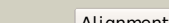


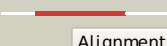
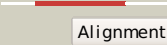
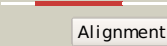
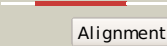
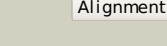
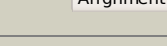
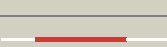
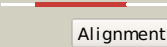
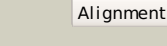
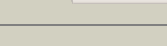
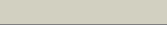
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z45A_	 Alignment		100.0	23	PDB header: isomerase Chain: A: PDB Molecule: gal10 bifunctional protein; PDBTitle: crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces3 cerevisiae complexed with nad, udp-glucose, and galactose
2	c1z7eC_	 Alignment		100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna
3	dli24a_	 Alignment		100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
4	c3oh8A_	 Alignment		100.0	11	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
5	c3e48B_	 Alignment		100.0	13	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
6	c2qx7A_	 Alignment		100.0	15	PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum
7	c2v6gA_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: progesterone 5-beta-reductase; PDBTitle: structure of progesterone 5beta-reductase from digitalis2 lanata in complex with nadp
8	c2vrcD_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: D: PDB Molecule: triphenylmethane reductase; PDBTitle: crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
9	c3c1oA_	 Alignment		100.0	14	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
10	d1xgka_	 Alignment		100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
11	c2zcuA_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized oxidoreductase ytfq; PDBTitle: crystal structure of a new type of nadph-dependent quinone2 oxidoreductase (qor2) from escherichia coli

12	d2c5aa1	Alignment		100.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
13	d1qyda_	Alignment		100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
14	d2b69a1	Alignment		100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
15	c2b69A_	Alignment		100.0	15	PDB header: lyase Chain: A: PDB Molecule: udp-glucuronate decarboxylase 1; PDBTitle: crystal structure of human udp-glucuronic acid decarboxylase
16	d1db3a_	Alignment		100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
17	d1e6ua_	Alignment		100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
18	d1qyca_	Alignment		100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
19	c2gn9B_	Alignment		100.0	17	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
20	d1oc2a_	Alignment		100.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
21	c2x4gA_	Alignment	not modelled	100.0	18	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
22	c2z1mC_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: C: PDB Molecule: gdp-d-mannose dehydratase; PDBTitle: crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
23	c3i5mA_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative leucoanthocyanidin reductase 1; PDBTitle: structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera
24	d1vl0a_	Alignment	not modelled	100.0	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
25	c2gasA_	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: isoflavone reductase; PDBTitle: crystal structure of isoflavone reductase
26	c2c20D_	Alignment	not modelled	100.0	15	PDB header: isomerase Chain: D: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of udp-glucose 4-epimerase
27	c3m2pD_	Alignment	not modelled	100.0	16	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
28	c3sc6F_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: F: PDB Molecule: ddtp-4-dehydrorhamnose reductase; PDBTitle: 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfd) from bacillus anthracis str.

						ames in complex with3 nadp PDB header: unknown function Chain: B: PDB Molecule: hscarg protein; PDBTitle: crystal structure of hscarg from homo sapiens in complex with nadp
29	c2exxB_	Alignment	not modelled	100.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
30	d1ek6a_	Alignment	not modelled	100.0	19	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
31	c2iodD_	Alignment	not modelled	100.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
32	d1n2sa_	Alignment	not modelled	100.0	13	PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei
33	c3enkB_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: l-threonine dehydrogenase; PDBTitle: crystal structure of thermolabile l-threonine dehydrogenase from2 flavobacterium frigidimaris kuc-1
34	c2yy7B_	Alignment	not modelled	100.0	13	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
35	c2p5uC_	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
36	d1wvga1	Alignment	not modelled	100.0	13	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
37	c2hrzA_	Alignment	not modelled	100.0	17	PDB header: sugar binding protein Chain: B: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme2 wbmj in complex with nad and udp
38	c2pzlB_	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
39	d1z45a2	Alignment	not modelled	100.0	21	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.
40	d1y1pa1	Alignment	not modelled	100.0	15	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+
41	c1n7gB_	Alignment	not modelled	100.0	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
42	c2q1wC_	Alignment	not modelled	100.0	14	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
43	d1t2aa_	Alignment	not modelled	100.0	15	PDB header: sugar binding protein Chain: A: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmj in2 complex with nad+ and udp
44	d1rkxa_	Alignment	not modelled	100.0	13	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
45	c1t2aC_	Alignment	not modelled	100.0	15	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
46	c2q1uA_	Alignment	not modelled	100.0	16	PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
47	c2pk3B_	Alignment	not modelled	100.0	14	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
48	c3eheB_	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
49	c2zklA_	Alignment	not modelled	100.0	15	PDB header: plant protein Chain: X: PDB Molecule: vestitone reductase; PDBTitle: crystal structure of vestitone reductase from alfalfa2 (medicago sativa l.)
50	c2hunB_	Alignment	not modelled	100.0	15	
51	d1r6da_	Alignment	not modelled	100.0	15	
52	c2p4hX_	Alignment	not modelled	100.0	14	

