




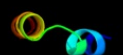















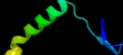











#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ms6A_	 Alignment		46.6	33	PDB header: protein binding Chain: A: PDB Molecule: hepatitis b virus x-interacting protein; PDBTitle: crystal structure of hepatitis b x-interacting protein (hbxi p)
2	c3kgkA_	 Alignment		35.7	21	PDB header: chaperone Chain: A: PDB Molecule: arsenical resistance operon trans-acting repressor arsd; PDBTitle: crystal structure of arsd
3	d1mxra_	 Alignment		29.5	14	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
4	c1yfdA_	 Alignment		27.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase 1 beta PDBTitle: crystal structure of the y122h mutant of ribonucleotide2 reductase r2 protein from e. coli
5	d1r2fa_	 Alignment		25.7	23	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
6	c3ee4A_	 Alignment		25.0	41	PDB header: oxidoreductase Chain: A: PDB Molecule: probable ribonucleoside-di-phosphate reductase; PDBTitle: r2-like ligand binding mn/fe oxidase from m. tuberculosis
7	c2o1zA_	 Alignment		25.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleotide reductase subunit r2; PDBTitle: plasmodium vivax ribonucleotide reductase subunit r22 (pv086155)
8	c1r2fB_	 Alignment		24.3	23	PDB header: oxidoreductase Chain: B: PDB Molecule: protein (ribonucleotide reductase r2); PDBTitle: ribonucleotide reductase r2f protein from salmonella2 typhimurium
9	d1uw0a_	 Alignment		24.2	13	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: PARP-type zinc finger
10	c2vuxB_	 Alignment		24.1	23	PDB header: oxidoreductase Chain: B: PDB Molecule: ribonucleoside-diphosphate reductase subunit m2 b; PDBTitle: human ribonucleotide reductase, subunit m2 b
11	c3pqaA_	 Alignment		23.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: lactaldehyde dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase gapn2 from methanocaldococcus jannaschii dsm 2661

12	d1w68a_	Alignment		23.2	9	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
13	c3ktbD_	Alignment		23.1	8	PDB header: transcription regulator Chain: D: PDB Molecule: arsenical resistance operon trans-acting repressor; PDBTitle: crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
14	c2rccC_	Alignment		23.0	5	PDB header: oxidoreductase Chain: C: PDB Molecule: ribonucleoside-diphosphate reductase subunit beta; PDBTitle: crystal structure of putative class i ribonucleotide reductase2 (np_241368.1) from bacillus halodurans at 1.90 a resolution
15	d1oquc_	Alignment		22.9	27	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
16	c1vluB_	Alignment		22.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: gamma-glutamyl phosphate reductase; PDBTitle: crystal structure of gamma-glutamyl phosphate reductase (yor323c) from2 saccharomyces cerevisiae at 2.40 a resolution
17	c3hf1B_	Alignment		22.5	23	PDB header: oxidoreductase Chain: B: PDB Molecule: ribonucleoside-diphosphate reductase subunit m2 PDBTitle: crystal structure of human p53r2
18	d1uzra_	Alignment		22.5	27	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
19	d1o20a_	Alignment		22.4	12	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
20	c1h0oA_	Alignment		22.1	9	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase; PDBTitle: cobalt substitution of mouse r2 ribonucleotide reductase to2 model the reactive diferrous state
21	c3ry0A_	Alignment	not modelled	21.8	12	PDB header: isomerase Chain: A: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
22	d1bjpa_	Alignment	not modelled	21.3	21	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
23	d3dhza1	Alignment	not modelled	21.2	27	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
24	d2doaa1	Alignment	not modelled	19.7	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ELL N2 domain-like
25	d1otfa_	Alignment	not modelled	19.2	16	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
26	c2op8A_	Alignment	not modelled	19.2	10	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase ywhb; PDBTitle: crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
27	c3fghA_	Alignment	not modelled	19.1	23	PDB header: transcription Chain: A: PDB Molecule: transcription factor a, mitochondrial; PDBTitle: human mitochondrial transcription factor a box b
28	d1v54d_	Alignment	not modelled	17.8	42	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit IV Family: Mitochondrial cytochrome c oxidase subunit IV
						PDB header: electron transport Chain: Q: PDB Molecule: cytochrome c oxidase subunit 4 isoform

