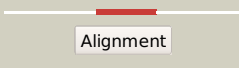

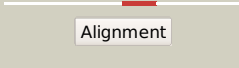
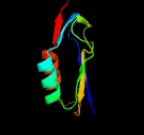
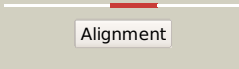

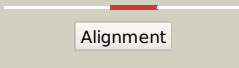
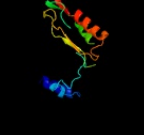
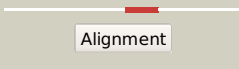

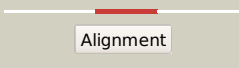

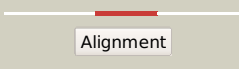

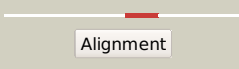

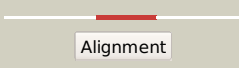

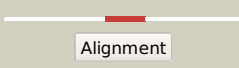

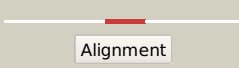

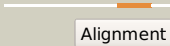
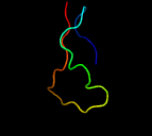
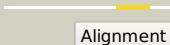
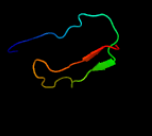
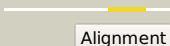

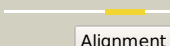

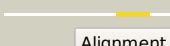

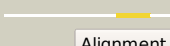
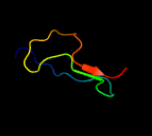
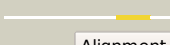
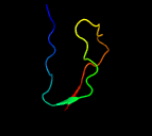
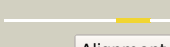
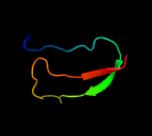
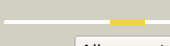

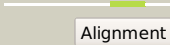
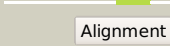
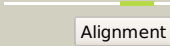
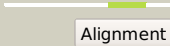
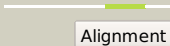

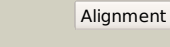
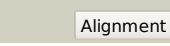


Phyre2

Email	mdejesus@rockefeller.edu
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Date	Wed Jul 31 22:05:38 BST 2019
Unique Job ID	133c7a458f0128b9

Detailed template information

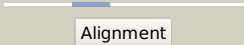
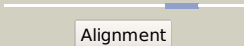
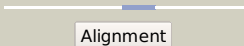
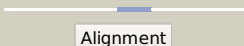
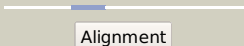

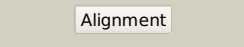
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2	d1brwa3	 Alignment		98.2	20	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
3	c2dsjA_	 Alignment		98.2	23	PDB header: transferase Chain: A; PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8
4	c1brwB_	 Alignment		98.1	19	PDB header: transferase Chain: B; PDB Molecule: protein (pyrimidine nucleoside phosphorylase); PDBTitle: the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
5	d1uoua3	 Alignment		98.0	22	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
6	c1otpA_	 Alignment		98.0	8	PDB header: phosphorylase Chain: A; PDB Molecule: thymidine phosphorylase; PDBTitle: structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
7	c2j0fC_	 Alignment		98.0	16	PDB header: transferase Chain: C; PDB Molecule: thymidine phosphorylase; PDBTitle: structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
8	d2tpta3	 Alignment		97.9	12	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
9	c4ga5H_	 Alignment		97.8	16	PDB header: transferase Chain: H; PDB Molecule: putative thymidine phosphorylase; PDBTitle: crystal structure of amp phosphorylase c-terminal deletion mutant in2 the apo-form
10	d1qapa2	 Alignment		93.7	14	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinat PRTase N-terminal domain-like Family: NadC N-terminal domain-like
11	c1qapA_	 Alignment		93.0	14	PDB header: glycosyltransferase Chain: A; PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid

12	c5nenA	 Alignment		80.3	22	PDB header: hydrolase Chain: A: PDB Molecule: lipase c; PDBTitle: crystal structure of the soluble domain of lipc, a membrane fusion2 protein of a type i secretion system
13	c1t5eB	 Alignment		79.9	19	PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance protein mexa; PDBTitle: the structure of mexa
14	c1o4uA	 Alignment		77.3	17	PDB header: transferase Chain: A: PDB Molecule: type ii quinolic acid phosphoribosyltransferase; PDBTitle: crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
15	c3pajA	 Alignment		76.9	13	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase, carboxylating; PDBTitle: 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
16	d1vf7a	 Alignment		75.3	19	Fold: HlyD-like secretion proteins Superfamily: HlyD-like secretion proteins Family: HlyD-like secretion proteins
17	c2f1mA	 Alignment		73.3	19	PDB header: transport protein Chain: A: PDB Molecule: acriflavine resistance protein a; PDBTitle: conformational flexibility in the multidrug efflux system protein acra
18	c5c22A	 Alignment		73.2	36	PDB header: protein transport Chain: A: PDB Molecule: chromosomal hemolysin d; PDBTitle: crystal structure of zn-bound hlyd from e. coli
19	c3lnnB	 Alignment		73.1	39	PDB header: metal transport Chain: B: PDB Molecule: membrane fusion protein (mfp) heavy metal cation efflux PDBTitle: crystal structure of zneb from cupriavidus metallidurans
20	c2jbmA	 Alignment		72.6	11	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: qprtase structure from human
21	d1qpoa2	 Alignment	not modelled	69.8	18	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
22	c4l8jA	 Alignment	not modelled	69.8	27	PDB header: transport protein Chain: A: PDB Molecule: putative efflux transporter; PDBTitle: crystal structure of a putative efflux transporter (bacegg_01895) from2 bacteroides eggerthii dsm 20697 at 2.06 a resolution
23	c2dn8A	 Alignment	not modelled	69.6	17	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
24	c1qpoA	 Alignment	not modelled	69.1	15	PDB header: transferase Chain: A: PDB Molecule: quinolinate acid phosphoribosyl transferase; PDBTitle: quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
25	c3gnnA	 Alignment	not modelled	68.5	11	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 burkholderi pseudomallei
26	c2k33A	 Alignment	not modelled	66.2	31	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: acra; PDBTitle: solution structure of an n-glycosylated protein using in2 vitro glycosylation
27	c3fppB	 Alignment	not modelled	66.2	43	PDB header: membrane protein Chain: B: PDB Molecule: macrolide-specific efflux protein maca; PDBTitle: crystal structure of e.coli maca
28	c3l0gD	 Alignment	not modelled	66.0	6	PDB header: transferase Chain: D: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide

						pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
29	c3tqvA	Alignment	not modelled	64.8	8	
30	d2gyqa1	Alignment	not modelled	63.2	10	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ycif-like
31	d1qjoa	Alignment	not modelled	60.8	38	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
32	c3e8gB	Alignment	not modelled	57.8	20	PDB header: membrane protein Chain: B: PDB Molecule: potassium channel protein; PDBTitle: crystal structure of the the open nak channel-na+/ca2+ complex
33	c2v4dM	Alignment	not modelled	57.6	19	PDB header: membrane protein Chain: M: PDB Molecule: multidrug resistance protein mexa; PDBTitle: re-refinement of mexa adaptor protein
34	c5xu0B	Alignment	not modelled	57.5	24	PDB header: transport protein Chain: B: PDB Molecule: membrane-fusion protein; PDBTitle: structure of the membrane fusion protein spr0693 from streptococcus2 pneumoniae r6
35	c2b7pA	Alignment	not modelled	57.2	9	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori with phthalic acid
36	c4dk0A	Alignment	not modelled	57.0	27	PDB header: membrane protein Chain: A: PDB Molecule: putative maca; PDBTitle: crystal structure of maca from actinobacillus actinomycetemcomitans
37	c2kccA	Alignment	not modelled	56.9	16	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
38	c5huoH	Alignment	not modelled	55.9	20	PDB header: transferase Chain: H: PDB Molecule: nicotinate-nucleotide diphosphorylase (carboxylating); PDBTitle: crystal structure of nadc deletion mutant in c2221 space group
39	d1iyua	Alignment	not modelled	55.3	12	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
40	c5v5sH	Alignment	not modelled	54.9	19	PDB header: membrane protein Chain: H: PDB Molecule: multidrug efflux pump subunit acra; PDBTitle: multi-drug efflux; membrane transport; rnd superfamily; drug2 resistance
41	c3a5iB	Alignment	not modelled	53.6	21	PDB header: protein transport Chain: B: PDB Molecule: flagellar biosynthesis protein flha; PDBTitle: structure of the cytoplasmic domain of flha
42	d1o78a	Alignment	not modelled	53.3	24	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
43	c3lnnA	Alignment	not modelled	53.0	37	PDB header: metal transport Chain: A: PDB Molecule: membrane fusion protein (mfp) heavy metal cation efflux PDBTitle: crystal structure of zneb from cupriavidus metallidurans
44	c2b8gA	Alignment	not modelled	52.9	28	PDB header: biosynthetic protein Chain: A: PDB Molecule: biotin/lipoyl attachment protein; PDBTitle: solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
45	d2pnrc1	Alignment	not modelled	52.2	17	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
46	c1x1oC	Alignment	not modelled	50.6	20	PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermus thermophilus hb8
47	c2ejmA	Alignment	not modelled	50.1	12	PDB header: ligase Chain: A: PDB Molecule: methylcrotonoyl-coa carboxylase subunit alpha; PDBTitle: solution structure of ruh-072, an apo-biotnyl domain form2 human acetyl coenzyme a carboxylase
48	c5nilG	Alignment	not modelled	49.6	41	PDB header: transport protein Chain: G: PDB Molecule: macrolide export protein maca; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump-2 macb section
49	c3mixA	Alignment	not modelled	47.7	15	PDB header: protein transport Chain: A: PDB Molecule: flagellar biosynthesis protein flha; PDBTitle: crystal structure of the cytosolic domain of b. subtilis flha
50	c3na6A	Alignment	not modelled	47.5	14	PDB header: hydrolase Chain: A: PDB Molecule: succinylglutamate desuccinylase/aspartoacylase; PDBTitle: crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
51	c3h9iB	Alignment	not modelled	47.2	26	PDB header: transport protein Chain: B: PDB Molecule: cation efflux system protein cusb; PDBTitle: crystal structure of the membrane fusion protein cusb from escherichia2 coli
52	c3c2vA	Alignment	not modelled	45.9	11	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of the quinolinate phosphoribosyl transferase (bna6)2 from saccharomyces cerevisiae complexed with prpp and the inhibitor3 phthalate
53	c6hcyA	Alignment	not modelled	45.4	14	PDB header: membrane protein Chain: A: PDB Molecule: metalloreductase steap4;