53	c3iusB	Alignment	not modelled	100.0	16	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
54	dlorra	Alignment	not modelled	100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
55	dlkewa	Alignment	not modelled	100.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
56	din7ha	Alignment	not modelled	100.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
57	c2vdyA	Alignment	not modelled	100.0	17	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	c3lu1C	Alignment	not modelled	100.0	14	PDB header: isomerase Chain: C: PDB Molecule: wbgu; PDBTitle: crystal structure analysis of wbgu: a udp-galnac 4-epimerase
59	dlbxka	Alignment	not modelled	100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
60	dlgy8a	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
61	c3gpiA	Alignment	not modelled	100.0	20	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
62	dlrpna	Alignment	not modelled	100.0	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
63	c3icpA	Alignment	not modelled	100.0	18	PDB header: isomerase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of udp-galactose 4-epimerase
64	c2rh8A	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: anthocyanidin reductase; PDBTitle: structure of apo anthocyanidin reductase from vitis vinifera
65	dl5b8a	Alignment	not modelled	100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
66	d2bla1	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
67	c3a1nB	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: ndp-sugar epimerase; PDBTitle: crystal structure of l-threonine dehydrogenase from2 hyperthermophilic archaeon thermoplasma volcanium
68	c3ay3C	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of glucuronic acid dehydrogeanse from2 chromahalobacter salexigens
69	c3qvoA	Alignment	not modelled	100.0	24	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.
70	dludca	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
71	c3slgB	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: pbgp3 protein; PDBTitle: crystal structure of pbgp3 protein from burkholderia pseudomallei
72	d2q46a1	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
73	c3e8xA	Alignment	not modelled	100.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative nad-dependent epimerase/dehydratase; PDBTitle: putative nad-dependent epimerase/dehydratase from bacillus halodurans.
74	c2ggsB	Alignment	not modelled	100.0	16	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
75	c3nzoB	Alignment	not modelled	100.0	12	PDB header: lyase Chain: B: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri.
76	c3rfxB	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: uronate dehydrogenase; PDBTitle: crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
77	dlhdoa	Alignment	not modelled	100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
78	dleq2a	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

						Family: Tyrosine-dependent oxidoreductases
79	c3dqpA	Alignment	not modelled	99.9	20	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.
80	c2x86K	Alignment	not modelled	99.9	17	PDB header: isomerase Chain: K: PDB Molecule: adp-l-glycero-d-manno-heptose-6-epimerase; PDBTitle: agme bound to adp-b-mannose
81	c3ew7A	Alignment	not modelled	99.9	17	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.
82	c3dhnA	Alignment	not modelled	99.9	17	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.
83	d2bkaa1	Alignment	not modelled	99.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
84	d2fmua1	Alignment	not modelled	99.9	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
85	d2a35a1	Alignment	not modelled	99.9	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
86	c3h2sA	Alignment	not modelled	99.9	20	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.
87	c2uv9B	Alignment		99.9	15	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase alpha subunits; PDBTitle: crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the alpha subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
88	c3r6dA	Alignment	not modelled	99.9	16	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
89	c2uv8C	Alignment	not modelled	99.9	12	PDB header: transferase Chain: C: PDB Molecule: fatty acid synthase subunit alpha (fas2); PDBTitle: crystal structure of yeast fatty acid synthase with stalled2 acyl carrier protein at 3.1 angstrom resolution
90	c2vkzC	Alignment	not modelled	99.8	15	PDB header: transferase Chain: C: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
91	c2vz8B	Alignment	not modelled	99.7	20	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
92	c2fr1A	Alignment	not modelled	99.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: erythromycin synthase, eryai; PDBTitle: the first ketoreductase of the erythromycin synthase2 (crystal form 2)
93	c2z5lA	Alignment	not modelled	99.6	19	PDB header: transferase Chain: A: PDB Molecule: tylactone synthase starter module and modules 1 PDBTitle: the first ketoreductase of the tylosin pks
94	c3mjsA	Alignment	not modelled	99.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: amphb; PDBTitle: structure of a-type ketoreductases from modular polyketide synthase
95	c3qp9C	Alignment	not modelled	99.6	21	PDB header: oxidoreductase Chain: C: PDB Molecule: type i polyketide synthase pikaii; PDBTitle: the structure of a c2-type ketoreductase from a modular polyketide2 synthase
96	c3p19A	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: putative blue fluorescent protein; PDBTitle: improved nadph-dependent blue fluorescent protein
97	c2jahB	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: clavulanic acid dehydrogenase; PDBTitle: biochemical and structural analysis of the clavulanic acid2 dehydrogenase (cad) from streptomyces clavuligerus
98	d1mlda1	Alignment	not modelled	99.5	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
99	c3llsB	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-ketoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase from2 mycobacterium tuberculosis
100	c3lylB	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: structure of 3-oxoacyl-acylcarrier protein reductase, fabg2 from francisella tularensis
101	c2cfcB	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-(r)-hydroxypropyl-com dehydrogenase; PDBTitle: structural basis for stereo selectivity in the (r)- and2 (s)-hydroxypropylethane thiosulfonate dehydrogenases PDB header: oxidoreductase