29	c2y69Q_	Alignment	not modelled	17.8	42	1; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
30	c3mb2G_	Alignment	not modelled	17.7	12	PDB header: isomerase Chain: G: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - alpha subunit; PDBTitle: kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
31	c3r64A_	Alignment	not modelled	17.3	11	PDB header: oxidoreductase Chain: A: PDB Molecule: nad dependent benzaldehyde dehydrogenase; PDBTitle: crystal structure of a nad-dependent benzaldehyde dehydrogenase from2 corynebacterium glutamicum
32	c2e5nA_	Alignment	not modelled	16.4	10	PDB header: transcription Chain: A: PDB Molecule: rna polymerase ii elongation factor eli2; PDBTitle: solution structure of the eli_n2 domain of target of rna2 polymerase ii elongation factor eli2
33	d1vlua_	Alignment	not modelled	16.1	12	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
34	c1v9xA_	Alignment	not modelled	16.1	11	PDB header: transferase Chain: A: PDB Molecule: poly (adp-ribose) polymerase; PDBTitle: solution structure of the first zn-finger domain of2 poly(adp-ribose) polymerase-1
35	c2kzyA_	Alignment	not modelled	16.0	26	PDB header: metal binding protein Chain: A: PDB Molecule: zfpand5 protein (zinc finger protein 216 (predicted), PDBTitle: solution nmr structure of the znf216 a20 zinc finger
36	c3ed6B_	Alignment	not modelled	15.4	12	PDB header: oxidoreductase Chain: B: PDB Molecule: betaine aldehyde dehydrogenase; PDBTitle: 1.7 angstrom resolution crystal structure of betaine aldehyde2 dehydrogenase (betb) from staphylococcus aureus
37	c3v4cB_	Alignment	not modelled	15.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde dehydrogenase (nadh+); PDBTitle: crystal structure of a semialdehyde dehydrogenase from sinorhizobium2 meliloti 1021
38	d1uzba_	Alignment	not modelled	14.9	13	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
39	d1bc6a_	Alignment	not modelled	14.8	39	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
40	c2zetD_	Alignment	not modelled	14.8	16	PDB header: signaling protein Chain: D: PDB Molecule: melanophilin; PDBTitle: crystal structure of the small gtpase rab27b complexed with2 the slp homology domain of slac2-a/melanophilin
41	c2eqzA_	Alignment	not modelled	14.6	22	PDB header: transcription Chain: A: PDB Molecule: high mobility group protein b3; PDBTitle: solution structure of the first hmg-box domain from high2 mobility group protein b3
42	c3m20A_	Alignment	not modelled	14.4	16	PDB header: isomerase Chain: A: PDB Molecule: 4-oxalocrotonate tautomerase, putative; PDBTitle: crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
43	c2ormA_	Alignment	not modelled	14.4	16	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase hp0924; PDBTitle: crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.
44	c1j3xA_	Alignment	not modelled	13.8	26	PDB header: dna binding protein Chain: A: PDB Molecule: high mobility group protein 2; PDBTitle: solution structure of the n-terminal domain of the hmgb2
45	d1j3xa_	Alignment	not modelled	13.8	26	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
46	d1wt8a1	Alignment	not modelled	13.8	57	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
47	c2x4kB_	Alignment	not modelled	13.4	16	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
48	c2h5gA_	Alignment	not modelled	13.4	7	PDB header: oxidoreductase Chain: A: PDB Molecule: delta 1-pyrroline-5-carboxylate synthetase; PDBTitle: crystal structure of human pyrroline-5-carboxylate synthetase
49	d1k99a_	Alignment	not modelled	13.3	11	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
50	d1o9ja_	Alignment	not modelled	13.2	17	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
51	c2d4eB_	Alignment	not modelled	13.1	11	PDB header: oxidoreductase Chain: B: PDB Molecule: 5-carboxymethyl-2-hydroxyuconate semialdehyde PDBTitle: crystal structure of the hpcc from thermus thermophilus hb8
52	c2co9A_	Alignment	not modelled	13.1	15	PDB header: transcription Chain: A: PDB Molecule: thymus high mobility group box protein tox; PDBTitle: solution structure of the hmg_box domain of thymus high2 mobility group box protein tox from mouse
53	c2criA_	Alignment	not modelled	13.1	27	PDB header: gene regulation Chain: A: PDB Molecule: swi/snf-related matrix-associated actin-

53	c2v1jA_	Alignment	not modelled	13.1	27	PDBTitle: solution structure of the hmg domain of mouse hmg domain2 protein hmgx2
54	d1smaA_	Alignment	not modelled	12.9	20	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
55	d1jk0b_	Alignment	not modelled	12.9	18	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
56	d1bi9a_	Alignment	not modelled	12.7	23	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
57	d1ad3a_	Alignment	not modelled	12.6	12	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
58	d1oqen_	Alignment	not modelled	12.5	25	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: BAFF receptor-like
59	c2k9mA_	Alignment	not modelled	12.4	22	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: structure of the core binding domain of sigma54
60	c3k9dD_	Alignment	not modelled	12.2	8	PDB header: oxidoreductase Chain: D: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of probable aldehyde dehydrogenase from listeria2 monocytogenes egd-e
61	c3odeA_	Alignment	not modelled	12.1	8	PDB header: dna binding protein/dna Chain: A: PDB Molecule: poly [adp-ribose] polymerase 1; PDBTitle: human parp-1 zinc finger 2 (zn2) bound to dna
62	c2w8qA_	Alignment	not modelled	11.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate-semialdehyde dehydrogenase, PDBTitle: the crystal structure of human ssadh in complex with ssa.
63	d1o04a_	Alignment	not modelled	11.9	16	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
64	c3qpiA_	Alignment	not modelled	11.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: chlorite dismutase; PDBTitle: crystal structure of dimeric chlorite dismutases from nitrobacter2 winogradskyi
65	c3abfB_	Alignment	not modelled	11.7	16	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
66	c3b4wA_	Alignment	not modelled	11.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of mycobacterium tuberculosis aldehyde dehydrogenase2 complexed with nad+
67	c3k2wD_	Alignment	not modelled	11.7	21	PDB header: oxidoreductase Chain: D: PDB Molecule: betaine-aldehyde dehydrogenase; PDBTitle: crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
68	c3qanB_	Alignment	not modelled	11.6	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-pyrroline-5-carboxylate dehydrogenase 1; PDBTitle: crystal structure of 1-pyrroline-5-carboxylate dehydrogenase from2 bacillus halodurans
69	c2jg7G_	Alignment	not modelled	11.6	19	PDB header: oxidoreductase Chain: G: PDB Molecule: antiquitin; PDBTitle: crystal structure of seabream antiquitin and elucidation of2 its substrate specificity
70	c2hg2A_	Alignment	not modelled	11.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase a; PDBTitle: structure of lactaldehyde dehydrogenase
71	d1bxsa_	Alignment	not modelled	11.3	20	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
72	d1ag8a_	Alignment	not modelled	11.2	20	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
73	d1gt0d_	Alignment	not modelled	11.1	14	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
74	c3lnsD_	Alignment	not modelled	10.9	11	PDB header: oxidoreductase Chain: D: PDB Molecule: benzaldehyde dehydrogenase; PDBTitle: benzaldehyde dehydrogenase, a class 3 aldehyde dehydrogenase, with2 bound nadp+ and benzoate adduct
75	c3ju8B_	Alignment	not modelled	10.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: succinylglutamic semialdehyde dehydrogenase; PDBTitle: crystal structure of succinylglutamic semialdehyde dehydrogenase from2 pseudomonas aeruginosa.
76	c2ivfB_	Alignment	not modelled	10.7	28	PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
77	c1wz6A_	Alignment	not modelled	10.7	19	PDB header: transcription Chain: A: PDB Molecule: hmg-box transcription factor bbx; PDBTitle: solution structure of the hmg_box domain of murine bobby2 sox homolog
78	c2p1iA_	Alignment	not modelled	10.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleotide reductase, small chain; PDBTitle: plasmodium yoelii ribonucleotide reductase subunit r2 (py03671)
						PDB header: transferase Chain: A: PDB Molecule: poly (adp-ribose) polymerase family,