						PDBTitle: human steap4 bound to nadp, fad, heme and fe(iii)-nta.
54	d1o4ua2	Alignment	not modelled	44.9	12	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
55	d1k8ma_	Alignment	not modelled	42.9	11	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
56	c6bi6A_	Alignment	not modelled	41.3	29	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yejg; PDBTitle: solution nmr structure of uncharacterized protein yejg
57	c4dk1B_	Alignment	not modelled	41.0	27	PDB header: membrane protein Chain: B: PDB Molecule: putative maca, multidrug resistance protein mexa; PDBTitle: crystal structure of maca-mexa chimeric protein, containing the2 pseudomonas aeruginosa mexa alpha-hairpin domain.
58	c5nj3B_	Alignment	not modelled	40.9	15	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: complete structure
59	c2ejgD_	Alignment	not modelled	39.9	15	PDB header: ligase Chain: D: PDB Molecule: 149aa long hypothetical methylmalonyl-coa decarboxylase PDBTitle: crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
60	d1bdoa_	Alignment	not modelled	39.9	23	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
61	c4tkoB_	Alignment	not modelled	39.1	35	PDB header: membrane protein Chain: B: PDB Molecule: emra; PDBTitle: structure of the periplasmic adaptor protein emra
62	d1ghja_	Alignment	not modelled	38.9	39	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
63	d1gjxa_	Alignment	not modelled	38.7	16	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
64	c5do7B_	Alignment	not modelled	38.5	9	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 8; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8
65	c4pkcA_	Alignment	not modelled	37.7	17	PDB header: lyase Chain: A: PDB Molecule: tutd; PDBTitle: benzylsuccinate alpha-gamma complex
66	d1dcza_	Alignment	not modelled	37.3	27	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
67	c2f3oB_	Alignment	not modelled	37.2	21	PDB header: unknown function Chain: B: PDB Molecule: pyruvate formate-lyase 2; PDBTitle: crystal structure of a glycol radical enzyme from archaeoglobus2 fulgidus
68	d1de4c3	Alignment	not modelled	37.0	14	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: FolH catalytic domain-like
69	c5gt1A_	Alignment	not modelled	36.5	20	PDB header: choline-binding protein Chain: A: PDB Molecule: choline binding protein a; PDBTitle: crystal structure of cbpa from l. salivarius ren
70	c4rcnA_	Alignment	not modelled	33.8	22	PDB header: ligase Chain: A: PDB Molecule: long-chain acyl-coa carboxylase; PDBTitle: structure and function of a single-chain, multi-domain long-chain2 acyl-coa carboxylase
71	c2jkuA_	Alignment	not modelled	33.5	17	PDB header: ligase Chain: A: PDB Molecule: propionyl-coa carboxylase alpha chain, mitochondrial; PDBTitle: crystal structure of the n-terminal region of the biotin acceptor2 domain of human propionyl-coa carboxylase
72	c2kb1A_	Alignment	not modelled	32.2	8	PDB header: membrane protein Chain: A: PDB Molecule: wsk3; PDBTitle: nmr studies of a channel protein without membrane:2 structure and dynamics of water-solubilized kcsa
73	d2gs4a1	Alignment	not modelled	31.8	22	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ycif-like
74	c5kc1A_	Alignment	not modelled	31.3	86	PDB header: endocytosis Chain: A: PDB Molecule: autophagy-related protein 38; PDBTitle: structure of the c-terminal dimerization domain of atg38
75	d1laba_	Alignment	not modelled	30.9	14	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
76	c5kc1E_	Alignment	not modelled	30.9	86	PDB header: endocytosis Chain: E: PDB Molecule: autophagy-related protein 38; PDBTitle: structure of the c-terminal dimerization domain of atg38
77	c3vouB_	Alignment	not modelled	30.8	17	PDB header: transport protein Chain: B: PDB Molecule: ion transport 2 domain protein, voltage-gated sodium PDBTitle: the crystal structure of nak-navsulp chimera channel
78	d1twda_	Alignment	not modelled	30.4	13	Fold: TIM beta/alpha-barrel Superfamily: CutC-like Family: CutC-like

