Phyre^2

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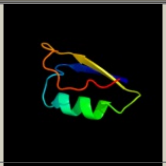
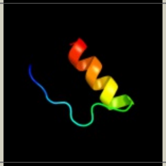
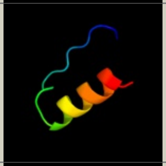
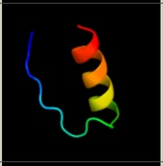
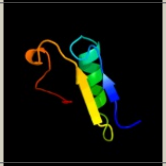
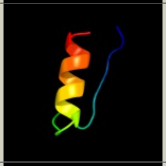
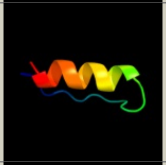
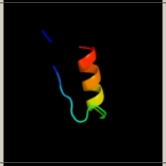
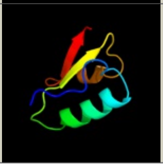
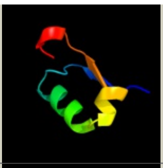
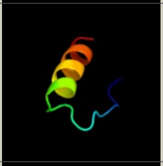
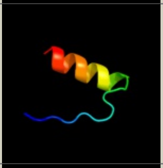
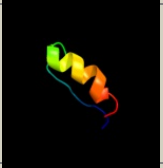
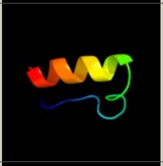
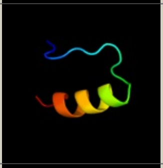
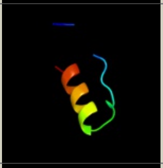
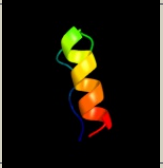
Description	Q2EER5
Date	Thu Jan 5 12:33:45 GMT 2012
Unique Job ID	915ec2341283d93a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qvoA_	Alignment		95.7	100	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nmra family protein; **PDBTitle:** structure of a rossmann-fold nad(p)-binding family protein from2 shigella flexneri.
2	c3dhnA_	Alignment		95.5	21	**PDB header:**isomerase, lyase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
3	d1oc2a_	Alignment		95.3	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
4	c2q1wC_	Alignment		95.0	42	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
5	d1hdoa_	Alignment		94.9	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
6	d1bxka_	Alignment		94.8	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
7	c3c1oA_	Alignment		94.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**eugenol synthase; **PDBTitle:** the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
8	c3e48B_	Alignment		93.3	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative nucleoside-diphosphate-sugar epimerase; **PDBTitle:** crystal structure of a nucleoside-diphosphate-sugar epimerase2 (sav0421) from staphylococcus aureus, northeast structural genomics3 consortium target zr319
9	c3gpiA_	Alignment		93.0	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** structure of putative nad-dependent epimerase/dehydratase2 from methylobacillus flagellatus
10	c2qx7A_	Alignment		93.0	33	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**eugenol synthase 1; **PDBTitle:** structure of eugenol synthase from ocimum basilicum
11	d2blla1	Alignment		92.9	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases

12	c2vrcD_	Alignment		92.7	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**triphenylmethane reductase; **PDBTitle:** crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
13	c3icpA_	Alignment		92.6	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of udp-galactose 4-epimerase
14	d1r6da_	Alignment		92.4	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
15	c3rfxB_	Alignment		92.2	42	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uronate dehydrogenase; **PDBTitle:** crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
16	d1udca_	Alignment		91.8	39	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
17	c2ggsB_	Alignment		91.7	35	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**273aa long hypothetical dtdp-4-dehydrorhamnose **PDBTitle:** crystal structure of hypothetical dtdp-4-dehydrorhamnose2 reductase from sulfolobus tokodaii
18	c2hunB_	Alignment		91.5	29	**PDB header:**lyase **Chain:** B: **PDB Molecule:**336aa long hypothetical dtdp-glucose 4,6-dehydratase; **PDBTitle:** crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3
19	c3m2pD_	Alignment		91.4	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine 4-epimerase; **PDBTitle:** the crystal structure of udp-n-acetylglucosamine 4-epimerase2 from bacillus cereus
20	c2pk3B_	Alignment		91.2	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gdp-6-deoxy-d-lyxo-4-hexulose reductase; **PDBTitle:** crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
21	d2c5aa1	Alignment	not modelled	90.9	38	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
22	d2q46a1	Alignment	not modelled	90.8	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
23	d2b69a1	Alignment	not modelled	90.5	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
24	c2b69A_	Alignment	not modelled	90.5	30	**PDB header:**lyase **Chain:** A: **PDB Molecule:**udp-glucuronate decarboxylase 1; **PDBTitle:** crystal structure of human udp-glucoronic acid decarboxylase
25	c2pzlB_	Alignment	not modelled	90.5	26	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**putative nucleotide sugar epimerase/dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme2 wbmg in complex with nad and udp
26	c2p5uC_	Alignment	not modelled	90.3	35	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** crystal structure of thermus thermophilus hb8 udp-glucose 4-2 epimerase complex with nad