79	c2dmjA_	Alignment	not modelled	10.7	12	member 1; PDBTitle: solution structure of the first zf-parp domain of human2 poly(adp-ribose)polymerase-1
80	d1mwwa_	Alignment	not modelled	10.7	17	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: Hypothetical protein HI1388.1
81	d1lwma_	Alignment	not modelled	10.7	19	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
82	d3c7bb1	Alignment	not modelled	10.4	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
83	c2cs1A_	Alignment	not modelled	10.3	23	PDB header: dna binding protein Chain: A: PDB Molecule: pms1 protein homolog 1; PDBTitle: solution structure of the hmg domain of human dna mismatch2 repair protein
84	c2c7mA_	Alignment	not modelled	9.9	39	PDB header: protein-binding Chain: A: PDB Molecule: rab guanine nucleotide exchange factor 1; PDBTitle: human rabex-5 residues 1-74 in complex with ubiquitin
85	c2kn0A_	Alignment	not modelled	9.8	36	PDB header: apoptosis Chain: A: PDB Molecule: fn14; PDBTitle: solution nmr structure of xenopus fn14
86	c3iwkB_	Alignment	not modelled	9.8	21	PDB header: oxidoreductase Chain: B: PDB Molecule: aminoaldehyde dehydrogenase; PDBTitle: crystal structure of aminoaldehyde dehydrogenase 1 from2 pisum sativum (psamadh1)
87	c2gmhA_	Alignment	not modelled	9.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: electron transfer flavoprotein-ubiquinone PDBTitle: structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
88	c2k9lA_	Alignment	not modelled	9.8	24	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: structure of the core binding domain of sigma54
89	d1hsma_	Alignment	not modelled	9.7	15	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
90	c1mv4B_	Alignment	not modelled	9.5	36	PDB header: de novo protein Chain: B: PDB Molecule: tropomyosin 1 alpha chain; PDBTitle: tm9a251-284: a peptide model of the c-terminus of a rat2 striated alpha tropomyosin
91	d2c7na1	Alignment	not modelled	9.5	39	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: A20-like zinc finger
92	c1hmfA_	Alignment	not modelled	9.4	15	PDB header: dna-binding Chain: A: PDB Molecule: high mobility group protein fragment-b; PDBTitle: structure of the hmg box motif in the b-domain of hmg1
93	d1hmfa_	Alignment	not modelled	9.4	15	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
94	d1a4sa_	Alignment	not modelled	9.4	19	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
95	c2vroB_	Alignment	not modelled	9.2	12	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400
96	c3mhsE_	Alignment	not modelled	9.2	29	PDB header: hydrolase/transcription regulator/protei Chain: E: PDB Molecule: saga-associated factor 73; PDBTitle: structure of the saga ubp8/sgf11/sus1/sgf73 dub module bound to2 ubiquitin aldehyde
97	c3ifgH_	Alignment	not modelled	9.1	15	PDB header: oxidoreductase Chain: H: PDB Molecule: succinate-semialdehyde dehydrogenase (nadp+); PDBTitle: crystal structure of succinate-semialdehyde dehydrogenase from2 burkholderia pseudomallei, part 1 of 2
98	c1t90B_	Alignment	not modelled	9.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: probable methylmalonate-semialdehyde PDBTitle: crystal structure of methylmalonate semialdehyde2 dehydrogenase from bacillus subtilis
99	c3my7A_	Alignment	not modelled	9.0	8	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase/acetaldehyde dehydrogenase; PDBTitle: the crystal structure of the acdh domain of an alcohol dehydrogenase2 from vibrio parahaemolyticus to 2.25a