

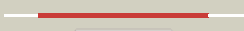






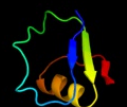









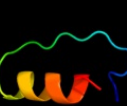

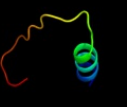

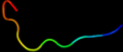




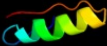

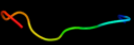


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2p2vA_	 Alignment		99.6	20	PDB header: transferase Chain: A: PDB Molecule: alpha-2,3-sialyltransferase; PDBTitle: crystal structure analysis of monofunctional alpha-2,3-2 sialyltransferase cst-i from campylobacter jejuni
2	dlro7a_	 Alignment		99.5	19	Fold: Alpha-2,3/8-sialyltransferase CstII Superfamily: Alpha-2,3/8-sialyltransferase CstII Family: Alpha-2,3/8-sialyltransferase CstII
3	c2wqqA_	 Alignment		99.5	20	PDB header: transferase Chain: A: PDB Molecule: alpha-2,3-/2,8-sialyltransferase; PDBTitle: crystallographic analysis of monomeric cstii
4	c3lm8D_	 Alignment		91.1	22	PDB header: transferase Chain: D: PDB Molecule: thiamine pyrophosphokinase; PDBTitle: crystal structure of thiamine pyrophosphokinase from2 bacillus subtilis, northeast structural genomics consortium3 target sr677
5	c3melC_	 Alignment		87.3	13	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: thiamin pyrophosphokinase family protein; PDBTitle: crystal structure of thiamin pyrophosphokinase family protein from2 enterococcus faecalis, northeast structural genomics consortium3 target efr150
6	c3k94A_	 Alignment		81.9	18	PDB header: transferase Chain: A: PDB Molecule: thiamin pyrophosphokinase; PDBTitle: crystal structure of thiamin pyrophosphokinase from geobacillus2 thermodenitrificans, northeast structural genomics consortium target3 gtr2
7	c3cq9C_	 Alignment		79.9	22	PDB header: transferase Chain: C: PDB Molecule: uncharacterized protein lp_1622; PDBTitle: crystal structure of the lp_1622 protein from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr114
8	c3l8mA_	 Alignment		76.3	17	PDB header: transferase Chain: A: PDB Molecule: probable thiamine pyrophosphokinase; PDBTitle: crystal structure of a probable thiamine pyrophosphokinase2 from staphylococcus saprophyticus subsp. saprophyticus.3 northeast structural genomics consortium target id syr86
9	c3ihkC_	 Alignment		75.5	14	PDB header: transferase Chain: C: PDB Molecule: thiamin pyrophosphokinase; PDBTitle: crystal structure of thiamin pyrophosphokinase from2 s.mutans, northeast structural genomics consortium target3 smr83
10	d2gv8a2	 Alignment		44.2	8	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
11	d1nhpa2	 Alignment		41.2	11	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains

12	dlf8fa1	Alignment		39.3	25	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
13	dlseza1	Alignment		34.8	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
14	c2r70A	Alignment		33.9	16	PDB header: transferase Chain: A: PDB Molecule: infectious bursal virus vp1 polymerase; PDBTitle: crystal structure of infectious bursal disease virus vp12 polymerase, cocrystallized with an oligopeptide mimicking3 the vp3 c-terminus.
15	d2pgga1	Alignment		29.1	16	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
16	c3nksA	Alignment		26.7	17	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: structure of human protoporphyrinogen ix oxidase
17	dlqo8a2	Alignment		25.7	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
18	c2k0zA	Alignment		25.6	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein hp1203; PDBTitle: solution nmr structure of protein hp1203 from helicobacter pylori2 26695. northeast structural genomics consortium (nesg) target3 pt1/ontario center for structural proteomics target hp1203
19	dl1jqa3	Alignment		25.4	32	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: N-terminal domain of adrenodoxin reductase-like
20	dltrba1	Alignment		25.3	33	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
21	dly0pa2	Alignment	not modelled	25.2	28	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
22	d2io8a1	Alignment	not modelled	25.1	18	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Glutathionylspermidine synthase substrate-binding domain-like
23	d2gv8a1	Alignment	not modelled	25.1	27	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
24	d2bi7a1	Alignment	not modelled	24.8	23	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: UDP-galactopyranose mutase, N-terminal domain
25	c3v76A	Alignment	not modelled	24.6	36	PDB header: flavoprotein Chain: A: PDB Molecule: flavoprotein; PDBTitle: the crystal structure of a flavoprotein from sinorhizobium meliloti
26	dlhyua1	Alignment	not modelled	24.0	30	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
27	c2jtqA	Alignment	not modelled	23.8	22	PDB header: transferase Chain: A: PDB Molecule: phage shock protein e; PDBTitle: rhodanese from e.coli
28	dlh6va1	Alignment	not modelled	22.7	40	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
						Fold: FAD/NAD(P)-binding domain

29	dlq1ra1	Alignment	not modelled	21.9	31	Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
30	dlw4xa2	Alignment	not modelled	21.7	9	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
31	c3jskN_	Alignment	not modelled	21.7	19	PDB header: biosynthetic protein Chain: N: PDB Molecule: cypbp37 protein; PDBTitle: thiazole synthase from neurospora crassa
32	clju2A_	Alignment	not modelled	21.6	30	PDB header: lyase Chain: A: PDB Molecule: hydroxynitrile lyase; PDBTitle: crystal structure of the hydroxynitrile lyase from almond
33	dl1lsa_	Alignment	not modelled	21.3	16	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
34	dlfl2a1	Alignment	not modelled	21.2	60	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
35	c2ywlA_	Alignment	not modelled	21.1	50	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase related protein; PDBTitle: crystal structure of thioredoxin reductase-related protein ttha03702 from thermus thermophilus hb8
36	clqlwA_	Alignment	not modelled	21.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: putidaredoxin reductase; PDBTitle: crystal structure of putidaredoxin reductase from2 pseudomonas putida
37	clfcdB_	Alignment	not modelled	21.0	15	PDB header: electron transport(flavocytochrome) Chain: B: PDB Molecule: flavocytochrome c sulfide dehydrogenase (flavin- PDBTitle: the structure of flavocytochrome c sulfide dehydrogenase2 from a purple phototrophic bacterium chromatium vinosum at3 2.5 angstroms resolution
38	c2vdcI_	Alignment	not modelled	20.8	23	PDB header: oxidoreductase Chain: I: PDB Molecule: glutamate synthase [nadh] small chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
39	dlw4xa1	Alignment	not modelled	20.7	30	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
40	dl1pfa1	Alignment	not modelled	20.1	40	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
41	dlvdca1	Alignment	not modelled	18.8	40	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
42	d3grsa1	Alignment	not modelled	18.8	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
43	c3s5wB_	Alignment	not modelled	18.6	40	PDB header: oxidoreductase Chain: B: PDB Molecule: l-ornithine 5-monooxygenase; PDBTitle: ornithine hydroxylase (pvda) from pseudomonas aeruginosa
44	dlq1ra2	Alignment	not modelled	18.3	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
45	c2l1nA_	Alignment	not modelled	18.2	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the protein yp_399305.1
46	dlldxa1	Alignment	not modelled	17.8	42	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
47	d2i0za1	Alignment	not modelled	17.3	50	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
48	dl0jta1	Alignment	not modelled	17.1	40	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
49	c3l80A_	Alignment	not modelled	17.1	10	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
50	dlreoa1	Alignment	not modelled	17.1	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
51	c3dlcA_	Alignment	not modelled	16.9	30	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-containing putative monooxygenase; PDBTitle: crystal structure of flavin-containing putative monooxygenase2 (np_373108.1) from staphylococcus aureus mu50 at 2.40 a resolution
52	dla9xa3	Alignment	not modelled	16.7	30	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
53	dlrp0a1	Alignment	not modelled	16.5	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Thi4-like

