















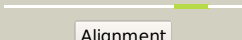
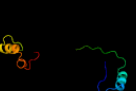
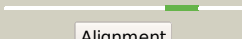
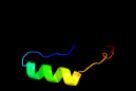
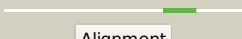
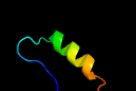

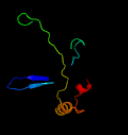



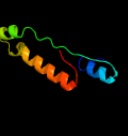
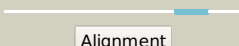
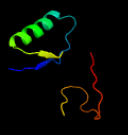
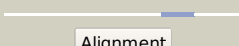

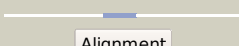

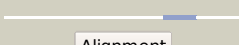


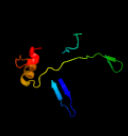

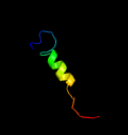
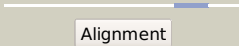
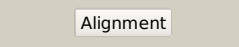
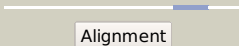
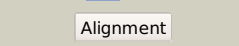
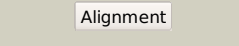
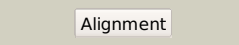




Phyre2

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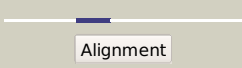
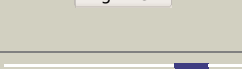
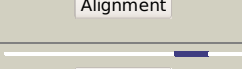
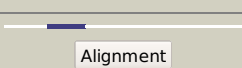
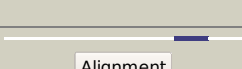
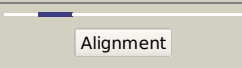
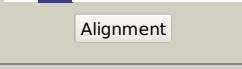
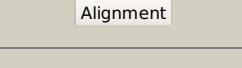
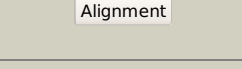
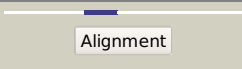
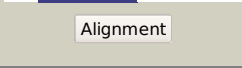
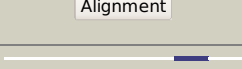
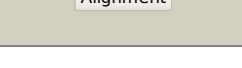
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4kp1A_	 Alignment		100.0	36	PDB header: isomerase Chain: A: PDB Molecule: isopropylmalate/citramalate isomerase large subunit; PDBTitle: crystal structure of ipm isomerase large subunit from methanococcus2 jannaschii (mj0499)
2	c4kp2A_	 Alignment		100.0	34	PDB header: lyase Chain: A: PDB Molecule: homoaconitase large subunit; PDBTitle: crystal structure of homoaconitase large subunit from methanococcus2 jannaschii (mj1003)
3	d1acoa2	 Alignment		100.0	26	Fold: Aconitase iron-sulfur domain Superfamily: Aconitase iron-sulfur domain Family: Aconitase iron-sulfur domain
4	d1l5ja3	 Alignment		100.0	24	Fold: Aconitase iron-sulfur domain Superfamily: Aconitase iron-sulfur domain Family: Aconitase iron-sulfur domain
5	c5acnA_	 Alignment		100.0	26	PDB header: lyase(carbon-oxygen) Chain: A: PDB Molecule: aconitase; PDBTitle: structure of activated aconitase. formation of the (4fe-4s) cluster in2 the crystal
6	d2b3ya2	 Alignment		100.0	22	Fold: Aconitase iron-sulfur domain Superfamily: Aconitase iron-sulfur domain Family: Aconitase iron-sulfur domain
7	c2b3yB_	 Alignment		100.0	22	PDB header: lyase Chain: B: PDB Molecule: iron-responsive element binding protein 1; PDBTitle: structure of a monoclinic crystal form of human cytosolic aconitase2 (irp1)
8	c1l5jB_	 Alignment		100.0	25	PDB header: lyase Chain: B: PDB Molecule: aconitate hydratase 2; PDBTitle: crystal structure of e. coli aconitase b.
9	c3bolB_	 Alignment		63.7	23	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
10	d3bofa2	 Alignment		57.7	23	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
11	c4cczA_	 Alignment		57.2	26	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: crystal structure of human 5-methyltetrahydrofolate-homocysteine2 methyltransferase, the homocysteine and folate binding domains

