



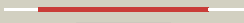




















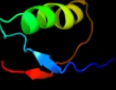

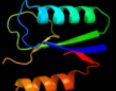



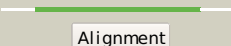
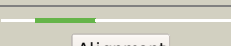

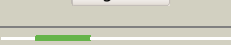
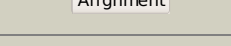


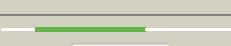
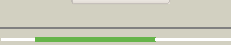
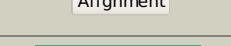
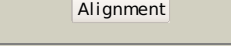
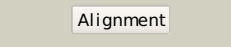

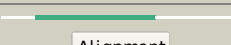
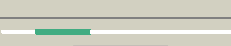
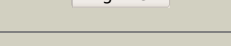

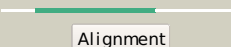
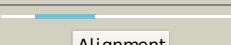


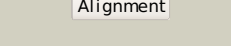
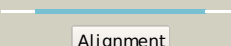
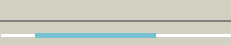
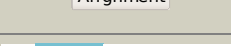
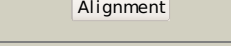


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2d1pa1</a>	 Alignment		100.0	100	<b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrEF-like
2	<a href="#">d2hy5a1</a>	 Alignment		100.0	45	<b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrEF-like
3	<a href="#">d1jx7a_</a>	 Alignment		100.0	23	<b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrEF-like
4	<a href="#">d2hy5b1</a>	 Alignment		100.0	16	<b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrEF-like
5	<a href="#">d2d1pb1</a>	 Alignment		99.9	23	<b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrEF-like
6	<a href="#">c3mc3A_</a>	 Alignment		99.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dsre/dsrf-like family protein; <b>PDBTitle:</b> crystal structure of dsre/dsrf-like family protein (np_342589.1) from2 sulfolobus solfataricus at 1.49 a resolution
7	<a href="#">c2qs7D_</a>	 Alignment		99.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase of the dsre/dsrf-like2 family (sso1126) from sulfolobus solfataricus p2 at 2.09 a resolution
8	<a href="#">c3pnxF_</a>	 Alignment		99.4	13	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> putative sulfurtransferase dsre; <b>PDBTitle:</b> crystal structure of a putative sulfurtransferase dsre (swol_2425)2 from syntrophomonas wolfei str. goettingen at 1.92 a resolution
9	<a href="#">d2hy5c1</a>	 Alignment		99.2	22	<b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrH-like
10	<a href="#">c2pd2A_</a>	 Alignment		98.4	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein st0148; <b>PDBTitle:</b> crystal structure of (st0148) conserved hypothetical from sulfolobus2 tokodaii strain7
11	<a href="#">c2fb6A_</a>	 Alignment		98.3	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> structure of conserved protein of unknown function bt1422 from2 bacteroides thetaiotaomicron

12	<a href="#">d2d1pc1</a>	Alignment		98.3	14	<b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrH-like
13	<a href="#">d1l1sa_</a>	Alignment		98.1	17	<b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrEF-like
14	<a href="#">d1x9aa_</a>	Alignment		98.0	18	<b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrH-like
15	<a href="#">c3oy2A_</a>	Alignment		90.5	20	<b>PDB header:</b> viral protein,transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyltransferase b736l; <b>PDBTitle:</b> crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
16	<a href="#">c3lcmB_</a>	Alignment		88.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of smu.1420 from streptococcus mutans ua159
17	<a href="#">c2gejA_</a>	Alignment		88.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol mannosyltransferase (pima); <b>PDBTitle:</b> crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
18	<a href="#">c2qzsA_</a>	Alignment		88.3	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen synthase; <b>PDBTitle:</b> crystal structure of wild-type e.coli gs in complex with adp2 and glucose(wtgsb)
19	<a href="#">d1gsaa1</a>	Alignment		87.3	20	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> Prokaryotic glutathione synthetase, N-terminal domain
20	<a href="#">c1gshA_</a>	Alignment		86.9	22	<b>PDB header:</b> glutathione biosynthesis ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione biosynthetic ligase; <b>PDBTitle:</b> structure of escherichia coli glutathione synthetase at ph 7.5
21	<a href="#">d1rzua_</a>	Alignment	not modelled	86.3	19	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
22	<a href="#">d1pn3a_</a>	Alignment	not modelled	86.0	21	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
23	<a href="#">c2p6pB_</a>	Alignment	not modelled	85.4	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase; <b>PDBTitle:</b> x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
24	<a href="#">d2bisa1</a>	Alignment	not modelled	84.9	26	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
25	<a href="#">d1rrva_</a>	Alignment	not modelled	84.7	24	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
26	<a href="#">d1iira_</a>	Alignment	not modelled	81.7	15	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
27	<a href="#">d1qrda_</a>	Alignment	not modelled	81.6	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
28	<a href="#">c3ia7A_</a>	Alignment	not modelled	76.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calg4; <b>PDBTitle:</b> crystal structure of calg4, the calicheamicin glycosyltransferase
						<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> glycosyl transferase, group 1 family

29	<a href="#">c2jlmH</a>	Alignment	not modelled	76.1	18	protein; <b>PDBTitle:</b> crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.
30	<a href="#">c2gk4A</a>	Alignment	not modelled	75.8	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> the crystal structure of the dna/pantothenate metabolism flavoprotein2 from streptococcus pneumoniae
31	<a href="#">c3c4vB</a>	Alignment	not modelled	75.8	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted glycosyltransferases; <b>PDBTitle:</b> structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
32	<a href="#">d1pvdal</a>	Alignment	not modelled	75.4	15	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
33	<a href="#">d1rtta</a>	Alignment	not modelled	73.4	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> NADPH-dependent FMN reductase
34	<a href="#">d1f0ka</a>	Alignment	not modelled	70.7	16	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Peptidoglycan biosynthesis glycosyltransferase MurG
35	<a href="#">d1udca</a>	Alignment	not modelled	69.4	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
36	<a href="#">c3iaaB</a>	Alignment	not modelled	68.9	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> calg2; <b>PDBTitle:</b> crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
37	<a href="#">c3hbjA</a>	Alignment	not modelled	68.2	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> flavonoid 3-o-glucosyltransferase; <b>PDBTitle:</b> structure of ugt78g1 complexed with udp
38	<a href="#">c2iv3B</a>	Alignment	not modelled	66.0	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyltransferase; <b>PDBTitle:</b> crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
39	<a href="#">c2q1wC</a>	Alignment	not modelled	63.9	23	<b>PDB header:</b> sugar binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> putative nucleotide sugar epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
40	<a href="#">c3icpA</a>	Alignment	not modelled	62.2	43	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of udp-galactose 4-epimerase
41	<a href="#">d2blna2</a>	Alignment	not modelled	62.0	17	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
42	<a href="#">c2iyaB</a>	Alignment	not modelled	61.3	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> oleandomycin glycosyltransferase; <b>PDBTitle:</b> the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
43	<a href="#">d1p9oa</a>	Alignment	not modelled	61.2	30	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> CoaB-like <b>Family:</b> CoaB-like
44	<a href="#">c2iyfA</a>	Alignment	not modelled	60.4	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oleandomycin glycosyltransferase; <b>PDBTitle:</b> the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
45	<a href="#">d1kewa</a>	Alignment	not modelled	60.4	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
46	<a href="#">c1hyqA</a>	Alignment	not modelled	60.2	28	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division inhibitor (mind-1); <b>PDBTitle:</b> mind bacterial cell division regulator from a. fulgidus
47	<a href="#">d1hyqa</a>	Alignment	not modelled	60.2	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
48	<a href="#">d1fmta2</a>	Alignment	not modelled	60.1	19	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
49	<a href="#">c2pk3B</a>	Alignment	not modelled	59.3	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gdp-6-deoxy-d-lyxo-4-hexulose reductase; <b>PDBTitle:</b> crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
50	<a href="#">d1bxka</a>	Alignment	not modelled	58.3	28	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
51	<a href="#">c2pzlB</a>	Alignment	not modelled	57.4	33	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative nucleotide sugar epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of the bordetella bronchiseptica enzyme2 wbmh in complex with nad and udp
52	<a href="#">d1v59a2</a>	Alignment	not modelled	57.0	14	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
53	<a href="#">c3othB</a>	Alignment	not modelled	56.7	19	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> calg1; <b>PDBTitle:</b> crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
54	<a href="#">c2p5uC</a>	Alignment	not modelled	56.5	37	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> crystal structure of thermus thermophilus hb8 udp-glucose 4-2 epimerase complex with nad

55	<a href="#">d2bw0a2</a>	 Alignment	not modelled	56.1	18	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
56	<a href="#">c3m2pD</a>	 Alignment	not modelled	54.3	23	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine 4-epimerase; <b>PDBTitle:</b> the crystal structure of udp-n-acetylglucosamine 4-epimerase2 from bacillus cereus
57	<a href="#">d1u7za</a>	 Alignment	not modelled	53.0	18	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> CoaB-like <b>Family:</b> CoaB-like
58	<a href="#">d1r6da</a>	 Alignment	not modelled	52.9	37	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
59	<a href="#">d1ubea1</a>	 Alignment	not modelled	52.1	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
60	<a href="#">c3fmfA</a>	 Alignment	not modelled	51.7	28	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
61	<a href="#">d1ebda2</a>	 Alignment	not modelled	51.4	12	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
62	<a href="#">c2recB</a>	 Alignment	not modelled	50.3	20	<b>PDB header:</b> helicase <b>PDB COMPND:</b>
63	<a href="#">d1s3ia2</a>	 Alignment	not modelled	49.5	16	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
64	<a href="#">c3io5B</a>	 Alignment	not modelled	47.3	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> recombination and repair protein; <b>PDBTitle:</b> crystal structure of a dimeric form of the uvsx recombinase core2 domain from enterobacteria phage t4
65	<a href="#">d1vhta</a>	 Alignment	not modelled	45.0	29	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
66	<a href="#">c3cr8C</a>	 Alignment	not modelled	44.2	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sulfate adenyllyltransferase, adenyllylsulfate <b>PDBTitle:</b> hexameric aps kinase from thiobacillus denitrificans
67	<a href="#">c3d0qB</a>	 Alignment	not modelled	43.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein calg3; <b>PDBTitle:</b> crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
68	<a href="#">c2ggsB</a>	 Alignment	not modelled	42.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 273aa long hypothetical dtdp-4-dehydrorhamnose <b>PDBTitle:</b> crystal structure of hypothetical dtdp-4-dehydrorhamnose2 reductase from sulfolobus tokodaii
69	<a href="#">d2qwxal</a>	 Alignment	not modelled	41.7	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
70	<a href="#">d2c1xa1</a>	 Alignment	not modelled	39.8	18	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
71	<a href="#">d1hdoa</a>	 Alignment	not modelled	39.7	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
72	<a href="#">c2x4gA</a>	 Alignment	not modelled	38.9	30	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside-diphosphate-sugar epimerase; <b>PDBTitle:</b> crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
73	<a href="#">c2w93A</a>	 Alignment	not modelled	38.4	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate decarboxylase isozyme 1; <b>PDBTitle:</b> crystal structure of the saccharomyces cerevisiae pyruvate2 decarboxylase variant e477q in complex with the surrogate3 pyruvamide
74	<a href="#">c3ouzA</a>	 Alignment	not modelled	38.2	9	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> biotin carboxylase; <b>PDBTitle:</b> crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
75	<a href="#">c2x0dA</a>	 Alignment	not modelled	37.0	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> wsaf; <b>PDBTitle:</b> apo structure of wsaf
76	<a href="#">d2pq6a1</a>	 Alignment	not modelled	36.9	16	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
77	<a href="#">d1ydga</a>	 Alignment	not modelled	36.7	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
78	<a href="#">d1oc2a</a>	 Alignment	not modelled	36.5	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
79	<a href="#">d1zpdal</a>	 Alignment	not modelled	36.3	16	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
80	<a href="#">c3kjbB</a>	 Alignment	not modelled	36.0	18	<b>PDB header:</b> hydrolase, metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> co dehydrogenase/acetyl-coa synthase complex, accessory

						<b>PDBTitle:</b> adp-bound state of cooc1 <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
81	<a href="#">d1jjva_</a>	Alignment	not modelled	35.7	23	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
82	<a href="#">d1dsla2</a>	Alignment	not modelled	35.7	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uronate dehydrogenase; <b>PDBTitle:</b> crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
83	<a href="#">c3rfxB_</a>	Alignment	not modelled	35.6	26	<b>PDB header:</b> chromosome segregation <b>Chain:</b> B: <b>PDB Molecule:</b> segregation protein; <b>PDBTitle:</b> structure of the bacterial chromosome segregation protein2 soj
84	<a href="#">c2bekB_</a>	Alignment	not modelled	35.2	18	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
85	<a href="#">d3lada2</a>	Alignment	not modelled	35.0	12	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanine-d-alanine ligase a; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
86	<a href="#">c3e5nA_</a>	Alignment	not modelled	35.0	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 336aa long hypothetical dtdp-glucose 4,6-dehydratase; <b>PDBTitle:</b> crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3
87	<a href="#">c2hunB_</a>	Alignment	not modelled	34.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> atpase, subunit of the get complex; <b>PDBTitle:</b> crystal structure of aspergillus fumigatus get3 with bound2 adp
88	<a href="#">c3ibgF_</a>	Alignment	not modelled	34.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atp synthase subunit alpha; <b>PDBTitle:</b> crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
89	<a href="#">c2qe7C_</a>	Alignment	not modelled	33.6	17	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> biotin carboxylase; <b>PDBTitle:</b> crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.
90	<a href="#">c2gpwC_</a>	Alignment	not modelled	33.1	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
91	<a href="#">c3of5A_</a>	Alignment	not modelled	32.5	3	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> azoreductase; <b>PDBTitle:</b> crystal structure of azoreductase from bacillus anthracis str. Sterne
92	<a href="#">c3p0rA_</a>	Alignment	not modelled	32.3	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
93	<a href="#">d2q46a1</a>	Alignment	not modelled	32.3	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
94	<a href="#">d1n2sa_</a>	Alignment	not modelled	31.9	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
95	<a href="#">d1nksa_</a>	Alignment	not modelled	30.5	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
96	<a href="#">c2r60A_</a>	Alignment	not modelled	30.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl transferase, group 1; <b>PDBTitle:</b> structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
97	<a href="#">c1ulzA_</a>	Alignment	not modelled	29.9	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate carboxylase n-terminal domain; <b>PDBTitle:</b> crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
98	<a href="#">d1ovma1</a>	Alignment	not modelled	29.7	20	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
99	<a href="#">d2bla1a1</a>	Alignment	not modelled	29.0	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
100	<a href="#">d1nhpa2</a>	Alignment	not modelled	28.5	10	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
101	<a href="#">c3sc6F_</a>	Alignment	not modelled	28.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> dtdp-4-dehydrorhamnose reductase; <b>PDBTitle:</b> 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
102	<a href="#">c2vedA_</a>	Alignment	not modelled	28.2	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> membrane protein capa1, protein tyrosine kinase; <b>PDBTitle:</b> crystal structure of the chimerical mutant capabk55m2 protein
103	<a href="#">c1w0jB_</a>	Alignment	not modelled	27.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp synthase alpha chain heart isoform, <b>PDBTitle:</b> beryllium fluoride inhibited bovine f1-atpase
104	<a href="#">c3okaA_</a>	Alignment	not modelled	27.2	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gdp-mannose-dependent al pha-(1-6)-phosphatidylinositol <b>PDBTitle:</b> crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)
105	<a href="#">d1onfa2</a>	Alignment	not modelled	26.6	8	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central



						domains
106	<a href="#">d1ojta2</a>	Alignment	not modelled	26.5	20	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
107	<a href="#">c3bjrA</a>	Alignment	not modelled	25.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative carboxylesterase; <b>PDBTitle:</b> crystal structure of a putative carboxylesterase (lp_1002) from <i>lactobacillus plantarum</i> wcf51 at 2.09 a resolution
108	<a href="#">d1vmda</a>	Alignment	not modelled	25.0	19	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Methylglyoxal synthase, MgsA
109	<a href="#">c1qzuB</a>	Alignment	not modelled	24.8	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein mds018; <b>PDBTitle:</b> crystal structure of human phosphopantothenoylcysteine decarboxylase
110	<a href="#">d1t5ba</a>	Alignment	not modelled	24.0	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
111	<a href="#">d2c5aa1</a>	Alignment	not modelled	23.8	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
112	<a href="#">c2x6rA</a>	Alignment	not modelled	23.8	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose-synthase tret; <b>PDBTitle:</b> crystal structure of trehalose synthase tret from p.2 horikoshi produced by soaking in trehalose
113	<a href="#">d3grsa2</a>	Alignment	not modelled	23.7	24	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
114	<a href="#">c3cioA</a>	Alignment	not modelled	23.3	11	<b>PDB header:</b> signaling protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase etk; <b>PDBTitle:</b> the kinase domain of escherichia coli tyrosine kinase etk
115	<a href="#">d1fjha</a>	Alignment	not modelled	23.2	31	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
116	<a href="#">c2w0mA</a>	Alignment	not modelled	22.4	25	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sso2452; <b>PDBTitle:</b> crystal structure of sso2452 from <i>sulfolobus solfataricus</i> 2 p2
117	<a href="#">d2acva1</a>	Alignment	not modelled	22.3	20	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
118	<a href="#">d2afhe1</a>	Alignment	not modelled	21.6	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
119	<a href="#">c2derA</a>	Alignment	not modelled	21.6	17	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> trna-specific 2-thiouridylase mnma; <b>PDBTitle:</b> cocrystal structure of an rna sulfuration enzyme mnma and 2 trna-glu in the initial trna binding state
120	<a href="#">d1djqa2</a>	Alignment	not modelled	21.4	14	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> C-terminal domain of adrenodoxin reductase-like