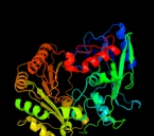


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pm9A_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative dehydrogenase (rpa1076) from <i>Rhodopseudomonas palustris</i> cga009 at 2.57 Å resolution
2	c1ahuB_	 Alignment		100.0	18	PDB header: flavoenzyme Chain: B: PDB Molecule: vanillyl-alcohol oxidase; PDBTitle: structure of the octameric flavoenzyme vanillyl-alcohol 2 oxidase in complex with p-cresol
3	c2uuvC_	 Alignment		100.0	21	PDB header: transferase Chain: C: PDB Molecule: alkyl dihydroxyacetonephosphate synthase; PDBTitle: alkyl dihydroxyacetonephosphate synthase in p1
4	c1f0xA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase, a peripheral 2 membrane respiratory enzyme.
5	c1wveB_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-cresol dehydrogenase [hydroxylating] PDBTitle: p-cresol methylhydroxylase: alteration of the structure of 2 the flavoprotein subunit upon its binding to the 3 cytochrome subunit
6	c3bw7A_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 1; PDBTitle: maize cytokinin oxidase/dehydrogenase complexed with the allenic 2 cytokinin analog ha-1
7	c2exrA_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 7; PDBTitle: x-ray structure of cytokinin oxidase/dehydrogenase (ckx)2 from <i>Arabidopsis thaliana</i> at5g21482
8	c2bvfA_	 Alignment		100.0	16	PDB header: oxidase Chain: A: PDB Molecule: 6-hydroxy-d-nicotine oxidase; PDBTitle: crystal structure of 6-hydroxy-d-nicotine oxidase from <i>Arthrobacter nicotinovorans</i> . crystal form 3 (p1)
9	c3fwaA_	 Alignment		100.0	13	PDB header: flavoprotein Chain: A: PDB Molecule: reticuline oxidase; PDBTitle: structure of berberine bridge enzyme, c166a variant in complex with 2 (s)-reticuline
10	c1zr6A_	 Alignment		100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: glucooligosaccharide oxidase; PDBTitle: the crystal structure of an <i>Acremonium strictum</i> glucooligosaccharide 2 oxidase reveals a novel flavinylation
11	c3d2hA_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: berberine bridge-forming enzyme; PDBTitle: structure of berberine bridge enzyme from <i>Eschscholzia californica</i> , 2 monoclinic crystal form

12	c2ipiD_	Alignment		100.0	13	PDB header: oxidoreductase Chain: D: PDB Molecule: aclacinomycin oxidoreductase (aknox); PDBTitle: crystal structure of aclacinomycin oxidoreductase
13	c3popD_	Alignment		100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: gilr oxidase; PDBTitle: the crystal structure of gilr, an oxidoreductase that catalyzes the2 terminal step of gilvocarcin biosynthesis
14	c2wdwB_	Alignment		100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: putative hexose oxidase; PDBTitle: the native crystal structure of the primary hexose oxidase (2 dbv29) in antibiotic a40926 biosynthesis
15	c2y3rC_	Alignment		100.0	15	PDB header: oxidoreductase Chain: C: PDB Molecule: taml; PDBTitle: structure of the tirandamycin-bound fad-dependent2 tirandamycin oxidase taml in p21 space group
16	c2vfvA_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: xylitol oxidase; PDBTitle: alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite
17	cli19B_	Alignment		100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: cholesterol oxidase; PDBTitle: crystal structure of cholesterol oxidase from b.sterolicum
18	c3js8A_	Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: solvent-stable cholesterol oxidase
19	dlwvfa2	Alignment		100.0	22	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
20	dlf0xa2	Alignment		100.0	22	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
21	dle8ga2	Alignment	not modelled	100.0	21	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
22	dlw1oa2	Alignment	not modelled	100.0	20	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
23	d2i0ka2	Alignment	not modelled	100.0	22	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
24	dlhskal	Alignment	not modelled	100.0	19	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
25	dle8ga1	Alignment	not modelled	100.0	16	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
26	dluxyal	Alignment	not modelled	100.0	12	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
27	clhskA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: crystal structure of s. aureus murb
28	dlwvfa1	Alignment	not modelled	100.0	20	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
						Fold: Ferredoxin-like

29	d1f0xa1	Alignment	not modelled	100.0	20	Superfamily: FAD-linked oxidases, C-terminal domain Family: D-lactate dehydrogenase
