







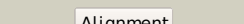

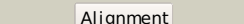

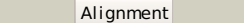

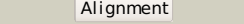

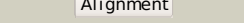

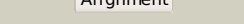

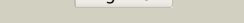




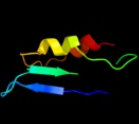

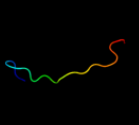



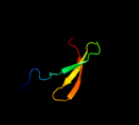

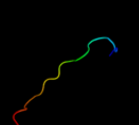







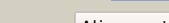


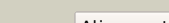






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fug4_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: 4: PDB Molecule: nadh-quinone oxidoreductase chain 4; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
2	d2fug41	 Alignment		100.0	31	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nqo4-like
3	d1e3db_	 Alignment		100.0	22	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
4	d1yq9h1	 Alignment		100.0	22	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
5	d1frfl_	 Alignment		100.0	21	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
6	d1cc1l_	 Alignment		100.0	20	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
7	c2wpmB_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: periplasmic [nifese] hydrogenase, large subunit, PDBTitle: structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
8	c1h2aL_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: L: PDB Molecule: hydrogenase; PDBTitle: single crystals of hydrogenase from desulfovibrio vulgaris
9	c3myrB_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: nickel-dependent hydrogenase large subunit; PDBTitle: crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
10	d1wuil1	 Alignment		100.0	19	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
11	d2fug51	 Alignment		100.0	25	Fold: Nqo5-like Superfamily: Nqo5-like Family: Nqo5-like

12	c3mcrA	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase, subunit c; PDBTitle: crystal structure of nadh dehydrogenase subunit c (tfu_2693) from2 thermobifida fusca yx-er1 at 2.65 a resolution
13	d1v97a4	 Alignment		44.9	8	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
14	d2zjrg1	 Alignment		43.8	17	Fold: Ribosomal protein L13 Superfamily: Ribosomal protein L13 Family: Ribosomal protein L13
15	c3cf5G	 Alignment		43.8	17	PDB header: ribosome/antibiotic Chain: G: PDB Molecule: 50s ribosomal protein l13; PDBTitle: thiopeptide antibiotic thiostrepton bound to the large ribosomal2 subunit of deinococcus radiodurans
16	c2dgyA	 Alignment		33.8	8	PDB header: translation Chain: A: PDB Molecule: mgc11102 protein; PDBTitle: solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
17	c2ftcH	 Alignment		33.3	17	PDB header: ribosome Chain: H: PDB Molecule: 39s ribosomal protein l13, mitochondrial; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
18	c3d5bN	 Alignment		31.5	26	PDB header: ribosome Chain: N: PDB Molecule: 50s ribosomal protein l13; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
19	c3bboL	 Alignment		31.5	22	PDB header: ribosome Chain: L: PDB Molecule: ribosomal protein l13; PDBTitle: homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
20	d1ffvc1	 Alignment		29.5	16	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
21	d1knya2	 Alignment	not modelled	28.6	16	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Kanamycin nucleotidyltransferase (KNTase), N-terminal domain
22	d1r9da	 Alignment	not modelled	28.1	14	Fold: PFL-like glycyl radical enzymes Superfamily: PFL-like glycyl radical enzymes Family: PFL-like
23	d2j01n1	 Alignment	not modelled	24.2	26	Fold: Ribosomal protein L13 Superfamily: Ribosomal protein L13 Family: Ribosomal protein L13
24	d1ni2a3	 Alignment	not modelled	23.9	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: First domain of FERM
25	d1gg3a3	 Alignment	not modelled	23.6	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: First domain of FERM
26	d1u07a	 Alignment	not modelled	23.0	14	Fold: TolA/TonB C-terminal domain Superfamily: TolA/TonB C-terminal domain Family: TonB
27	d1ef1a3	 Alignment	not modelled	22.8	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: First domain of FERM
28	d2zpya3	 Alignment	not modelled	22.1	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: First domain of FERM
29	d2ntka1	 Alignment	not modelled	21.9	27	Fold: Ntn hydrolase-like Superfamily: Archaeal IMP cyclohydrolase PurO

						Family: Archaeal IMP cyclohydrolase PurO
30	c2grxC_	Alignment	not modelled	21.6	8	PDB header: metal transport Chain: C: PDB Molecule: protein tonb; PDBTitle: crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
31	c2f3oB_	Alignment	not modelled	21.4	14	PDB header: unknown function Chain: B: PDB Molecule: pyruvate formate-lyase 2; PDBTitle: crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus
32	c3kwIA_	Alignment	not modelled	21.0	5	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein from helicobacter pylori
33	clufiD_	Alignment	not modelled	19.9	50	PDB header: dna binding protein Chain: D: PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of the dimerization domain of human cenp-b
34	d1vqza1	Alignment	not modelled	19.8	13	Fold: SufE/NifU Superfamily: SufE/NifU Family: SP1160 C-terminal domain-like
35	d1ufia_	Alignment	not modelled	19.7	50	Fold: ROP-like Superfamily: Dimerisation domain of CENP-B Family: Dimerisation domain of CENP-B
36	d2gych1	Alignment	not modelled	19.4	18	Fold: Ribosomal protein L13 Superfamily: Ribosomal protein L13 Family: Ribosomal protein L13
37	c2dnwA_	Alignment	not modelled	19.4	11	PDB header: transport protein Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
38	c1xx3A_	Alignment	not modelled	18.1	6	PDB header: transport protein Chain: A: PDB Molecule: tonb protein; PDBTitle: solution structure of escherichia coli tonb-ctd
39	c2ibpB_	Alignment	not modelled	18.1	22	PDB header: transferase Chain: B: PDB Molecule: citrate synthase; PDBTitle: crystal structure of citrate synthase from pyrobaculum aerophilum
40	c2oqkA_	Alignment	not modelled	17.9	8	PDB header: translation Chain: A: PDB Molecule: putative translation initiation factor eif-1a; PDBTitle: crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
41	d2q22a1	Alignment	not modelled	17.8	28	Fold: Ava3019-like Superfamily: Ava3019-like Family: Ava3019-like
42	d2gskb1	Alignment	not modelled	16.9	8	Fold: TolA/TonB C-terminal domain Superfamily: TolA/TonB C-terminal domain Family: TonB
43	d1d7qa_	Alignment	not modelled	16.0	8	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
44	c3hrdC_	Alignment	not modelled	15.8	12	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinate dehydrogenase fad-subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
45	d3c7bb2	Alignment	not modelled	15.0	7	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: DsrA/DsrB N-terminal-domain-like
46	d1ghha_	Alignment	not modelled	14.6	17	Fold: DNA damage-inducible protein DinI Superfamily: DNA damage-inducible protein DinI Family: DNA damage-inducible protein DinI
47	d1n62c1	Alignment	not modelled	13.1	15	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
48	d1qxha_	Alignment	not modelled	13.1	10	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
49	c1bl1A_	Alignment	not modelled	13.0	54	PDB header: hormone receptor Chain: A: PDB Molecule: parathyroid hormone receptor; PDBTitle: pth receptor n-terminus fragment, nmr, 1 structure
50	d1yeya2	Alignment	not modelled	13.0	10	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
51	c2kzxA_	Alignment	not modelled	12.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of a3dht5 from clostridium thermocellum,2 northeast structural genomics consortium target cmr116
52	d2cfua2	Alignment	not modelled	12.5	14	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Alkylsulfatase-like
53	c2cfuA_	Alignment	not modelled	12.3	14	PDB header: hydrolase Chain: A: PDB Molecule: sdsa1; PDBTitle: crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
54	d1rtyb_	Alignment	not modelled	12.2	15	Fold: Ferritin-like Superfamily: Cobalamin adenosyltransferase-like Family: Cobalamin adenosyltransferase
55	c1wvtA_	Alignment	not modelled	12.2	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein st2180; PDBTitle: crystal structure of uncharacterized protein st2180 from

						sulfolobus2 tokodaii
56	c2w3zA_	Alignment	not modelled	11.9	10	PDB header: hydrolase Chain: A: PDB Molecule: putative deacetylase; PDBTitle: structure of a streptococcus mutans ce4 esterase
57	c3echC_	Alignment	not modelled	11.5	36	PDB header: transcription, transcription regulation Chain: C: PDB Molecule: 25-mer fragment of protein armr; PDBTitle: the marr-family repressor mexr in complex with its antirepressor armr
58	d1es6a2	Alignment	not modelled	11.4	36	Fold: EV matrix protein Superfamily: EV matrix protein Family: EV matrix protein
59	c2l9fA_	Alignment	not modelled	11.4	15	PDB header: transferase Chain: A: PDB Molecule: cale8; PDBTitle: nmr solution structure of meacp
60	c1es6A_	Alignment	not modelled	11.4	36	PDB header: viral protein Chain: A: PDB Molecule: matrix protein vp40; PDBTitle: crystal structure of the matrix protein of ebola virus
61	c2kboA_	Alignment	not modelled	11.3	50	PDB header: hydrolase Chain: A: PDB Molecule: dna dc->du-editing enzyme apobec-3g; PDBTitle: structure, interaction, and real-time monitoring of the2 enzymatic reaction of wild type apobec3g
62	c2fq2A_	Alignment	not modelled	11.3	10	PDB header: lipid transport Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of minor conformation of holo-acyl2 carrier protein from malaria parasite plasmodium falciparum
63	d1h4ra3	Alignment	not modelled	11.2	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: First domain of FERM
64	c2jisA_	Alignment	not modelled	11.1	17	PDB header: lyase Chain: A: PDB Molecule: cysteine sulfinic acid decarboxylase; PDBTitle: human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
65	c2zhzC_	Alignment	not modelled	10.6	14	PDB header: transferase Chain: C: PDB Molecule: atp:cob(i)alamin adenosyltransferase, putative; PDBTitle: crystal structure of a pduo-type atp:cobalamin adenosyltransferase2 from burkholderia thailandensis
66	d1o98a1	Alignment	not modelled	10.3	14	Fold: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Superfamily: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
67	d1mixa2	Alignment	not modelled	10.0	16	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Third domain of FERM
68	d1zday1	Alignment	not modelled	10.0	21	Fold: Antiparallel beta/alpha barrel (PT-barrel) Superfamily: Prenyltransferase-like Family: Prenyltransferase-like
69	c2yvzA_	Alignment	not modelled	9.9	18	PDB header: transport protein Chain: A: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
70	c2g40A_	Alignment	not modelled	9.8	24	PDB header: unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of a duf162 family protein (dr_1909) from2 deinococcus radiodurans at 1.70 a resolution
71	d2g40a1	Alignment	not modelled	9.8	24	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: YkgG-like
72	d1x2ga1	Alignment	not modelled	9.8	11	Fold: SufE/NifU Superfamily: SufE/NifU Family: SP1160 C-terminal domain-like
73	d2hc5a1	Alignment	not modelled	9.5	12	Fold: FlaG-like Superfamily: FlaG-like Family: FlaG-like
74	d1t3qc1	Alignment	not modelled	9.5	13	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
75	d1gxma_	Alignment	not modelled	9.4	31	Fold: alpha/alpha toroid Superfamily: Family 10 polysaccharide lyase Family: Family 10 polysaccharide lyase
76	c2ks1B_	Alignment	not modelled	9.4	28	PDB header: transferase Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation
77	d1r6ta2	Alignment	not modelled	9.4	23	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
78	d1jt8a_	Alignment	not modelled	9.3	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
79	c1mbbA_	Alignment	not modelled	9.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: uridine diphospho-n-acetylenolpyruvylglucosamine PDBTitle: oxidoreductase
80	c2k9kA_	Alignment	not modelled	9.0	13	PDB header: metal transport Chain: A: PDB Molecule: tonb2; PDBTitle: molecular characterization of the tonb2 protein from vibrio2 anguillarum
81	c2kw0A_	Alignment	not modelled	8.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: ccmh protein; PDBTitle: solution structure of n-terminal domain of ccmh from

					escherichia.coli
82	c2ip1A_	Alignment	not modelled	8.9	31 PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
83	c1usdA_	Alignment	not modelled	8.8	13 PDB header: signaling protein Chain: A: PDB Molecule: vasodilator-stimulated phosphoprotein; PDBTitle: human vasp tetramerisation domain l352m
84	c1hucC_	Alignment	not modelled	8.7	18 PDB header: thiol protease Chain: C: PDB Molecule: cathepsin b; PDBTitle: the refined 2.15 angstroms x-ray crystal structure of human2 liver cathepsin b: the structural basis for its specificity
85	c3gdzA_	Alignment	not modelled	8.6	12 PDB header: ligase Chain: A: PDB Molecule: arginyl-trna synthetase; PDBTitle: crystal structure of arginyl-trna synthetase from klebsiella2 pneumoniae subsp. pneumoniae
86	d1jrma_	Alignment	not modelled	8.6	16 Fold: YggU-like Superfamily: YggU-like Family: YggU-like
87	c2l4bA_	Alignment	not modelled	8.6	16 PDB header: transferase Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of a putative acyl carrier protein from anaplasma2 phagocytophilum. seattle structural genomics center for infectious3 disease target anpha.01018.a
88	d1jroa3	Alignment	not modelled	8.6	17 Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
89	c3jxeB_	Alignment	not modelled	8.6	23 PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
90	c3a05A_	Alignment	not modelled	8.5	31 PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from2 hyperthermophilic archaeon, aeropyrum pernix k1 complex3 with tryptophan
91	d1xhja_	Alignment	not modelled	8.5	28 Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
92	c2vgpD_	Alignment	not modelled	8.4	19 PDB header: transferase Chain: D: PDB Molecule: inner centromere protein a; PDBTitle: crystal structure of aurora b kinase in complex with a2 aminothiazole inhibitor
93	c2kciA_	Alignment	not modelled	8.4	11 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative acyl carrier protein; PDBTitle: solution nmr structure of gmet_2339 from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr141
94	d1ihra_	Alignment	not modelled	8.3	8 Fold: TolA/TonB C-terminal domain Superfamily: TolA/TonB C-terminal domain Family: TonB
95	c3hztD_	Alignment	not modelled	8.3	15 PDB header: ligase Chain: D: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase homolog from entamoeba histolytica
96	c3g59A_	Alignment	not modelled	8.3	12 PDB header: transferase Chain: A: PDB Molecule: fmn adenyltransferase; PDBTitle: crystal structure of candida glabrata fmn2 adenyltransferase in complex with atp
97	c2ouxB_	Alignment	not modelled	8.0	16 PDB header: transport protein Chain: B: PDB Molecule: magnesium transporter; PDBTitle: crystal structure of the soluble part of a magnesium transporter
98	c3sc0A_	Alignment	not modelled	8.0	38 PDB header: oxidoreductase Chain: A: PDB Molecule: methylmalonic aciduria and homocystinuria type c protein; PDBTitle: crystal structure of mmachc (1-238), a human b12 processing enzyme,2 complexed with methylcobalamin
99	d1tifa_	Alignment	not modelled	7.9	10 Fold: beta-Grasp (ubiquitin-like) Superfamily: Translation initiation factor IF3, N-terminal domain Family: Translation initiation factor IF3, N-terminal domain