




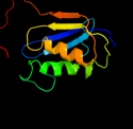


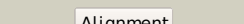

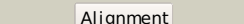

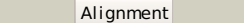
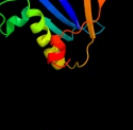
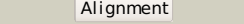
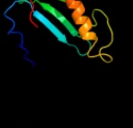
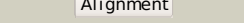

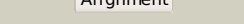

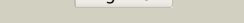












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2qalk1	 Alignment		100.0	100	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
2	d2uubk1	 Alignment		100.0	54	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
3	c3bbnK_	 Alignment		100.0	54	PDB header: ribosome Chain: K: PDB Molecule: ribosomal protein s11; PDBTitle: homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
4	c2zkqk_	 Alignment		100.0	43	PDB header: ribosomal protein/rna Chain: K: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
5	c3jyvK_	 Alignment		100.0	41	PDB header: ribosome Chain: K: PDB Molecule: 40s ribosomal protein s14(a); PDBTitle: structure of the 40s rna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
6	d1vqon1	 Alignment		97.4	19	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
7	d2gycm1	 Alignment		96.8	21	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
8	c2jl8S_	 Alignment		96.7	20	PDB header: ribosome Chain: S: PDB Molecule: 50s ribosomal protein l18; PDBTitle: insights into translational termination from the structure2 of rf2 bound to the ribosome (part 4 of 4).3 this file contains the 50s subunit.
9	d1ovya_	 Alignment		96.5	23	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
10	c3bboQ_	 Alignment		96.3	22	PDB header: ribosome Chain: Q: PDB Molecule: ribosomal protein l18; PDBTitle: homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
11	d2j01s1	 Alignment		96.2	20	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11

12	d2zjrl1	Alignment		95.2	22	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
13	dlbgva1	Alignment		74.9	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
14	c4a1aM_	Alignment		73.9	21	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l5; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rna,3 5.8s rna and proteins of molecule 3.
15	c2zkrn_	Alignment		68.8	20	PDB header: ribosomal protein/rna Chain: N: PDB Molecule: rna expansion segment es27; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
16	dlv9la1	Alignment		66.7	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
17	c3izcQ_	Alignment		65.6	18	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein rp15 (l18p); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
18	clv9laA_	Alignment		60.5	24	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad
19	c2yfqA_	Alignment		57.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: nad-specific glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase from2 peptoniphilus asaccharolyticus
20	c2bmaA_	Alignment		56.7	11	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase (nadp+); PDBTitle: the crystal structure of plasmodium falciparum glutamate2 dehydrogenase, a putative target for novel antimalarial3 drugs
21	dleuza1	Alignment	not modelled	56.2	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
22	dlgado1	Alignment	not modelled	51.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
23	c3aogA_	Alignment	not modelled	49.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
24	dlgtma1	Alignment	not modelled	49.2	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
25	dlbvua1	Alignment	not modelled	49.1	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
26	c3aoeC_	Alignment	not modelled	47.8	17	PDB header: oxidoreductase Chain: C: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
27	c2jvfA_	Alignment	not modelled	47.4	26	PDB header: de novo protein Chain: A: PDB Molecule: de novo protein m7; PDBTitle: solution structure of m7, a computationally-designed2 artificial protein
28	dlb26a1	Alignment	not modelled	46.8	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
						PDB header: de novo protein

29	c1qysA_	Alignment	not modelled	46.2	23	Chain: A: PDB Molecule: top7; PDBTitle: crystal structure of top7: a computationally designed2 protein with a novel fold
30	d1u8fo1	Alignment	not modelled	45.6	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
31	d3cmco1	Alignment	not modelled	45.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
32	d1hwxal	Alignment	not modelled	44.4	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
33	c1hrdA_	Alignment	not modelled	43.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: glutamate dehydrogenase
34	d1j0xo1	Alignment	not modelled	39.5	35	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
35	d1cf2o1	Alignment	not modelled	38.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
36	d3gpdg1	Alignment	not modelled	33.2	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
37	c2vyvB_	Alignment	not modelled	28.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase
38	c1bvuf_	Alignment	not modelled	28.0	16	PDB header: oxidoreductase Chain: F: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: glutamate dehydrogenase from thermococcus litoralis
39	d2czca2	Alignment	not modelled	27.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
40	c3klja_	Alignment	not modelled	27.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: nad(fad)-dependent dehydrogenase, nirb-family (n-terminal PDBTitle: crystal structure of nadh:rubredoxin oxidoreductase from clostridium2 acetobutylicum
41	d2g82a1	Alignment	not modelled	26.9	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
42	c2tmgD_	Alignment	not modelled	24.7	21	PDB header: oxidoreductase Chain: D: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: thermotoga maritima glutamate dehydrogenase mutant s128r,2 t158e, n117r, s160e
43	d1vc2a1	Alignment	not modelled	23.8	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
44	d1ueha_	Alignment	not modelled	23.7	17	Fold: Undecaprenyl diphosphate synthase Superfamily: Undecaprenyl diphosphate synthase Family: Undecaprenyl diphosphate synthase
45	c3iz5Q_	Alignment	not modelled	23.7	21	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein l5 (l18p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
46	d2b4ro1	Alignment	not modelled	23.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
47	d2pkqo1	Alignment	not modelled	21.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
48	c2yh5A_	Alignment	not modelled	21.0	20	PDB header: lipid binding protein Chain: A: PDB Molecule: dapx protein; PDBTitle: structure of the c-terminal domain of bamc
49	c3hq4R_	Alignment	not modelled	20.6	26	PDB header: oxidoreductase Chain: R: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase 1; PDBTitle: crystal structure of c151s mutant of glyceraldehyde-3-phosphate2 dehydrogenase 1 (gapdh1) complexed with nad from staphylococcus3 aureus mrsa252 at 2.2 angstrom resolution
50	d2g3qa1	Alignment	not modelled	20.5	29	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
51	c3k8zD_	Alignment	not modelled	19.4	24	PDB header: oxidoreductase Chain: D: PDB Molecule: nad-specific glutamate dehydrogenase; PDBTitle: crystal structure of gudb1 a decyptified secondary glutamate2 dehydrogenase from b. subtilis
52	c2czcD_	Alignment	not modelled	18.9	23	PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 pyrococcus horikoshii ot3
53	c3ga9S_	Alignment	not modelled	17.6	26	PDB header: hydrolase Chain: S: PDB Molecule: capsule biosynthesis protein capd; PDBTitle: crystal structure of bacillus anthracis transpeptidase enzyme capd,2 crystal form ii

54	d1hpla2	Alignment	not modelled	17.6	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
55	c2v36D	Alignment	not modelled	16.9	35	PDB header: transferase Chain: D: PDB Molecule: gamma-glutamyltranspeptidase small chain; PDBTitle: crystal structure of gamma-glutamyl transferase from2 bacillus subtilis
56	c2ep7B	Alignment	not modelled	16.6	26	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: structural study of project id aq_1065 from aquifex aeolicus vf5
57	c1s7cA	Alignment	not modelled	16.6	26	PDB header: structural genomics, oxidoreductase Chain: A: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase a; PDBTitle: crystal structure of mes buffer bound form of glyceraldehyde 3-2 phosphate dehydrogenase from escherichia coli
58	c2e0yB	Alignment	not modelled	16.2	26	PDB header: transferase Chain: B: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: crystal structure of the samarium derivative of mature gamma-2 glutamyltranspeptidase from escherichia coli
59	c1gv4A	Alignment	not modelled	15.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: programed cell death protein 8; PDBTitle: murine apoptosis-inducing factor (aif)
60	d1etha2	Alignment	not modelled	12.7	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
61	c3h9eA	Alignment	not modelled	12.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: PDBTitle: crystal structure of human sperm-specific glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate
62	c1cf2Q	Alignment	not modelled	12.0	15	PDB header: oxidoreductase Chain: Q: PDB Molecule: protein (glyceraldehyde-3-phosphate PDBTitle: three-dimensional structure of d-glyceraldehyde-3-phosphate2 dehydrogenase from the hyperthermophilic archaeon3 methanothermus fervidus
63	c1jp3A	Alignment	not modelled	11.8	17	PDB header: transferase Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: structure of e.coli undecaprenyl pyrophosphate synthase
64	c1cerC	Alignment	not modelled	11.7	26	PDB header: oxidoreductase (aldehyde(d)-nad(a)) Chain: C: PDB Molecule: holo-d-glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: determinants of enzyme thermostability observed in the2 molecular structure of thermus aquaticus d-glyceraldehyde-3 3-phosphate dehydrogenase at 2.5 angstroms resolution
65	c1b7gO	Alignment	not modelled	11.6	18	PDB header: oxidoreductase Chain: O: PDB Molecule: protein (glyceraldehyde 3-phosphate dehydrogenase); PDBTitle: glyceraldehyde 3-phosphate dehydrogenase
66	c3hjaB	Alignment	not modelled	11.4	21	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase from borrelia burgdorferi
67	c2b4rQ	Alignment	not modelled	10.5	20	PDB header: oxidoreductase Chain: Q: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 plasmodium falciparum at 2.25 angstrom resolution reveals intriguing3 extra electron density in the active site
68	d1j1xa2	Alignment	not modelled	10.3	27	Fold: beta-Trefoil Superfamily: Agglutinin Family: Agglutinin
69	c2gd1P	Alignment	not modelled	10.2	26	PDB header: oxidoreductase(aldehyde(d)-nad(a)) Chain: P: PDB Molecule: apo-d-glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: coenzyme-induced conformational changes in glyceraldehyde-3-2 phosphate dehydrogenase from bacillus stearothermophilus
70	d1j1xa1	Alignment	not modelled	10.2	36	Fold: beta-Trefoil Superfamily: Agglutinin Family: Agglutinin
71	c1nr1A	Alignment	not modelled	9.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase 1; PDBTitle: crystal structure of the r463a mutant of human glutamate2 dehydrogenase
72	c1hplB	Alignment	not modelled	9.3	12	PDB header: hydrolase(carboxylic esterase) Chain: B: PDB Molecule: lipase; PDBTitle: horse pancreatic lipase. the crystal structure at 2.32 angstroms resolution
73	c2nqoB	Alignment	not modelled	8.5	26	PDB header: transferase Chain: B: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: crystal structure of helicobacter pylori gamma-glutamyltranspeptidase
74	d1t57a	Alignment	not modelled	8.5	24	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
75	c2j3eA	Alignment	not modelled	8.3	24	PDB header: protein transport Chain: A: PDB Molecule: t7i23.11 protein; PDBTitle: dimerization is important for the gtpase activity of2 chloroplast translocon components atoc33 and pstoc159
76	d1gpla2	Alignment	not modelled	7.6	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain

77	d1v95a_	Alignment	not modelled	7.4	13	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
78	d1lpbb2	Alignment	not modelled	7.2	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
79	c3kwsB_	Alignment	not modelled	6.8	16	PDB header: isomerase Chain: B: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
80	d1g8ma1	Alignment	not modelled	6.8	24	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
81	c2hcuA_	Alignment	not modelled	6.8	38	PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: crystal structure of smu.1381 (or leud) from streptococcus2 mutans
82	c3sthA_	Alignment	not modelled	6.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 toxoplasma gondii
83	c3q3wB_	Alignment	not modelled	6.7	38	PDB header: transferase Chain: B: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: isopropylmalate isomerase small subunit from campylobacter jejuni.
84	c1gplA_	Alignment	not modelled	6.6	12	PDB header: serine esterase Chain: A: PDB Molecule: rp2 lipase; PDBTitle: rp2 lipase
85	c2pvsB_	Alignment	not modelled	6.5	17	PDB header: hydrolase Chain: B: PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 22 mutant n336q
86	c3h5jA_	Alignment	not modelled	6.3	43	PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from2 mycobacterium tuberculosis
87	c2e0wA_	Alignment	not modelled	6.2	26	PDB header: transferase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: t391a precursor mutant protein of gamma-glutamyltranspeptidase from2 escherichia coli
88	d1htwa_	Alignment	not modelled	6.0	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: YjeE-like
89	d1v7la_	Alignment	not modelled	5.9	43	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: LeuD-like
90	d1bu8a2	Alignment	not modelled	5.7	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
91	c3efhB_	Alignment	not modelled	5.7	17	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase 1; PDBTitle: crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
92	d1pkxa1	Alignment	not modelled	5.7	21	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Inosicase
93	c2p9wA_	Alignment	not modelled	5.5	15	PDB header: allergen Chain: A: PDB Molecule: mal s 1 allergenic protein; PDBTitle: crystal structure of the major malassezia sympodialis allergen mala s2 1
94	d2cyga1	Alignment	not modelled	5.5	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
95	d2dsta1	Alignment	not modelled	5.2	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: TTHA1544-like
96	c3b4nB_	Alignment	not modelled	5.2	19	PDB header: lyase Chain: B: PDB Molecule: endo-pectate lyase; PDBTitle: crystal structure analysis of pectate lyase peli from2 erwinia chrysanthemi