30	c2yvsA	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: glycolate oxidase subunit glce; PDBTitle: crystal structure of glycolate oxidase subunit glce from thermus2 thermophilus hb8
31	c1mbbA	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: uridine diphospho-n-acetylenolpyruvylglucosamine PDBTitle: oxidoreductase
32	c3i99A	Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: the crystal structure of the udp-n-acetylenolpyruvylglucosamine2 reductase from the vibrio cholerae o1 biovar tor
33	c2gquA	Alignment	not modelled	99.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvylglucosamine reductase; PDBTitle: crystal structure of udp-n-acetylenolpyruvylglucosamine2 reductase (murb) from thermus caldophilus
34	d1w1oa1	Alignment	not modelled	99.3	16	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cytokinin dehydrogenase 1
35	d1ffvc2	Alignment	not modelled	97.8	19	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
36	c1n62C	Alignment	not modelled	97.8	17	PDB header: oxidoreductase Chain: C: PDB Molecule: carbon monoxide dehydrogenase medium chain; PDBTitle: crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state
37	c1ffuF	Alignment	not modelled	97.7	20	PDB header: hydrolase Chain: F: PDB Molecule: cutm, flavoprotein of carbon monoxide PDBTitle: carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
38	c1t3qF	Alignment	not modelled	97.5	14	PDB header: oxidoreductase Chain: F: PDB Molecule: quinoline 2-oxidoreductase medium subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
39	d3b9jb2	Alignment	not modelled	97.5	10	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
40	c3etrM	Alignment	not modelled	97.5	8	PDB header: oxidoreductase Chain: M: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of xanthine oxidase in complex with2 lumazine
41	c3b9jl	Alignment	not modelled	97.5	8	PDB header: oxidoreductase Chain: J: PDB Molecule: xanthine oxidase; PDBTitle: structure of xanthine oxidase with 2-hydroxy-6-methylpurine
42	c3hrdC	Alignment	not modelled	97.4	17	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinate dehydrogenase fad-subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
43	d1v97a6	Alignment	not modelled	97.4	10	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
44	d1t3qc2	Alignment	not modelled	97.3	15	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
45	d1n62c2	Alignment	not modelled	97.3	18	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
46	d1jroa4	Alignment	not modelled	97.2	13	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
47	c1rm6E	Alignment	not modelled	97.0	20	PDB header: oxidoreductase Chain: E: PDB Molecule: 4-hydroxybenzoyl-coa reductase beta subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
48	c2w3rG	Alignment	not modelled	96.9	16	PDB header: oxidoreductase Chain: G: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
49	d1rm6b2	Alignment	not modelled	96.3	21	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CO dehydrogenase flavoprotein N-terminal domain-like
50	c1wygA	Alignment	not modelled	95.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
51	d2i0ka1	Alignment	not modelled	86.0	13	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cholesterol oxidase
52	d1jaka1	Alignment	not modelled	67.9	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
53	d1yhta1	Alignment	not modelled	64.9	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain

54	d1qbaa3	Alignment	not modelled	64.2	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
55	d1nowa1	Alignment	not modelled	63.7	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
56	c3nsnA	Alignment	not modelled	63.2	10	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosaminidase; PDBTitle: crystal structure of insect beta-n-acetyl-d-hexosaminidase ofhex12 complexed with tmg-chitotriomycin
57	c1nouA	Alignment	not modelled	63.1	10	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase beta chain; PDBTitle: native human lysosomal beta-hexosaminidase isoform b
58	d2gja1	Alignment	not modelled	63.0	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
59	c3gh7A	Alignment	not modelled	62.8	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of beta-hexosaminidase from paenibacillus2 sp. ts12 in complex with galnac
60	c1m04A	Alignment	not modelled	61.9	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcnac)
61	c3rcnA	Alignment	not modelled	61.5	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aureus
62	c2yl8A	Alignment	not modelled	61.4	10	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
63	c2uval	Alignment	not modelled	61.3	17	PDB header: transferase Chain: I: PDB Molecule: fatty acid synthase beta subunits; PDBTitle: crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
64	c2ylaA	Alignment	not modelled	61.1	10	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
65	c2dgaA	Alignment	not modelled	59.9	16	PDB header: rna binding protein Chain: A: PDB Molecule: kiaa0430 protein; PDBTitle: solution structure of the rna recognition motif in kiaa04302 protein
66	c2gjeE	Alignment	not modelled	59.7	10	PDB header: hydrolase Chain: E: PDB Molecule: beta-hexosaminidase alpha chain; PDBTitle: crystallographic structure of human beta-hexosaminidase a
67	c3lmyA	Alignment	not modelled	59.6	10	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase subunit beta; PDBTitle: the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
68	c1qpaA	Alignment	not modelled	59.1	11	PDB header: chaperone Chain: A: PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide2 dismutase
69	c2vkzH	Alignment	not modelled	58.9	19	PDB header: transferase Chain: H: PDB Molecule: fatty acid synthase subunit beta; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
70	c3rpmA	Alignment	not modelled	56.5	10	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetyl-hexosaminidase; PDBTitle: crystal structure of the first gh20 domain of a novel beta-n-acetyl-2 hexosaminidase strh from streptococcus pneumoniae r6
71	c1qbaA	Alignment	not modelled	52.4	10	PDB header: glycosyl hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: bacterial chitinase, glycosyl hydrolase family 20
72	c1jk9D	Alignment	not modelled	51.1	11	PDB header: oxidoreductase Chain: D: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: heterodimer between h48f-yso1 and yccs
73	c2epoB	Alignment	not modelled	50.1	10	PDB header: hydrolase Chain: B: PDB Molecule: n-acetyl-beta-d-glucosaminidase; PDBTitle: n-acetyl-b-d-glucosaminidase (gcna) from streptococcus gordonii
74	c2bp7F	Alignment	not modelled	46.6	10	PDB header: oxidoreductase Chain: F: PDB Molecule: 2-oxoisovalerate dehydrogenase beta subunit; PDBTitle: new crystal form of the pseudomonas putida branched-chain2 dehydrogenase (e1)
75	d2p0la1	Alignment	not modelled	45.9	16	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like
76	d2p5ia1	Alignment	not modelled	44.1	33	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: LplA-like
77	c2yswB	Alignment	not modelled	39.2	16	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: crystal structure of the 3-dehydroquinate dehydratase from aquifex2 aeolicus vf5
78	d2bi7a1	Alignment	not modelled	39.1	19	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: UDP-galactopyranose mutase, N-terminal domain

79	d2cqpa1	Alignment	not modelled	38.5	19	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
80	c3s01A	Alignment	not modelled	38.0	12	PDB header: rna binding protein Chain: A: PDB Molecule: heterogeneous nuclear ribonucleoprotein l; PDBTitle: crystal structure of a heterogeneous nuclear ribonucleoprotein l2 (hnrlp) from mus musculus at 2.15 a resolution
81	c2do0A	Alignment	not modelled	37.4	16	PDB header: rna binding protein Chain: A: PDB Molecule: heterogeneous nuclear ribonucleoprotein m; PDBTitle: solution structure of the rna binding domain of2 heterogeneous nuclear ribonucleoprotein m
82	d1a9xb2	Alignment	not modelled	36.8	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
83	c2x24B	Alignment	not modelled	36.6	22	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: bovine acc2 ct domain in complex with inhibitor
84	d1itza2	Alignment	not modelled	35.5	11	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
85	c3ff6D	Alignment	not modelled	34.3	22	PDB header: ligase Chain: D: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: human acc2 ct domain with cp-640186
86	d1wexa	Alignment	not modelled	33.5	17	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
87	d1umdb1	Alignment	not modelled	33.3	26	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
88	d2r8oa1	Alignment	not modelled	32.8	11	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
89	c1od4C	Alignment	not modelled	32.7	19	PDB header: ligase Chain: C: PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain
90	d2plsa1	Alignment	not modelled	32.4	7	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
91	c2f3ja	Alignment	not modelled	31.2	16	PDB header: transport protein Chain: A: PDB Molecule: rna and export factor binding protein 2; PDBTitle: the solution structure of the ref2-i mrna export factor2 (residues 1-155).
92	d1no8a	Alignment	not modelled	29.8	16	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
93	c1no8A	Alignment	not modelled	29.8	16	PDB header: rna binding protein Chain: A: PDB Molecule: aly; PDBTitle: solution structure of the nuclear factor aly rbd domain
94	d1qupa2	Alignment	not modelled	29.6	14	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
95	c2dnoA	Alignment	not modelled	29.3	21	PDB header: rna binding protein Chain: A: PDB Molecule: trinucleotide repeat containing 4 variant; PDBTitle: solution structure of rna binding domain in trinucleotide2 repeat containing 4 variant
96	c2e44A	Alignment	not modelled	28.8	15	PDB header: rna binding protein Chain: A: PDB Molecule: insulin-like growth factor 2 mrna binding PDBTitle: solution structure of rna binding domain in insulin-like2 growth factor 2 mrna binding protein 3
97	d1r9ja1	Alignment	not modelled	28.3	22	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like Pyr module
98	c2fy1A	Alignment	not modelled	28.2	21	PDB header: structural protein/rna Chain: A: PDB Molecule: rna-binding motif protein, y chromosome, family PDBTitle: a dual mode of rna recognition by the rbmy protein
99	d2ozlb1	Alignment	not modelled	27.8	30	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
100	dlik6a1	Alignment	not modelled	27.3	30	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
101	d1w85b1	Alignment	not modelled	27.1	26	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
102	c2gvsA	Alignment	not modelled	26.8	38	PDB header: lipid binding protein Chain: A: PDB Molecule: chemosensory protein csp-sg4; PDBTitle: nmr solution structure of cspsg4
103	c2rneA	Alignment	not modelled	26.2	17	PDB header: rna binding protein Chain: A: PDB Molecule: tia1 protein; PDBTitle: solution structure of the second rna recognition motif2 (rrm) of tia-1
104	d1fhta	Alignment	not modelled	26.1	9	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
105	c3h0ja	Alignment	not modelled	25.0	19	PDB header: transferase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the carboxyltransferase domain of2

					acetyl-coenzyme a carboxylase in complex with compound 2
106	d1kx9b_	Alignment	not modelled	24.6	29 Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2
107	d1n8va_	Alignment	not modelled	22.1	25 Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2
108	d1qs0b1	Alignment	not modelled	22.0	19 Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
109	c2crlA_	Alignment	not modelled	22.0	3 PDB header: chaperone Chain: A: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: the apo form of hma domain of copper chaperone for2 superoxide dismutase
110	d1x5oa1	Alignment	not modelled	22.0	17 Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
111	c1uytC_	Alignment	not modelled	21.9	19 PDB header: transferase Chain: C: PDB Molecule: acetyl-coa carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain
112	d1pixa3	Alignment	not modelled	21.7	22 Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
113	c2i38A_	Alignment	not modelled	21.6	22 PDB header: rna binding protein/chimera Chain: A: PDB Molecule: fusion protein consists of immunoglobulin g- PDBTitle: solution structure of the rrm of srp20
114	c2rd5D_	Alignment	not modelled	21.5	31 PDB header: protein binding Chain: D: PDB Molecule: pii protein; PDBTitle: structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
115	c2do4A_	Alignment	not modelled	21.2	11 PDB header: immune system Chain: A: PDB Molecule: squamous cell carcinoma antigen recognized by t- PDBTitle: solution structure of the rna binding domain of squamous2 cell carcinoma antigen recognized by t cells 3
116	d2bfdb1	Alignment	not modelled	20.9	26 Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
117	c3qxbB_	Alignment	not modelled	20.8	7 PDB header: isomerase Chain: B: PDB Molecule: putative xylose isomerase; PDBTitle: crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution