






























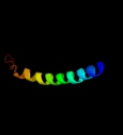
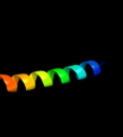
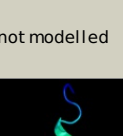

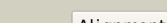

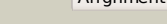







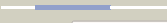
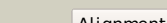

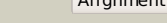
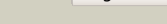


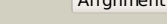
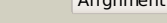
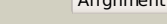
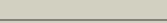





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rgwS_	 Alignment		100.0	76	PDB header: oxidoreductase/oxidoreductase Chain: S: PDB Molecule: membrane-bound hydrogenase (nife) small subunit hoxk; PDBTitle: crystal structure at 1.5 a resolution of an h2-reduced, o2-tolerant2 hydrogenase from ralstonia eutropha unmasks a novel iron-sulfur3 cluster
2	c3myrE_	 Alignment		100.0	47	PDB header: oxidoreductase Chain: E: PDB Molecule: hydrogenase (nife) small subunit hyda; PDBTitle: crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
3	dlwuis1	 Alignment		100.0	41	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
4	c1h2aS_	 Alignment		100.0	41	PDB header: oxidoreductase Chain: S: PDB Molecule: hydrogenase; PDBTitle: single crystals of hydrogenase from desulfovibrio vulgaris
5	dlfrfs_	 Alignment		100.0	45	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
6	dle3da_	 Alignment		100.0	42	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
7	dlyq9a1	 Alignment		100.0	42	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
8	dlcc1s_	 Alignment		100.0	36	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nickel-iron hydrogenase, small subunit
9	c2wpaA_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic [nifese] hydrogenase, small subunit; PDBTitle: structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
10	d2fug61	 Alignment		99.6	23	Fold: HydA/Nqo6-like Superfamily: HydA/Nqo6-like Family: Nqo6-like
11	c2g4rB_	 Alignment		89.6	11	PDB header: biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis mog protein; PDBTitle: anomalous substructure of moga

12	d2ftsa3	Alignment		88.7	17	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
13	c2is8A_	Alignment		86.7	12	PDB header: structural protein Chain: A: PDB Molecule: molybdopterin biosynthesis enzyme, moab; PDBTitle: crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
14	d1y5ea1	Alignment		85.8	7	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
15	d1xi8a3	Alignment		84.9	7	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
16	c2nqqA_	Alignment		84.8	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin biosynthesis protein moea; PDBTitle: moea r137q
17	c2fu3A_	Alignment		84.6	16	PDB header: biosynthetic protein/structural protein Chain: A: PDB Molecule: gephyrin; PDBTitle: crystal structure of gephyrin e-domain
18	c2pjka_	Alignment		83.2	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 178aa long hypothetical molybdenum cofactor PDBTitle: structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfobus tokodaii
19	d2nqra3	Alignment		82.1	14	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
20	d1ilja_	Alignment		81.4	19	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
21	c2e76D_	Alignment		80.0	11	PDB header: photosynthesis Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
22	c2fynO_	Alignment		78.2	42	PDB header: oxidoreductase Chain: O: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
23	c2pq4B_	Alignment	not modelled	73.8	35	PDB header: chaperone/oxidoreductase Chain: B: PDB Molecule: periplasmic nitrate reductase precursor; PDBTitle: nmr solution structure of napd in complex with napa1-352 signal peptide
24	c1p84E_	Alignment		73.7	18	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
25	d1wu2a3	Alignment	not modelled	68.5	11	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
						Fold: Molybdenum cofactor biosynthesis proteins

