modelled	32.5	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
75	c1zrsB_	Alignment	not modelled	31.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** wild-type ld-carboxypeptidase
76	c3g0sA_	Alignment	not modelled	31.8	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
77	c3i09A_	Alignment	not modelled	31.4	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic branched-chain amino acid-binding protein; **PDBTitle:** crystal structure of a periplasmic binding protein (bma2936) from2 burkholderia mallei at 1.80 a resolution
78	c2x7xA_	Alignment	not modelled	31.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** fructose binding periplasmic domain of hybrid two component2 system bt1754
79	c3daqB_	Alignment	not modelled	30.6	7	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
						PDB header:isomerase

80	c3gvgA_	Alignment	not modelled	30.6	19	**Chain:** A: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from mycobacterium2 tuberculosis
81	c3n5lA_	Alignment	not modelled	30.4	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**binding protein component of abc phosphonate transporter; **PDBTitle:** crystal structure of a binding protein component of abc phosphonate2 transporter (pa3383) from pseudomonas aeruginosa at 1.97 a resolution
82	c3noeA_	Alignment	not modelled	30.1	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
83	c3mjdA_	Alignment	not modelled	29.8	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.9 angstrom crystal structure of orotate2 phosphoribosyltransferase (pyre) francisella tularensis.
84	d1kv5a_	Alignment	not modelled	29.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
85	d1qs0a_	Alignment	not modelled	29.6	13	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
86	c3fluD_	Alignment	not modelled	29.6	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
87	c3r85H_	Alignment	not modelled	29.3	60	**PDB header:**apoptosis **Chain:** H: **PDB Molecule:**heme-binding protein 2; **PDBTitle:** crystal structure of human soul bh3 domain in complex with bcl-xl
88	d1o5ka_	Alignment	not modelled	29.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
89	c3cprB_	Alignment	not modelled	29.0	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
90	d1jpma1	Alignment	not modelled	28.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
91	c3o3nA_	Alignment	not modelled	28.6	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**alpha-subunit 2-hydroxyisocaproyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
92	c2l9dA_	Alignment	not modelled	28.6	42	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of the protein yp_546394.1, the first structural2 representative of the pfam family pf12112
93	d1mo0a_	Alignment	not modelled	28.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
94	c2vc6A_	Alignment	not modelled	28.3	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
95	d2liva_	Alignment	not modelled	28.3	10	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
96	c3th6B_	Alignment	not modelled	28.2	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from rhipicephalus2 (boophilus) microplus.
97	d2a6na1	Alignment	not modelled	28.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
98	c2yxgD_	Alignment	not modelled	27.7	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
99	c2r94B_	Alignment	not modelled	27.6	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxy-(6-phospho-)gluconate aldolase; **PDBTitle:** crystal structure of kd(p)ga from t.tenax
100	d1sw3a_	Alignment	not modelled	27.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
101	c3r85E_	Alignment	not modelled	27.2	60	**PDB header:**apoptosis **Chain:** E: **PDB Molecule:**heme-binding protein 2; **PDBTitle:** crystal structure of human soul bh3 domain in complex with bcl-xl
102	c3r85G_	Alignment	not modelled	27.0	60	**PDB header:**apoptosis **Chain:** G: **PDB Molecule:**heme-binding protein 2; **PDBTitle:** crystal structure of human soul bh3 domain in complex with bcl-xl
103	d2arka1	Alignment	not modelled	26.9	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
104	c3lerA_	Alignment	not modelled	26.7	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
105	c3sg0A_	Alignment	not modelled	26.5	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2

106	d1uz5a3	Alignment	not modelled	26.2	12	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
107	c3eb2A_	Alignment	not modelled	25.9	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
108	c3n0xA_	Alignment	not modelled	25.7	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**possible substrate binding protein of abc transporter **PDBTitle:** crystal structure of an abc-type branched-chain amino acid transporter2 (rpa4397) from rhodopseudomonas palustris cga009 at 1.50 a resolution
109	d1vmea1	Alignment	not modelled	25.5	6	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
110	c2p1nD_	Alignment	not modelled	24.8	16	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**skp1-like protein 1a; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase
111	c2uuvC_	Alignment	not modelled	24.7	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**alkyldihydroxyacetonephosphate synthase; **PDBTitle:** alkyldihydroxyacetonephosphate synthase in p1
112	d2btma_	Alignment	not modelled	24.5	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
113	c3pueA_	Alignment	not modelled	24.3	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
114	d1f74a_	Alignment	not modelled	24.2	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
115	c3eo5A_	Alignment	not modelled	24.0	36	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**resuscitation-promoting factor rpfb; **PDBTitle:** crystal structure of the resuscitation promoting factor rpfb
116	c2v9dB_	Alignment	not modelled	23.6	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
117	c3n2lA_	Alignment	not modelled	23.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar eltor3 str. n16961
118	c3n2xB_	Alignment	not modelled	22.8	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uncharacterized protein yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
119	c3g23A_	Alignment	not modelled	22.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ld-carboxypeptidase a; **PDBTitle:** crystal structure of a ld-carboxypeptidase a (saro_1426) from2 novosphingobium aromaticivorans dsm at 1.89 a resolution
120	d2dara1	Alignment	not modelled	22.3	40	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain