






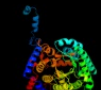























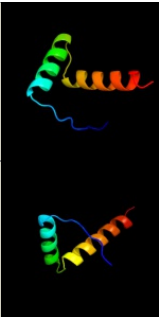
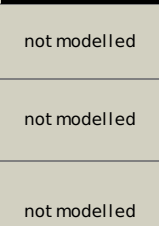


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3hazA_</a>	 Alignment		100.0	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dehydrogenase; <b>PDBTitle:</b> crystal structure of bifunctional proline utilization a2 (puta) protein
2	<a href="#">c1k87A_</a>	 Alignment		100.0	99	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dehydrogenase; <b>PDBTitle:</b> crystal structure of e.coli puta (residues 1-669)
3	<a href="#">c3e2sA_</a>	 Alignment		100.0	100	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dehydrogenase; <b>PDBTitle:</b> crystal structure reduced puta86-630 mutant y540s complexed with l-2 proline
4	<a href="#">c1tj2A_</a>	 Alignment		100.0	100	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional puta protein; <b>PDBTitle:</b> crystal structure of e. coli puta proline dehydrogenase domain2 (residues 86-669) complexed with acetate
5	<a href="#">c3qanB_</a>	 Alignment		100.0	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-pyrroline-5-carboxylate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of 1-pyrroline-5-carboxylate dehydrogenase from2 bacillus halodurans
6	<a href="#">d1uzba_</a>	 Alignment		100.0	37	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
7	<a href="#">c3ed6B_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> betaine aldehyde dehydrogenase; <b>PDBTitle:</b> 1.7 angstrom resolution crystal structure of betaine aldehyde2 dehydrogenase (betb) from staphylococcus aureus
8	<a href="#">d1a4sa_</a>	 Alignment		100.0	25	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
9	<a href="#">c2o2qA_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formyltetrahydrofolate dehydrogenase; <b>PDBTitle:</b> crystal structure of the c-terminal domain of rat2 10'formyltetrahydrofolate dehydrogenase in complex with nadp
10	<a href="#">c2d4eB_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 5-carboxymethyl-2-hydroxymuconate semialdehyde <b>PDBTitle:</b> crystal structure of the hpcc from thermus thermophilus hb8
11	<a href="#">c2jg7G_</a>	 Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> antiquitin; <b>PDBTitle:</b> crystal structure of seabream antiquitin and elucidation of2 its substrate specificity

12	<a href="#">d1bxsA_</a>	Alignment		100.0	30	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
13	<a href="#">c2ve5H_</a>	Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> betaine aldehyde dehydrogenase; <b>PDBTitle:</b> crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa
14	<a href="#">c3iwbB_</a>	Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aminoaldehyde dehydrogenase 1 from2 pisum sativum (psamadh1)
15	<a href="#">c3rh9A_</a>	Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> succinate-semialdehyde dehydrogenase (nad(p)(+)); <b>PDBTitle:</b> the crystal structure of oxidoreductase from marinobacter aquaeolei
16	<a href="#">d1o9ja_</a>	Alignment		100.0	29	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
17	<a href="#">c1t90B_</a>	Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable methylmalonate-semialdehyde dehydrogenase from bacillus subtilis
18	<a href="#">d1ag8a_</a>	Alignment		100.0	28	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
19	<a href="#">d1o04a_</a>	Alignment		100.0	28	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
20	<a href="#">c3b4wA_</a>	Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aldehyde dehydrogenase2 complexed with nad+
21	<a href="#">c3ifgH_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> succinate-semialdehyde dehydrogenase (nadp+); <b>PDBTitle:</b> crystal structure of succinate-semialdehyde dehydrogenase from2 burkholderia pseudomallei, part 1 of 2
22	<a href="#">c3ek1C_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aldehyde dehydrogenase from brucella2 melitensis biovar abortus 2308
23	<a href="#">d1wnda_</a>	Alignment	not modelled	100.0	33	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
24	<a href="#">c3k2wD_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> betaine-aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
25	<a href="#">d1ky8a_</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
26	<a href="#">c3i44A_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aldehyde dehydrogenase from bartonella2 henselae at 2.0a resolution
27	<a href="#">d1euha_</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
28	<a href="#">c2vroB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400

29	<a href="#">d1tj1a2</a>	Alignment	not modelled	100.0	100	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FAD-linked oxidoreductase <b>Family:</b> Proline dehydrogenase domain of bifunctional PutA protein
30	<a href="#">c3r31A</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> betaine aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of betaine aldehyde dehydrogenase from agrobacterium2 tumefaciens
31	<a href="#">c3prlD</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nadp-dependent glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of nadp-dependent glyceraldehyde-3-phosphate2 dehydrogenase from bacillus halodurans c-125
32	<a href="#">c2w8qA</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> succinate-semialdehyde dehydrogenase, <b>PDBTitle:</b> the crystal structure of human ssadh in complex with ssa.
33	<a href="#">c2hg2A</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde dehydrogenase a; <b>PDBTitle:</b> structure of lactaldehyde dehydrogenase
34	<a href="#">c3jz4C</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> succinate-semialdehyde dehydrogenase [nadp+]; <b>PDBTitle:</b> crystal structure of e. coli nadp dependent enzyme
35	<a href="#">c3ju8B</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> succinylglutamic semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of succinylglutamic semialdehyde dehydrogenase from2 pseudomonas aeruginosa.
36	<a href="#">c3rosA</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of nad-dependent aldehyde dehydrogenase from2 lactobacillus acidophilus
37	<a href="#">c3efvC</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative succinate-semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative succinate-semialdehyde dehydrogenase2 from salmonella typhimurium lt2 with bound nad
38	<a href="#">c3pqaA</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lactaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase gapn2 from methanocaldococcus jannaschii dsm 2661
39	<a href="#">c3r64A</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad dependent benzaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of a nad-dependent benzaldehyde dehydrogenase from2 corynebacterium glutamicum
40	<a href="#">d1ez0a</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
41	<a href="#">d1bi9a</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
42	<a href="#">c3v4cB</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aldehyde dehydrogenase (nadp+); <b>PDBTitle:</b> crystal structure of a semialdehyde dehydrogenase from sinorhizobium2 meliloti 1021
43	<a href="#">d1ad3a</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
44	<a href="#">c3lnsD</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> benzaldehyde dehydrogenase; <b>PDBTitle:</b> benzaldehyde dehydrogenase, a class 3 aldehyde dehydrogenase, with2 bound nadp+ and benzoate adduct
45	<a href="#">c3k9dD</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of probable aldehyde dehydrogenase from listeria2 monocytogenes egd-e
46	<a href="#">d1o20a</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
47	<a href="#">c3my7A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase/acetaldehyde dehydrogenase; <b>PDBTitle:</b> the crystal structure of the acdh domain of an alcohol dehydrogenase2 from vibrio parahaemolyticus to 2.25a
48	<a href="#">d1vlua</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
49	<a href="#">c2ekgB</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> proline dehydrogenase/delta-1-pyrroline-5-carboxylate <b>PDBTitle:</b> structure of thermus thermophilus proline dehydrogenase inactivated by2 n-propargylglycine
50	<a href="#">c2h5gA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> delta 1-pyrroline-5-carboxylate synthetase; <b>PDBTitle:</b> crystal structure of human pyrroline-5-carboxylate synthetase
51	<a href="#">c1vlub</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-glutamyl phosphate reductase; <b>PDBTitle:</b> crystal structure of gamma-glutamyl phosphate reductase (yor323c) from2 saccharomyces cerevisiae at 2.40 a resolution
52	<a href="#">d1tj1a1</a>	Alignment	not modelled	100.0	100	<b>Fold:</b> N-terminal domain of bifunctional PutA protein <b>Superfamily:</b> N-terminal domain of bifunctional PutA protein <b>Family:</b> N-terminal domain of bifunctional PutA protein

53	<a href="#">d2ay0a1</a>	Alignment		99.7	98	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> PutA pre-N-terminal region-like
54	<a href="#">c2rbfB</a>	Alignment		99.5	100	<b>PDB header:</b> oxidoreductase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein puta; <b>PDBTitle:</b> structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
55	<a href="#">d1tz9a</a>	Alignment	not modelled	92.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> UxuA-like
56	<a href="#">c3bdkB</a>	Alignment	not modelled	84.9	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> d-mannonate dehydratase; <b>PDBTitle:</b> crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
57	<a href="#">c3cnyA</a>	Alignment	not modelled	64.9	8	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> inositol catabolism protein iole; <b>PDBTitle:</b> crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcfs1 at 1.85 a3 resolution
58	<a href="#">d1eucb1</a>	Alignment	not modelled	61.4	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
59	<a href="#">d1k75a</a>	Alignment	not modelled	59.6	17	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> L-histidinol dehydrogenase HisD
60	<a href="#">c3k2gA</a>	Alignment	not modelled	56.9	14	<b>PDB header:</b> resiniferatoxin binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> resiniferatoxin-binding, phosphotriesterase- <b>PDBTitle:</b> crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
61	<a href="#">c2ixaA</a>	Alignment	not modelled	54.3	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-n-acetyl galactosaminidase; <b>PDBTitle:</b> a-zyme, n-acetyl galactosaminidase
62	<a href="#">d2nu7a1</a>	Alignment	not modelled	54.0	27	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
63	<a href="#">c1v9nA</a>	Alignment	not modelled	49.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> structure of malate dehydrogenase from pyrococcus horikoshii ot3
64	<a href="#">c2g8yB</a>	Alignment	not modelled	48.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> malate/l-lactate dehydrogenases; <b>PDBTitle:</b> the structure of a putative malate/lactate dehydrogenase from e. coli.
65	<a href="#">c1vbiA</a>	Alignment	not modelled	46.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> type 2 malate/lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
66	<a href="#">d1xrha</a>	Alignment	not modelled	45.5	22	<b>Fold:</b> L-sulfolactate dehydrogenase-like <b>Superfamily:</b> L-sulfolactate dehydrogenase-like <b>Family:</b> L-sulfolactate dehydrogenase-like
67	<a href="#">c2yvqA</a>	Alignment	not modelled	44.8	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase; <b>PDBTitle:</b> crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
68	<a href="#">d1bh9b</a>	Alignment	not modelled	40.1	27	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> TBP-associated factors, TAFs
69	<a href="#">d1i60a</a>	Alignment	not modelled	38.4	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> loll-like
70	<a href="#">d1rfma</a>	Alignment	not modelled	38.3	17	<b>Fold:</b> L-sulfolactate dehydrogenase-like <b>Superfamily:</b> L-sulfolactate dehydrogenase-like <b>Family:</b> L-sulfolactate dehydrogenase-like
71	<a href="#">c3dx5A</a>	Alignment	not modelled	37.2	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein asbf; <b>PDBTitle:</b> crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
72	<a href="#">c3uoeB</a>	Alignment	not modelled	37.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> the crystal structure of dehydrogenase from sinorhizobium meliloti
73	<a href="#">d1nxua</a>	Alignment	not modelled	36.6	20	<b>Fold:</b> L-sulfolactate dehydrogenase-like <b>Superfamily:</b> L-sulfolactate dehydrogenase-like <b>Family:</b> L-sulfolactate dehydrogenase-like
74	<a href="#">c3i0pA</a>	Alignment	not modelled	36.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of malate dehydrogenase from entamoeba histolytica
75	<a href="#">c1wtjB</a>	Alignment	not modelled	35.5	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ureidoglycolate dehydrogenase; <b>PDBTitle:</b> crystal structure of delta1-piperidine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
76	<a href="#">d1hn0a1</a>	Alignment	not modelled	34.5	16	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Chondroitin AC/alginate lyase <b>Family:</b> Hyaluronate lyase-like catalytic, N-terminal domain <b>PDB header:</b> transferase

77	<a href="#">c3pe3D_</a>	Alignment	not modelled	34.4	22	<b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine--peptide n- <b>PDBTitle:</b> structure of human o-glcna2 transferase and its complex with a peptide2 substrate
78	<a href="#">c3gkuB_</a>	Alignment	not modelled	33.0	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable rna-binding protein; <b>PDBTitle:</b> crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940
79	<a href="#">d2nu7b1</a>	Alignment	not modelled	32.5	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
80	<a href="#">d2g0wa1</a>	Alignment	not modelled	31.6	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> lol1-like
81	<a href="#">c2vsnB_</a>	Alignment	not modelled	31.1	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> xcogt; <b>PDBTitle:</b> structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of3 intracellular glycosylation
82	<a href="#">c3kwsB_</a>	Alignment	not modelled	30.2	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative sugar isomerase; <b>PDBTitle:</b> crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
83	<a href="#">d1s7ia_</a>	Alignment	not modelled	28.9	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> DGPF domain (Pfam 04946)
84	<a href="#">c3oqbF_</a>	Alignment	not modelled	28.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
85	<a href="#">c3cinA_</a>	Alignment	not modelled	28.9	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> myo-inositol-1-phosphate synthase-related protein; <b>PDBTitle:</b> crystal structure of a myo-inositol-1-phosphate synthase-related2 protein (tm_1419) from thermotoga maritima msb8 at 1.70 a resolution
86	<a href="#">d1sd4a_</a>	Alignment	not modelled	27.3	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Penicillinase repressor
87	<a href="#">d1a9xa2</a>	Alignment	not modelled	27.3	15	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
88	<a href="#">d1r30a_</a>	Alignment	not modelled	26.6	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Radical SAM enzymes <b>Family:</b> Biotin synthase
89	<a href="#">c1r30A_</a>	Alignment	not modelled	26.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> biotin synthase; <b>PDBTitle:</b> the crystal structure of biotin synthase, an s-2 adenosylmethionine-dependent radical enzyme
90	<a href="#">c1z2iA_</a>	Alignment	not modelled	26.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of agrobacterium tumefaciens malate2 dehydrogenase, new york structural genomics consortium
91	<a href="#">d2pb1a1</a>	Alignment	not modelled	25.4	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
92	<a href="#">d1xima_</a>	Alignment	not modelled	25.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Xylose isomerase
93	<a href="#">c1eucB_</a>	Alignment	not modelled	24.0	22	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> succinyl-coa synthetase, beta chain; <b>PDBTitle:</b> crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase
94	<a href="#">d2vgna3</a>	Alignment	not modelled	23.6	9	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> L30e-like <b>Family:</b> ERF1/Dom34 C-terminal domain-like
95	<a href="#">d2aaaa2</a>	Alignment	not modelled	23.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
96	<a href="#">c2hk1D_</a>	Alignment	not modelled	22.8	10	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> d-psicose 3-epimerase; <b>PDBTitle:</b> crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
97	<a href="#">d1oi7a1</a>	Alignment	not modelled	21.3	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
98	<a href="#">d1y5ea1</a>	Alignment	not modelled	20.4	19	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like
99	<a href="#">d1bofa2</a>	Alignment	not modelled	20.3	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
100	<a href="#">d1wu2a3</a>	Alignment	not modelled	20.3	15	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like