26	d1uuya_	Alignment	not modelled	68.4	12	Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
27	d1uz5a3	Alignment	not modelled	65.1	16	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
28	d1mkza_	Alignment	not modelled	60.8	12	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
29	c3rfqC_	Alignment	not modelled	60.1	9	PDB header: biosynthetic protein Chain: C: PDB Molecule: pterin-4-alpha-carbinolamine dehydratase moab2; PDBTitle: crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
30	c2wcvl_	Alignment	not modelled	59.8	27	PDB header: isomerase Chain: I: PDB Molecule: l-fucose mutarotase; PDBTitle: crystal structure of bacterial fucu
31	c2fyuE_	Alignment	not modelled	57.2	14	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit, PDBTitle: crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
32	d2h1qa1	Alignment	not modelled	56.7	9	Fold: PLP-dependent transferase-like Superfamily: Dhaf3308-like Family: Dhaf3308-like
33	d1ogda_	Alignment	not modelled	53.2	23	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
34	c1uz5A_	Alignment	not modelled	52.7	14	PDB header: molybdopterin biosynthesis Chain: A: PDB Molecule: 402aa long hypothetical molybdopterin PDBTitle: the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii
35	c3e7nB_	Alignment	not modelled	52.3	31	PDB header: transport protein Chain: B: PDB Molecule: d-ribose high-affinity transport system; PDBTitle: crystal structure of d-ribose high-affinity transport system from2 salmonella typhimurium lt2
36	d1ovma1	Alignment	not modelled	52.1	26	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
37	c3mvkA_	Alignment	not modelled	45.9	23	PDB header: isomerase Chain: A: PDB Molecule: protein fucu; PDBTitle: the crystal structure of fucu from bifidobacterium longum to 1.65a
38	d2ob5a1	Alignment	not modelled	44.0	23	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
39	d1pvda1	Alignment	not modelled	42.3	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
40	c2wcuB_	Alignment	not modelled	41.9	27	PDB header: isomerase Chain: B: PDB Molecule: protein fucu homolog; PDBTitle: crystal structure of mammalian fucu
41	c3ilhA_	Alignment	not modelled	40.0	14	PDB header: transcription regulator Chain: A: PDB Molecule: two component response regulator; PDBTitle: crystal structure of two component response regulator from cytophaga2 hutchinsonii
42	c3a52A_	Alignment	not modelled	38.9	21	PDB header: hydrolase Chain: A: PDB Molecule: cold-active alkaline phosphatase; PDBTitle: crystal structure of cold-active alkaliine phosphatase from2 psychrophile shewanella sp.
43	d2oa4a1	Alignment	not modelled	35.6	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: SPO1678-like
44	d1k7ha_	Alignment	not modelled	34.0	29	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
45	d1whza_	Alignment	not modelled	33.7	27	Fold: dsRBD-like Superfamily: YcfA/nrd intein domain Family: YcfA-like
46	d1y6va1	Alignment	not modelled	33.6	25	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
47	d2f7wa1	Alignment	not modelled	33.4	10	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
48	d2g2ca1	Alignment	not modelled	33.4	12	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
49	d1vmea1	Alignment	not modelled	32.8	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
50	c3e2dB_	Alignment	not modelled	30.8	21	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: the 1.4 a crystal structure of the large and cold-active2 vibrio sp. alkaline phosphatase
51	d1zpda1	Alignment	not modelled	30.1	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
52	c2x98A_	Alignment	not modelled	29.7	17	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase

53	c3fniA	 Alignment	not modelled	29.1	11	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
54	d1ozha1	 Alignment	not modelled	28.6	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
55	c1ew2A	 Alignment	not modelled	26.3	25	PDB header: hydrolase Chain: A: PDB Molecule: phosphatase; PDBTitle: crystal structure of a human phosphatase
56	d1zeda1	 Alignment	not modelled	26.3	25	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
57	d1xhja	 Alignment	not modelled	26.2	14	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
58	c2jnvA	 Alignment	not modelled	25.4	22	PDB header: metal transport Chain: A: PDB Molecule: nifu-like protein 1, chloroplast; PDBTitle: solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
59	c2iucB	 Alignment	not modelled	24.9	8	PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: structure of alkaline phosphatase from the antarctic2 bacterium tab5
60	c2jrtA	 Alignment	not modelled	24.5	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
61	dlik6a2	 Alignment	not modelled	24.2	12	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
62	c1wu2B	 Alignment	not modelled	23.9	19	PDB header: structural genomics, biosynthetic protein Chain: B: PDB Molecule: molybdopterin biosynthesis moea protein; PDBTitle: crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii ot3
63	c3hbcA	 Alignment	not modelled	22.4	12	PDB header: hydrolase Chain: A: PDB Molecule: choloylglycine hydrolase; PDBTitle: crystal structure of choloylglycine hydrolase from bacteroides2 thetaiotaomicron vpi
64	c3fq6A	 Alignment	not modelled	22.3	16	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi
65	d1rlja	 Alignment	not modelled	21.2	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavoprotein NrdI
66	d1ryda1	 Alignment	not modelled	19.7	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
67	d2djia1	 Alignment	not modelled	19.6	8	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
68	c3uhjE	 Alignment	not modelled	19.2	15	PDB header: oxidoreductase Chain: E: PDB Molecule: probable glycerol dehydrogenase; PDBTitle: crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
69	c2zwmA	 Alignment	not modelled	18.7	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
70	d2ez9a1	 Alignment	not modelled	18.6	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
71	c2oasA	 Alignment	not modelled	18.2	23	PDB header: transferase Chain: A: PDB Molecule: 4-hydroxybutyrate coenzyme a transferase; PDBTitle: crystal structure of 4-hydroxybutyrate coenzyme a transferase (atoa)2 in complex with coa from shewanella oneidensis, northeast structural3 genomics target sor119.
72	c3nhzA	 Alignment	not modelled	18.1	17	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
73	c2kveA	 Alignment	not modelled	17.1	67	PDB header: hormone Chain: A: PDB Molecule: mesencephalic astrocyte-derived neurotrophic factor; PDBTitle: c-terminal domain of mesencephalic astrocyte-derived neurotrophic2 factor (manf)
74	d1t9ba1	 Alignment	not modelled	17.0	22	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
75	d1zh2a1	 Alignment	not modelled	16.2	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
76	c3up8B	 Alignment	not modelled	15.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative 2,5-diketo-d-gluconic acid reductase b; PDBTitle: crystal structure of a putative 2,5-diketo-d-gluconic acid reductase b
77	d1kgsa2	 Alignment	not modelled	15.8	14	Fold: Flavodoxin-like Superfamily: CheY-like