79	c5hl8B_	Alignment	not modelled	30.4	12	PDB header: protein transport Chain: B: PDB Molecule: type ii secretion system protein I; PDBTitle: 1.93 angstrom resolution crystal structure of a pullulanase-specific2 type ii secretion system integral cytoplasmic membrane protein gspI3 (c-terminal fragment; residues 309-397) from klebsiella pneumoniae4 subsp. pneumoniae ntuH-k2044
80	c2w2eA_	Alignment	not modelled	30.1	10	PDB header: membrane protein Chain: A: PDB Molecule: aquaporin pip2-7 7; PDBTitle: 1.15 angstrom crystal structure of p.pastoris aquaporin, aqy1, in a2 closed conformation at ph 3.5
81	c2dneA_	Alignment	not modelled	29.7	20	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase
82	c2d57A_	Alignment	not modelled	29.7	19	PDB header: transport protein Chain: A: PDB Molecule: aquaporin-4; PDBTitle: double layered 2d crystal structure of aquaporin-4 (aqp4m23) at 3.2 a2 resolution by electron crystallography
83	c2b5fD_	Alignment	not modelled	29.0	19	PDB header: transport protein,membrane protein Chain: D: PDB Molecule: aquaporin; PDBTitle: crystal structure of the spinach aquaporin sopip2;1 in an2 open conformation to 3.9 resolution
84	c2dncA_	Alignment	not modelled	29.0	20	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase protein x component; PDBTitle: solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
85	c3mydA_	Alignment	not modelled	28.9	23	PDB header: protein transport Chain: A: PDB Molecule: flagellar biosynthesis protein flhA; PDBTitle: structure of the cytoplasmic domain of flhA from helicobacter pylori
86	c5kc1I_	Alignment	not modelled	28.8	86	PDB header: endocytosis Chain: I: PDB Molecule: autophagy-related protein 38; PDBTitle: structure of the c-terminal dimerization domain of atg38
87	c5kc1C_	Alignment	not modelled	28.0	86	PDB header: endocytosis Chain: C: PDB Molecule: autophagy-related protein 38; PDBTitle: structure of the c-terminal dimerization domain of atg38
88	c2l5tA_	Alignment	not modelled	27.4	15	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase; PDBTitle: solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
89	c5d0bB_	Alignment	not modelled	26.8	12	PDB header: oxidoreductase/rna Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: crystal structure of epoxyqueuosine reductase with a trna-tyr2 epoxyqueuosine-modified trna stem loop
90	c6dkuA_	Alignment	not modelled	26.8	54	PDB header: unknown function Chain: A: PDB Molecule: vp35; PDBTitle: crystal structure of myotis vp35 mutant of interferon inhibitory2 domain
91	c3iwpK_	Alignment	not modelled	26.6	10	PDB header: metal binding protein Chain: K: PDB Molecule: copper homeostasis protein cutc homolog; PDBTitle: crystal structure of human copper homeostasis protein cutc
92	d1q90n_	Alignment	not modelled	25.9	31	Fold: Single transmembrane helix Superfamily: PetN subunit of the cytochrome b6f complex Family: PetN subunit of the cytochrome b6f complex
93	c2qj8B_	Alignment	not modelled	25.5	15	PDB header: hydrolase Chain: B: PDB Molecule: mlr6093 protein; PDBTitle: crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
94	c2x49A_	Alignment	not modelled	25.4	16	PDB header: protein transport Chain: A: PDB Molecule: invasion protein inva; PDBTitle: crystal structure of the c-terminal domain of inva
95	c5n7sA_	Alignment	not modelled	25.2	9	PDB header: transport protein Chain: A: PDB Molecule: type ii secretion system protein I; PDBTitle: crystal structure of the periplasmic domain of xcpcy, op crystal form.
96	c2lowA_	Alignment	not modelled	25.2	13	PDB header: membrane protein Chain: A: PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfp
97	d1bg6a1	Alignment	not modelled	25.1	17	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: N-(1-D-carboxylethyl)-L-norvaline dehydrogenase
98	c2q8iB_	Alignment	not modelled	24.9	20	PDB header: transferase Chain: B: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase component of PDBTitle: pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
99	c6g2dC_	Alignment	not modelled	24.3	22	PDB header: ligase Chain: C: PDB Molecule: acetyl-coa carboxylase 1; PDBTitle: citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution
100	c3gd8A_	Alignment	not modelled	23.5	21	PDB header: membrane protein Chain: A: PDB Molecule: aquaporin-4; PDBTitle: crystal structure of human aquaporin 4 at 1.8 and its mechanism of2 conductance
101	c3hiuB_	Alignment	not modelled	23.1	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of protein (xcc3681) from xanthomonas2 campestris pv. campestris str. atcc 33913
102	c2b6pA_	Alignment	not modelled	23.1	19	PDB header: membrane protein Chain: A: PDB Molecule: lens fiber major intrinsic protein; PDBTitle: x-ray structure of lens aquaporin-0 (aqp0) (lens mip) in an open pore2 state
103	d1pmra_	Alignment	not modelled	22.9	23	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains

104	c3d9sB	 Alignment	not modelled	22.8	17	PDB header: membrane protein Chain: B: PDB Molecule: aquaporin-5; PDBTitle: human aquaporin 5 (aqp5) - high resolution x-ray structure
105	c4toiA	 Alignment	not modelled	22.7	22	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s2,ribosomal protein s1; PDBTitle: crystal structure of e.coli ribosomal protein s2 in complex with n-2 terminal domain of s1
106	c2gu1A	 Alignment	not modelled	22.5	16	PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae
107	c3u9sA	 Alignment	not modelled	21.7	29	PDB header: ligase Chain: A: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
108	c5i32A	 Alignment	not modelled	20.8	12	PDB header: membrane protein Chain: A: PDB Molecule: aquaporin tip2-1; PDBTitle: ammonia permeable aquaporin attip2;1
109	d1y8ob1	 Alignment	not modelled	20.8	20	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
110	c5do7A	 Alignment	not modelled	20.7	11	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family g member 5; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8