54	d3lada1	Alignment	not modelled	16.5	50	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
55	d2iida1	Alignment	not modelled	16.4	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
56	d2gjca1	Alignment	not modelled	16.2	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Thi4-like
57	d3coxa1	Alignment	not modelled	16.2	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
58	d1ps9a2	Alignment	not modelled	15.8	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: C-terminal domain of adrenodoxin reductase-like
59	d1fl2a2	Alignment	not modelled	15.8	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
60	c1lqtB_	Alignment	not modelled	15.6	40	PDB header: oxidoreductase Chain: B: PDB Molecule: fprra; PDBTitle: a covalent modification of nadp+ revealed by the atomic resolution2 structure of fprra, a mycobacterium tuberculosis oxidoreductase
61	c1vqwB_	Alignment	not modelled	15.5	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein with similarity to flavin-containing PDBTitle: crystal structure of a protein with similarity to flavin-2 containing monooxygenases and to mammalian dimethylalanine3 monooxygenases
62	c3e5bB_	Alignment	not modelled	15.4	22	PDB header: lyase Chain: B: PDB Molecule: isocitrate lyase; PDBTitle: 2.4 a crystal structure of isocitrate lyase from brucella2 melitensis
63	c3fkjA_	Alignment	not modelled	15.4	6	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerases; PDBTitle: crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
64	c2xdoC_	Alignment	not modelled	15.3	31	PDB header: oxidoreductase Chain: C: PDB Molecule: tbx2 protein; PDBTitle: structure of the tetracycline degrading monooxygenase tbx2 from2 bacteroides thetaiotaomicron
65	d2bcgg1	Alignment	not modelled	15.2	50	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
66	d1trba2	Alignment	not modelled	15.1	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
67	d2f5va1	Alignment	not modelled	15.0	60	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
68	c2bryA_	Alignment	not modelled	14.9	13	PDB header: transport Chain: A: PDB Molecule: nedd9 interacting protein with calponin homology PDBTitle: crystal structure of the native monooxygenase domain of2 mical at 1.45 a resolution
69	c3fimB_	Alignment	not modelled	14.9	20	PDB header: oxidoreductase Chain: B: PDB Molecule: aryl-alcohol oxidase; PDBTitle: crystal structure of aryl-alcohol-oxidase from pleurotus eryngii
70	c2omkB_	Alignment	not modelled	14.9	24	PDB header: transferase Chain: B: PDB Molecule: hypothetical protein; PDBTitle: structure of the bacteroides thetaiotaomicron thiamin2 pyrophosphokinase
71	d1igwa_	Alignment	not modelled	14.8	26	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
72	d1i8ta1	Alignment	not modelled	14.7	50	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: UDP-galactopyranose mutase, N-terminal domain
73	c2vq7B_	Alignment	not modelled	14.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: flavin-containing monooxygenase; PDBTitle: bacterial flavin-containing monooxygenase in complex with2 nadp: native data
74	d1d5ta1	Alignment	not modelled	14.5	50	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
75	c1zz0C_	Alignment	not modelled	14.5	16	PDB header: hydrolase Chain: C: PDB Molecule: histone deacetylase-like amidohydrolase; PDBTitle: crystal structure of a hdac-like protein with acetate bound
76	d1ps9a3	Alignment	not modelled	14.5	15	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: N-terminal domain of adrenodoxin reductase-like
77	c2jbvA_	Alignment	not modelled	14.3	30	PDB header: oxidoreductase Chain: A: PDB Molecule: choline oxidase; PDBTitle: crystal structure of choline oxidase reveals insights into2 the catalytic mechanism
78	c3f8rD_	Alignment	not modelled	14.1	50	PDB header: oxidoreductase Chain: D: PDB Molecule: thioredoxin reductase (trxb-3); PDBTitle: crystal structure of sulfobolus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
						PDB header: structural genomics, unknown function

79	c2gqfA_	Alignment	not modelled	14.1	30	Chain: A: PDB Molecule: hypothetical protein hi0933; PDBTitle: crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd
80	d1vdca2	Alignment	not modelled	13.9	7	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
81	d1chua2	Alignment	not modelled	13.8	50	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
82	d1jnra2	Alignment	not modelled	13.8	30	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
83	c2v6oA_	Alignment	not modelled	13.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: structure of schistosoma mansoni thioredoxin-gluthione2 reductase (smtgr)
84	c1sezA_	Alignment	not modelled	13.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase, mitochondrial; PDBTitle: crystal structure of protoporphyrinogen ix oxidase
85	d2bs2a2	Alignment	not modelled	13.6	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
86	d2gmha1	Alignment	not modelled	13.5	50	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
87	c3allA_	Alignment	not modelled	13.5	8	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; PDBTitle: crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
88	d1fecal	Alignment	not modelled	13.3	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
89	d1ebda1	Alignment	not modelled	13.2	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
90	c2pd2A_	Alignment	not modelled	13.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein st0148; PDBTitle: crystal structure of (st0148) conserved hypothetical from sulfobolus2 tokodaii strain7
91	c2jb1B_	Alignment	not modelled	13.2	31	PDB header: oxidoreductase Chain: B: PDB Molecule: l-amino acid oxidase; PDBTitle: the l-amino acid oxidase from rhodococcus opacus in complex2 with l-alanine
92	d2gqfa1	Alignment	not modelled	13.2	30	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
93	c3ctvA_	Alignment	not modelled	13.1	40	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of t. acidophilum thioredoxin reductase
94	d1gtea4	Alignment	not modelled	12.9	20	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: N-terminal domain of adrenodoxin reductase-like
95	c2gewA_	Alignment	not modelled	12.8	10	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)
96	d1n4wa1	Alignment	not modelled	12.8	10	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
97	c3rhaA_	Alignment	not modelled	12.8	33	PDB header: oxidoreductase Chain: A: PDB Molecule: putrescine oxidase; PDBTitle: the crystal structure of oxidoreductase from arthrobacter aureus
98	d2i71a1	Alignment	not modelled	12.8	35	Fold: SSO1389-like Superfamily: SSO1389-like Family: Cas DxTHG
99	c2bi8A_	Alignment	not modelled	12.8	23	PDB header: isomerase Chain: A: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from klebsiella pneumoniae with2 reduced fad