					Family: CheY-related
78	d2f6ma1	Alignment	not modelled	15.6	18 Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS23 C-terminal domain
79	c3p13B	Alignment	not modelled	15.6	19 PDB header: isomerase Chain: B: PDB Molecule: d-ribose pyranase; PDBTitle: complex structure of d-ribose pyranase sa240 with d-ribose
80	d1ys7a2	Alignment	not modelled	15.5	12 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
81	d1ofcx1	Alignment	not modelled	15.4	23 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
82	c2qvga	Alignment	not modelled	14.3	21 PDB header: transferase Chain: A: PDB Molecule: two component response regulator; PDBTitle: the crystal structure of a two-component response regulator2 from legionella pneumophila
83	d1uhua	Alignment	not modelled	13.7	18 Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: MMLV matrix protein-like
84	d1evsa	Alignment	not modelled	13.2	33 Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Long-chain cytokines
85	c3eh7A	Alignment	not modelled	13.1	21 PDB header: transferase Chain: A: PDB Molecule: 4-hydroxybutyrate coa-transferase; PDBTitle: the structure of a putative 4-hydroxybutyrate coa-transferase from2 porphyromonas gingivalis w83
86	d1peva	Alignment	not modelled	13.1	23 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
87	d1xhfa1	Alignment	not modelled	12.9	15 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
88	c1ovmC	Alignment	not modelled	12.7	26 PDB header: lyase Chain: C: PDB Molecule: indole-3-pyruvate decarboxylase; PDBTitle: crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
89	c2w0yB	Alignment	not modelled	12.7	12 PDB header: hydrolase Chain: B: PDB Molecule: alkaline phosphatase; PDBTitle: h.salinarum alkaline phosphatase
90	c3kcnA	Alignment	not modelled	12.6	18 PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase homolog; PDBTitle: the crystal structure of adenylate cyclase from2 rhodopirellula baltica
91	c2r8bA	Alignment	not modelled	12.3	18 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu2452; PDBTitle: the crystal structure of the protein atu2452 of unknown function from2 agrobacterium tumefaciens str. c58
92	d1hn4a	Alignment	not modelled	12.3	16 Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
93	d1ycga1	Alignment	not modelled	11.7	11 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
94	d1ny5a1	Alignment	not modelled	11.6	16 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
95	c3d7rB	Alignment	not modelled	11.6	8 PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of a putative esterase from staphylococcus aureus
96	c3eq2A	Alignment	not modelled	11.6	20 PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
97	d1veha	Alignment	not modelled	11.5	33 Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: Nifu C-terminal domain-like
98	d2r25b1	Alignment	not modelled	11.4	13 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
99	c3luaA	Alignment	not modelled	11.2	11 PDB header: transcription regulator Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of a signal receiver domain of two component signal2 transduction (histidine kinase) from clostridium thermocellum