27	d1sb8a_	Alignment	not modelled	90.0	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
28	d1n2sa_	Alignment	not modelled	89.9	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
						PDB header:oxidoreductase

29	c3sc6F_	Alignment	not modelled	89.9	29	**Chain:** F: **PDB Molecule:**dtdp-4-dehydrorhamnose reductase; **PDBTitle:** 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
30	d2fmua1	Alignment	not modelled	89.8	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
31	d1rpna_	Alignment	not modelled	89.8	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
32	c3ay3C_	Alignment	not modelled	89.5	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of glucuronic acid dehydrogeanse from2 chromohalobacter salexigens
33	c2x4gA_	Alignment	not modelled	89.2	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**nucleoside-diphosphate-sugar epimerase; **PDBTitle:** crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
34	d1kewa_	Alignment	not modelled	89.2	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
35	c2zklA_	Alignment	not modelled	88.9	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**capsular polysaccharide synthesis enzyme cap5f; **PDBTitle:** crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
36	c2yy7B_	Alignment	not modelled	88.7	35	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-threonine dehydrogenase; **PDBTitle:** crystal structure of thermolabile l-threonine dehydrogenase from2 flavobacterium frigidimaris kuc-1
37	d1db3a_	Alignment	not modelled	88.5	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
38	d1hyea1	Alignment	not modelled	88.4	39	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
39	d1npya1	Alignment	not modelled	88.4	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
40	c3slgB_	Alignment	not modelled	88.4	39	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pbgp3 protein; **PDBTitle:** crystal structure of pbgp3 protein from burkholderia pseudomallei
41	d1z45a2	Alignment	not modelled	88.0	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
42	d1wvga1	Alignment	not modelled	87.9	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
43	c2exxB_	Alignment	not modelled	87.8	26	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hscarg protein; **PDBTitle:** crystal structure of hscarg from homo sapiens in complex with nadp
44	c2rh8A_	Alignment	not modelled	87.7	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anthocyanidin reductase; **PDBTitle:** structure of apo anthocyanidin reductase from vitis vinifera
45	d1ek6a_	Alignment	not modelled	87.6	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
46	c3lu1C_	Alignment	not modelled	87.6	30	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**wbgu; **PDBTitle:** crystal structure analysis of wbgu: a udp-galnac 4-epimerase
47	d1e6ua_	Alignment	not modelled	87.6	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
48	c2q1uA_	Alignment	not modelled	87.4	22	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme wbmf in2 complex with nad+ and udp
49	d1xgka_	Alignment	not modelled	86.9	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
50	d1rkxa_	Alignment	not modelled	86.8	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
51	c2hrzA_	Alignment	not modelled	86.5	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nucleoside-diphosphate-sugar epimerase; **PDBTitle:** the crystal structure of the nucleoside-diphosphate-sugar epimerase2 from agrobacterium tumefaciens
52	d1n7ha_	Alignment	not modelled	86.3	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
53	d1gy8a_	Alignment	not modelled	86.2	40	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
54	d2a35a1	Alignment	not modelled	86.1	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases

55	c2iodD_	Alignment	not modelled	86.0	26	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydroflavonol 4-reductase; **PDBTitle:** binding of two substrate analogue molecules to2 dihydroflavonol-4-reductase alters the functional geometry3 of the catalytic site
56	c2z1mC_	Alignment	not modelled	85.8	35	**PDB header:**lyase **Chain:** C: **PDB Molecule:**gdp-d-mannose dehydratase; **PDBTitle:** crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
57	c2ydyA_	Alignment	not modelled	85.7	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine adenosyltransferase 2 subunit beta; **PDBTitle:** crystal structure of human s-adenosylmethionine synthetase2 2, beta subunit in orthorhombic crystal form
58	d2bkaa1	Alignment	not modelled	85.4	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
59	c3e8xA_	Alignment	not modelled	85.0	39	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative nad-dependent epimerase/dehydratase; **PDBTitle:** putative nad-dependent epimerase/dehydratase from bacillus halodurans.
60	c2c20D_	Alignment	not modelled	84.7	36	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** crystal structure of udp-glucose 4-epimerase
61	d1p77a1	Alignment	not modelled	84.3	40	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
62	c1t2aC_	Alignment	not modelled	83.6	30	**PDB header:**structural genomics,lyase **Chain:** C: **PDB Molecule:**gdp-mannose 4,6 dehydratase; **PDBTitle:** crystal structure of human gdp-d-mannose 4,6-dehydratase
63	d1t2aa_	Alignment	not modelled	83.6	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
64	c3l6eA_	Alignment	not modelled	83.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, short-chain dehydrogenase/reductase family; **PDBTitle:** crystal structure of putative short chain dehydrogenase/reductase2 family oxidoreductase from aeromonas hydrophila subsp. hydrophila3 atcc 7966
65	c3eheB_	Alignment	not modelled	82.0	29	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-glucose 4-epimerase (gale-1); **PDBTitle:** crystal structure of udp-glucose 4 epimerase (gale-1) from2 archaeoglobus fulgidus
66	c1npyA_	Alignment	not modelled	81.9	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical shikimate 5-dehydrogenase-like **PDBTitle:** structure of shikimate 5-dehydrogenase-like protein hi0607
67	d1y1pa1	Alignment	not modelled	81.8	43	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
68	c1n7gB_	Alignment	not modelled	81.4	35	**PDB header:**lyase **Chain:** B: **PDB Molecule:**gdp-d-mannose-4,6-dehydratase; **PDBTitle:** crystal structure of the gdp-mannose 4,6-dehydratase2 ternary complex with nadph and gdp-rhamnose.
69	c3i5mA_	Alignment	not modelled	81.2	43	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative leucoanthocyanidin reductase 1; **PDBTitle:** structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera
70	c3nzoB_	Alignment	not modelled	81.2	26	**PDB header:**lyase **Chain:** B: **PDB Molecule:**udp-n-acetylglucosamine 4,6-dehydratase; **PDBTitle:** udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri.
71	c3enkB_	Alignment	not modelled	80.8	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei
72	d2cmda1	Alignment	not modelled	80.7	39	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
73	c3a1nB_	Alignment	not modelled	80.5	38	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ndp-sugar epimerase; **PDBTitle:** crystal structure of l-threonine dehydrogenase from2 hyperthermophilic archaeon thermoplasma volcanium
74	c1z7eC_	Alignment	not modelled	80.0	38	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of full length arna
75	d1nvta1	Alignment	not modelled	79.8	41	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
76	c2gasA_	Alignment	not modelled	79.7	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isoflavone reductase; **PDBTitle:** crystal structure of isoflavone reductase
77	d1qyca_	Alignment	not modelled	79.6	39	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
78	c2gn9B_	Alignment	not modelled	79.2	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**udp-glcnac c6 dehydratase; **PDBTitle:** crystal structure of udp-glcnac inverting 4,6-dehydratase in complex2 with nadp and udp-glc
79	d1vl0a_	Alignment	not modelled	78.9	48	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases

80	c3ew7A_	Alignment	not modelled	78.8	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo0794 protein; **PDBTitle:** crystal structure of the lmo0794 protein from listeria2 monocytogenes. northeast structural genomics consortium3 target lmr162.
81	c3r6dA_	Alignment	not modelled	78.5	43	**PDB header:**lyase, isomerase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of nad-dependent epimerase/dehydratase from2 veillonella parvula dsm 2008 with cz-methylated lysine
82	c3oh8A_	Alignment	not modelled	78.1	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**nucleoside-diphosphate sugar epimerase (sula family); **PDBTitle:** crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
83	d1eq2a_	Alignment	not modelled	78.1	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
84	c2x86K_	Alignment	not modelled	77.5	29	**PDB header:**isomerase **Chain:** K: **PDB Molecule:**adp-l-glycero-d-manno-heptose-6-epimerase; **PDBTitle:** agme bound to adp-b-mannose
85	c3iusB_	Alignment	not modelled	77.4	32	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the structure of a functionally unknown conserved protein2 from silicibacter pomeroyi dss
86	c2p4hX_	Alignment	not modelled	77.1	22	**PDB header:**plant protein **Chain:** X: **PDB Molecule:**vestitone reductase; **PDBTitle:** crystal structure of vestitone reductase from alfalfa2 (medicago sativa l.)
87	c3dqpA_	Alignment	not modelled	75.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase ylbe; **PDBTitle:** crystal structure of the oxidoreductase ylbe from2 lactococcus lactis, northeast structural genomics3 consortium target kr121.
88	d1qyda_	Alignment	not modelled	75.4	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
89	c3l77A_	Alignment	not modelled	75.1	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain alcohol dehydrogenase; **PDBTitle:** x-ray structure alcohol dehydrogenase from archaeon thermococcus2 sibiricus complexed with 5-hydroxy-nadp
90	d1pqua1	Alignment	not modelled	74.8	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
91	c3h2sA_	Alignment	not modelled	73.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative nadh-flavin reductase; **PDBTitle:** crystal structure of the q03b84 protein from lactobacillus2 casei. northeast structural genomics consortium target3 lcr19.
92	d1e5qa1	Alignment	not modelled	73.3	41	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
93	c3o8qB_	Alignment	not modelled	71.7	42	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase i alpha; **PDBTitle:** 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
94	d1orra_	Alignment	not modelled	70.2	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
95	c3pwzA_	Alignment	not modelled	70.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase 3; **PDBTitle:** crystal structure of an ael1 enzyme from pseudomonas putida
96	c2zcuA_	Alignment	not modelled	68.8	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized oxidoreductase ytfg; **PDBTitle:** crystal structure of a new type of nadph-dependent quinone2 oxidoreductase (qor2) from escherichia coli
97	c1z45A_	Alignment	not modelled	67.1	35	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**gal10 bifunctional protein; **PDBTitle:** crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces3 cerevisiae complexed with nad, udp-glucose, and galactose
98	d1i24a_	Alignment	not modelled	66.5	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
99	c3donA_	Alignment	not modelled	66.5	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from staphylococcus2 epidermidis
100	c3etjB_	Alignment	not modelled	66.4	41	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure e. coli purk in complex with mg, adp, and2 pi
101	d1mlda1	Alignment	not modelled	66.2	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
102	d1fjha_	Alignment	not modelled	66.2	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
103	c2v6gA_	Alignment	not modelled	65.1	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**progesterone 5-beta-reductase; **PDBTitle:** structure of progesterone 5beta-reductase from digitalis2 lanata in complex with nadp

104	c3i4fD_	Alignment	not modelled	62.8	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**3-oxoacyl-[acyl-carrier protein] reductase; **PDBTitle:** structure of putative 3-oxoacyl-reductase from bacillus thuringiensis
105	c2hk8B_	Alignment	not modelled	62.1	43	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
106	c1e5lA_	Alignment	not modelled	61.9	41	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
107	d1vi2a1	Alignment	not modelled	61.7	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
108	c3tozA_	Alignment	not modelled	61.3	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
109	c2z2vA_	Alignment	not modelled	60.8	59	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1688; **PDBTitle:** crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
110	c1gpjA_	Alignment	not modelled	59.0	28	**PDB header:**reductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** glutamyl-trna reductase from methanopyrus kandleri
111	c2eggA_	Alignment	not modelled	57.1	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate 5-dehydrogenase (aroe) from2 geobacillus kaustophilus
112	c1nytC_	Alignment	not modelled	56.2	29	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** shikimate dehydrogenase aroe complexed with nadp+
113	c3orfC_	Alignment	not modelled	56.2	35	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dihydropteridine reductase; **PDBTitle:** crystal structure of dihydropteridine reductase from dictyostelium2 discoideum
114	c2nloA_	Alignment	not modelled	56.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum
115	c2axqA_	Alignment	not modelled	54.9	43	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
116	d1nyta1	Alignment	not modelled	52.5	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
117	c3fbtB_	Alignment	not modelled	52.2	33	**PDB header:**oxidoreductase, lyase **Chain:** B: **PDB Molecule:**chorismate mutase and shikimate 5-dehydrogenase **PDBTitle:** crystal structure of a chorismate mutase/shikimate 5-2 dehydrogenase fusion protein from clostridium3 acetobutylicum
118	c2jahB_	Alignment	not modelled	51.9	35	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**clavulanic acid dehydrogenase; **PDBTitle:** biochemical and structural analysis of the clavulanic acid2 dehydeogenase (cad) from streptomyces clavuligerus
119	d1mjfa_	Alignment	not modelled	51.7	50	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Spermidine synthase
120	d2b2ca1	Alignment	not modelled	51.6	63	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Spermidine synthase