102	c3grkE_	 Alignment	not modelled	99.5	15	Chain: E: PDB Molecule: enoyl-(acyl-carrier-protein) reductase (nadh); PDBTitle: crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
103	c3un1D_	 Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: D: PDB Molecule: probable oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from sinorhizobium meliloti2 1021
104	c3v8bC_	 Alignment	not modelled	99.4	16	PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase, possibly 3-oxoacyl-[acyl-carrier PDBTitle: crystal structure of a 3-ketoacyl-acp reductase from sinorhizobium2 meliloti 1021
105	c3ioyB_	 Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: structure of putative short-chain dehydrogenase (saro_0793)2 from novosphingobium aromaticivorans
106	c3ppiA_	 Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase type-2; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase type-2 from2 mycobacterium avium
107	c3gemC_	 Alignment	not modelled	99.4	20	PDB header: oxidoreductase Chain: C: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of short-chain dehydrogenase from pseudomonas2 syringae
108	c3m1IA_	 Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of a c-terminal truncated mutant of a putative2 ketoacyl reductase (fabg4) from mycobacterium tuberculosis h37rv at3 2.5 angstrom resolution
109	d2gdza1	 Alignment	not modelled	99.4	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
110	c3cxtA_	 Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
111	c2yutA_	 Alignment	not modelled	99.4	23	PDB header: oxidoreductase Chain: A: PDB Molecule: putative short-chain oxidoreductase; PDBTitle: crystal structure of putative short-chain oxidoreductase tthb094 from2 thermus thermophilus hb8
112	c2nwqA_	 Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: probable short-chain dehydrogenase; PDBTitle: short chain dehydrogenase from pseudomonas aeruginosa
113	c2dteB_	 Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: glucose 1-dehydrogenase related protein; PDBTitle: structure of thermoplasma acidophilum aldohexose dehydrogenase (aldt)2 in complex with nadh
114	d1iy8a_	 Alignment	not modelled	99.4	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
115	c3i4fD_	 Alignment	not modelled	99.4	13	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier protein] reductase; PDBTitle: structure of putative 3-oxoacyl-reductase from bacillus thuringiensis
116	c3k31B_	 Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of enoyl-(acyl-carrier-protein) reductase from2 anaplasma phagocytophilum in complex with nad at 1.9a resolution
117	c3toxG_	 Alignment	not modelled	99.4	18	PDB header: oxidoreductase Chain: G: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
118	c2qioA_	 Alignment	not modelled	99.3	15	PDB header: unknown function Chain: A: PDB Molecule: enoyl-(acyl-carrier-protein) reductase; PDBTitle: x-ray structure of enoyl-acyl carrier protein reductase from bacillus2 anthracis with triclosan
119	d1jiva_	 Alignment	not modelled	99.3	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
120	c3oidA_	 Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadph]; PDBTitle: crystal structure of enoyl-acp reductases iii (fabl) from b. subtilis2 (complex with nadp and tcl)