12	c4oc8A_	 Alignment		41.0	15	PDB header: hydrolase Chain: A: PDB Molecule: restriction endonuclease aspbhi; PDBTitle: dna modification-dependent restriction endonuclease aspbhi
13	c2e21A_	 Alignment		39.8	17	PDB header: ligase Chain: A: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
14	c1ni5A_	 Alignment		37.8	15	PDB header: cell cycle Chain: A: PDB Molecule: putative cell cycle protein mesj; PDBTitle: structure of the mesj pp-atpase from escherichia coli
15	c4yajA_	 Alignment		32.6	19	PDB header: ligase Chain: A: PDB Molecule: alpha subunit of acetyl-coenzyme a synthetase PDBTitle: ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
16	d1lt7a_	 Alignment		29.3	25	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
17	c4rz1A_	 Alignment		27.5	7	PDB header: dna binding protein Chain: A: PDB Molecule: restriction endonuclease lpnpi; PDBTitle: dna recognition domain of the cytosine modification-dependent2 restriction endonuclease lpnpi
18	d1umya_	 Alignment		26.2	22	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
19	c4oc8D_	 Alignment		25.3	17	PDB header: hydrolase Chain: D: PDB Molecule: restriction endonuclease aspbhi; PDBTitle: dna modification-dependent restriction endonuclease aspbhi
20	c5wusA_	 Alignment		24.5	31	PDB header: hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: crystal structure of a insect group iii chitinase (cad2) from ostrinia2 furnacalis
21	c3fseB_	 Alignment	not modelled	23.2	20	PDB header: hydrolase Chain: B: PDB Molecule: two-domain protein containing dj-1/thij/pfpi-like and PDBTitle: crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anaebaena variabilis3 atcc 29413 at 1.90 a resolution
22	c2gp4A_	 Alignment	not modelled	23.1	19	PDB header: lyase Chain: A: PDB Molecule: 6-phosphogluconate dehydratase; PDBTitle: structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
23	c5ze4A_	 Alignment	not modelled	20.7	15	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the structure of holo- structure of dhad complex with [2fe-2s] cluster
24	c2ox1A_	 Alignment	not modelled	20.7	47	PDB header: gene regulation Chain: A: PDB Molecule: hypothetical protein ymgb; PDBTitle: structure and function of the e. coli protein ymgb: a protein critical2 for biofilm formation and acid resistance
25	c3a2kB_	 Alignment	not modelled	20.3	24	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils complexed with trna
26	c5u32A_	 Alignment	not modelled	19.2	15	PDB header: transferase Chain: A: PDB Molecule: trna ligase; PDBTitle: crystal structure of fungal rna kinase
27	d1c0aa2	 Alignment	not modelled	18.6	21	Fold: DCoH-like Superfamily: GAD domain-like Family: GAD domain
28	c5fifD_	 Alignment	not modelled	18.5	15	PDB header: ligase Chain: D: PDB Molecule: carboxylase; PDBTitle: carboxyltransferase domain of a single-chain bacterial

						carboxylase
29	c4l6wA_	Alignment	not modelled	18.5	19	PDB header: ligase Chain: A: PDB Molecule: probable propionyl-coa carboxylase beta chain 6; PDBTitle: carboxyltransferase subunit (accd6) of mycobacterium tuberculosis2 acetyl-coa carboxylase
30	c2xivA_	Alignment	not modelled	18.4	17	PDB header: structural protein Chain: A: PDB Molecule: hypothetical invasion protein; PDBTitle: structure of rv1477, hypothetical invasion protein of mycobacterium2 tuberculosis
31	c4rcnA_	Alignment	not modelled	18.1	11	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
32	d1ejba_	Alignment	not modelled	17.9	14	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
33	c2jz2A_	Alignment	not modelled	17.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ssl0352 protein; PDBTitle: solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
34	d2gp4a2	Alignment	not modelled	16.4	19	Fold: lvD/EDD N-terminal domain-like Superfamily: lvD/EDD N-terminal domain-like Family: lvD/EDD N-terminal domain-like
35	c2kqvA_	Alignment	not modelled	15.8	39	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: sars coronavirus-unique domain (sud): three-domain molecular2 architecture in solution and rna binding. i: structure of the sud-m3 domain of sud-mc
36	c3uk7B_	Alignment	not modelled	15.8	26	PDB header: transferase Chain: B: PDB Molecule: class i glutamine amidotransferase-like domain-containing PDBTitle: crystal structure of arabidopsis thaliana dj-1d
37	d1ni5a1	Alignment	not modelled	15.5	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
38	c5mgyG_	Alignment	not modelled	15.5	11	PDB header: protein binding Chain: G: PDB Molecule: fad:protein fmn transferase; PDBTitle: crystal structure of pseudomonas stutzeri flavinyl transferase apbe,2 apo form
39	c2yb1A_	Alignment	not modelled	15.4	14	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
40	d1oi4a1	Alignment	not modelled	15.2	36	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
41	c3iz5Q_	Alignment	not modelled	14.8	9	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
42	c2gksB_	Alignment	not modelled	13.0	17	PDB header: transferase Chain: B: PDB Molecule: bifunctional sat/aps kinase; PDBTitle: crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
43	c2jzfA_	Alignment	not modelled	13.0	39	PDB header: viral protein Chain: A: PDB Molecule: replicase polyprotein 1ab; PDBTitle: nmr conformer closest to the mean coordinates of the domain 513-651 of2 the sars-cov nonstructural protein nsp3
44	c5uidC_	Alignment	not modelled	12.5	13	PDB header: transferase Chain: C: PDB Molecule: aminotransferase tlmj; PDBTitle: the crystal structure of an aminotransferase tlmj from2 streptoaloteichus hindustanus
45	c4lkrA_	Alignment	not modelled	12.4	16	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deod-type; PDBTitle: crystal structure of deod-3 gene product from shewanella oneidensis2 mr-1, nysgrc target 029437
46	c1htrP_	Alignment	not modelled	12.3	25	PDB header: aspartyl protease Chain: P: PDB Molecule: progastricsin (pro segment); PDBTitle: crystal and molecular structures of human progastricsin at 1.622 angstroms resolution
47	c2x24B_	Alignment	not modelled	12.1	16	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: bovine acc2 ct domain in complex with inhibitor
48	d1c41a_	Alignment	not modelled	11.7	16	Fold: Lumazine synthase Superfamily: Lumazine synthase Family: Lumazine synthase
49	c5yudA_	Alignment	not modelled	11.6	26	PDB header: immune system Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 1e; PDBTitle: flagellin derivative in complex with the nlr protein naip5
50	c6b4cH_	Alignment	not modelled	11.6	9	PDB header: antiviral protein Chain: H: PDB Molecule: viperin; PDBTitle: structure of viperin from trichoderma virens
51	c1x0uB_	Alignment	not modelled	11.5	20	PDB header: lyase Chain: B: PDB Molecule: hypothetical methylmalonyl-coa decarboxylase alpha subunit; PDBTitle: crystal structure of the carboxyl transferase subunit of putative pcc2 of sulfobobus tokodaii
52	c4m70E_	Alignment	not modelled	11.5	31	PDB header: plant protein Chain: E: PDB Molecule: ran gtpase activating protein 2; PDBTitle: crystal structure of potato rx-cc domain in complex with rangap2-wpp2 domain
53	c4mnnA_	Alignment	not modelled	11.4	11	PDB header: sugar binding protein Chain: A: PDB Molecule: n-acetylneuraminate-binding protein;

53	c4mmpA	Alignment	not modelled	11.4	11	PDBTitle: structure of the sialic acid binding protein from fusobacterium2 nucleatum subsp. nucleatum atcc 25586 PDB header: oxidoreductase
54	c5jw6A	Alignment	not modelled	11.3	19	Chain: A; PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: crystal structure of aspartate semialdehyde dehydrogenase from2 aspergillus fumigatus
55	c2w9mB	Alignment	not modelled	10.9	20	PDB header: dna replication Chain: B; PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
56	c3h8aF	Alignment	not modelled	10.9	27	PDB header: lyase/protein binding Chain: F; PDB Molecule: rnase e; PDBTitle: crystal structure of e. coli enolase bound to its cognate rnase e2 recognition domain
57	c1xovA	Alignment	not modelled	10.8	16	PDB header: hydrolase Chain: A; PDB Molecule: ply protein; PDBTitle: the crystal structure of the listeria monocytogenes bacteriophage psa2 endolysin plypsa
58	c3qpbB	Alignment	not modelled	10.8	18	PDB header: transferase Chain: B; PDB Molecule: uridine phosphorylase; PDBTitle: crystal structure of streptococcus pyogenes uridine phosphorylase2 reveals a subclass of the np-i superfamily
59	c2o2qA	Alignment	not modelled	10.7	17	PDB header: oxidoreductase Chain: A; PDB Molecule: formyltetrahydrofolate dehydrogenase; PDBTitle: crystal structure of the c-terminal domain of rat2 10'formyltetrahydrofolate dehydrogenase in complex with nadp
60	c5kf6B	Alignment	not modelled	10.6	17	PDB header: oxidoreductase Chain: B; PDB Molecule: bifunctional protein puta; PDBTitle: structure of proline utilization a from sinorhizobium meliloti2 complexed with l-tetrahydrofuroic acid and nad+ in space group p21
61	c3h8aE	Alignment	not modelled	10.3	27	PDB header: lyase/protein binding Chain: E; PDB Molecule: rnase e; PDBTitle: crystal structure of e. coli enolase bound to its cognate rnase e2 recognition domain
62	c3io1B	Alignment	not modelled	10.3	17	PDB header: hydrolase Chain: B; PDB Molecule: aminobenzoyl-glutamate utilization protein; PDBTitle: crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae
63	c4binA	Alignment	not modelled	10.3	12	PDB header: hydrolase Chain: A; PDB Molecule: n-acetylmuramoyl-l-alanine amidase amic; PDBTitle: crystal structure of the e. coli n-acetylmuramoyl-l-alanine amidase2 amic
64	d1sqda2	Alignment	not modelled	10.1	28	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Extradiol dioxygenases
65	c6b5bA	Alignment	not modelled	10.1	26	PDB header: immune system Chain: A; PDB Molecule: baculoviral iap repeat-containing protein 1e; PDBTitle: cryo-em structure of the naip5-nlr4-flagellin inflammasome
66	d1ppya	Alignment	not modelled	10.1	19	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Pyruvoyl dependent aspartate decarboxylase, ADC
67	d2a7sa1	Alignment	not modelled	10.1	15	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
68	d2ac7a1	Alignment	not modelled	10.0	15	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
69	c3pbiA	Alignment	not modelled	9.9	19	PDB header: hydrolase Chain: A; PDB Molecule: invasion protein; PDBTitle: structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
70	c5d3aA	Alignment	not modelled	9.8	50	PDB header: motor protein Chain: A; PDB Molecule: kinasin-like protein kif21a; PDBTitle: kif21a regulatory coiled coil
71	c3v9iD	Alignment	not modelled	9.7	9	PDB header: oxidoreductase Chain: D; PDB Molecule: delta-1-pyrroline-5-carboxylate dehydrogenase, PDBTitle: crystal structure of human 1-pyrroline-5-carboxylate dehydrogenase2 mutant s352l
72	c2nvgA	Alignment	not modelled	9.6	15	PDB header: oxidoreductase Chain: A; PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: soluble domain of rieske iron sulfur protein.
73	d1v8ba2	Alignment	not modelled	9.6	37	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: S-adenosylhomocystein hydrolase
74	c3hskB	Alignment	not modelled	9.5	13	PDB header: oxidoreductase Chain: B; PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: crystal structure of aspartate semialdehyde dehydrogenase with nadp2 from candida albicans
75	c4xb6D	Alignment	not modelled	9.5	14	PDB header: transferase Chain: D; PDB Molecule: alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; PDBTitle: structure of the e. coli c-p lyase core complex
76	c5ip4E	Alignment	not modelled	9.4	16	PDB header: transferase Chain: E; PDB Molecule: neuronal migration protein doublecortin; PDBTitle: x-ray structure of the c-terminal domain of human doublecortin
77	c5ux5C	Alignment	not modelled	9.4	23	PDB header: oxidoreductase/transferase Chain: C; PDB Molecule: bifunctional protein proline utilization a (puta); PDBTitle: structure of proline utilization a (puta) from corynebacterium2 freiburgense

78	c2ebbA		Alignment	not modelled	9.3	15	PDB header: lyase Chain: A: PDB Molecule: pterin-4-alpha-carbinolamine dehydratase; PDBTitle: crystal structure of pterin-4-alpha-carbinolamine2 dehydratase (pterin carbinolamine dehydratase) from3 geobacillus kaustophilus hta426
79	c2fgxA		Alignment	not modelled	9.2	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thioredoxin; PDBTitle: solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.
80	c4pfrB		Alignment	not modelled	9.1	18	PDB header: solute-binding protein Chain: B: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 rhodobacter sphaeroides (rsph17029_3541, target efi-510203), apo open3 partially disordered
81	c6hlwB		Alignment	not modelled	9.1	29	PDB header: viral protein Chain: B: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of human abcd3 gold domain in complex with 3a2 protein of enterovirus-a71 (fusion protein)
82	d1obra		Alignment	not modelled	9.0	33	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Carboxypeptidase T
83	c1od4C		Alignment	not modelled	9.0	16	PDB header: ligase Chain: C: PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain
84	c3ggyC		Alignment	not modelled	9.0	27	PDB header: transport protein Chain: C: PDB Molecule: periplasmic substrate binding protein; PDBTitle: the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state
85	c4m3nA		Alignment	not modelled	8.9	12	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deo-type; PDBTitle: crystal structure of purine nucleoside phosphorylase from meiothermus2 ruber dsm 1279, nysgrc target 029804.
86	c5ingC		Alignment	not modelled	8.8	12	PDB header: transferase Chain: C: PDB Molecule: putative carboxyl transferase; PDBTitle: a crotonyl-coa reductase-carboxylase independent pathway for assembly2 of unusual alkylmalonyl-coa polyketide synthase extender unit
87	d2ga5a1		Alignment	not modelled	8.7	29	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
88	c2k89A		Alignment	not modelled	8.7	21	PDB header: protein binding Chain: A: PDB Molecule: phospholipase a-2-activating protein; PDBTitle: solution structure of a novel ubiquitin-binding domain from2 human plaa (pfuc, gly76-pro77 cis isomer)
89	d1f0xa1		Alignment	not modelled	8.7	11	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: D-lactate dehydrogenase
90	d1wvfa1		Alignment	not modelled	8.6	11	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
91	d1woha		Alignment	not modelled	8.6	28	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
92	d1sp8a2		Alignment	not modelled	8.5	15	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Extradial dioxygenases
93	c4jc0B		Alignment	not modelled	8.5	14	PDB header: transferase Chain: B: PDB Molecule: ribosomal protein s12 methylthiotransferase rimo; PDBTitle: crystal structure of thermotoga maritima holo rimo in complex with2 pentasulfide, northeast structural genomics consortium target vr77
94	d2byea1		Alignment	not modelled	8.5	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
95	c1g8gB		Alignment	not modelled	8.3	13	PDB header: transferase Chain: B: PDB Molecule: sulfate adenylyltransferase; PDBTitle: atp sulfurylase from s. cerevisiae: the binary product complex with2 aps
96	d1iuka		Alignment	not modelled	8.3	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
97	c6hmvB		Alignment	not modelled	8.3	21	PDB header: viral protein Chain: B: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of human abcd3 gold domain in complex with 3a2 protein of enterovirus-d68 (fusion protein, lvvy mutant)
98	c4uoiB		Alignment	not modelled	8.2	28	PDB header: viral protein Chain: B: PDB Molecule: genome polyprotein; PDBTitle: unexpected structure for the n-terminal domain of hepatitis c virus2 envelope glycoprotein e1
99	d1skye2		Alignment	not modelled	8.1	17	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase