





















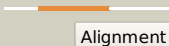

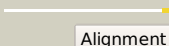

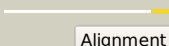

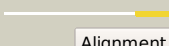

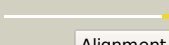

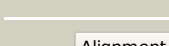

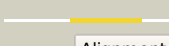

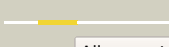



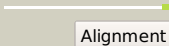
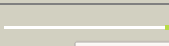
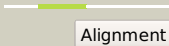
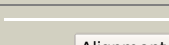

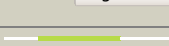
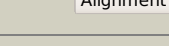
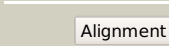


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0189c_(ilvD)_219994_221721
Date	Tue Jul 23 14:50:24 BST 2019
Unique Job ID	35d567dcd8d9584d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ze4A_	 Alignment		100.0	47	PDB header: lyase Chain: A; PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the structure of holo- structure of dhad complex with [2fe-2s] cluster
2	c5j84A_	 Alignment		100.0	37	PDB header: lyase Chain: A; PDB Molecule: dihydroxy-acid dehydratase; PDBTitle: crystal structure of l-arabinonate dehydratase in holo-form
3	c5oybB_	 Alignment		100.0	34	PDB header: lyase Chain: B; PDB Molecule: dehydratase, ilvd/edd family; PDBTitle: crystal structure of d-xylonate dehydratase in holo-form
4	c5ym0A_	 Alignment		100.0	49	PDB header: lyase Chain: A; PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the crystal structure of dhad
5	c2gp4A_	 Alignment		100.0	32	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
6	c2gp4B_	 Alignment		100.0	31	PDB header: lyase Chain: B; PDB Molecule: 6-phosphogluconate dehydratase; PDBTitle: structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
7	d2gp4a2	 Alignment		100.0	32	Fold: IlvD/EDD N-terminal domain-like Superfamily: IlvD/EDD N-terminal domain-like Family: IlvD/EDD N-terminal domain-like
8	d2gp4a1	 Alignment		100.0	31	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: IlvD/EDD C-terminal domain-like
9	c5fbtA_	 Alignment		96.7	24	PDB header: transferase/antibiotic Chain: A; PDB Molecule: phosphoenolpyruvate synthase; PDBTitle: crystal structure of rifampin phosphotransferase rph-Im from listeria2 monocytogenes in complex with rifampin
10	c3wrwE_	 Alignment		91.7	28	PDB header: transferase Chain: E; PDB Molecule: tm-1 protein; PDBTitle: crystal structure of the n-terminal domain of resistance protein
11	c4pe6B_	 Alignment		85.8	13	PDB header: solute-binding protein Chain: B; PDB Molecule: putative abc transporter; PDBTitle: crystal structure of abc transporter solute binding protein from2 thermobispora bispora dsm 43833

12	c3fijD_	 Alignment		82.1	27	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: lin1909 protein; PDBTitle: crystal structure of a uncharacterized protein lin1909
13	d1vba2	 Alignment		77.0	19	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
14	d1kbla2	 Alignment		75.7	28	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
15	c2e28A_	 Alignment		75.5	20	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
16	d1h6za2	 Alignment		75.4	20	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
17	c5woyA_	 Alignment		75.2	15	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: nmr solution structure of enzyme i (neit) protein using two 4d-spectra
18	c6gcsC_	 Alignment		71.6	14	PDB header: oxidoreductase Chain: C: PDB Molecule: 49-kda protein (nucm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
19	c4l8fA_	 Alignment		70.2	22	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: crystal structure of gamma-glutamyl hydrolase (c108a) complex with mtx
20	c6humH_	 Alignment		69.6	15	PDB header: proton transport Chain: H: PDB Molecule: nad(p)h-quinone oxidoreductase subunit h; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
21	c2osrA_	 Alignment	not modelled	68.7	19	PDB header: rna binding protein Chain: A: PDB Molecule: nucleolar protein 3; PDBTitle: nmr structure of rrm-2 of yeast npl3 protein
22	c2dh9A_	 Alignment	not modelled	67.9	25	PDB header: rna binding protein Chain: A: PDB Molecule: heterogeneous nuclear ribonucleoprotein m; PDBTitle: solution structure of the c-terminal rna binding domain in2 heterogeneous nuclear ribonucleoprotein m
23	c3nxkE_	 Alignment	not modelled	66.4	18	PDB header: hydrolase Chain: E: PDB Molecule: cytoplasmic l-asparaginase; PDBTitle: crystal structure of probable cytoplasmic l-asparaginase from2 campylobacter jejuni
24	d1zyma2	 Alignment	not modelled	64.5	13	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
25	d1fjca_	 Alignment	not modelled	63.9	41	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
26	c4lafB_	 Alignment	not modelled	62.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p)h dehydrogenase (quinone); PDBTitle: crystal structure of pnpb complex with fmn
27	c2pcnA_	 Alignment	not modelled	62.1	22	PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine:2-demethylmenaquinone PDBTitle: crystal structure of s-adenosylmethionine: 2-dimethylmenaquinone2 methyltransferase (gk_1813) from geobacillus kaustophilus hta426
28	c3ehkC_	 Alignment	not modelled	60.8	25	PDB header: plant protein Chain: C: PDB Molecule: prunin;

28	c2enlc_	Alignment	not modelled	60.8	23	PDBTitle: crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
29	d1rk8a_	Alignment	not modelled	60.6	26	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
30	c2jv2A_	Alignment	not modelled	60.0	25	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein ph1500; PDBTitle: solution structure of the n-terminal domain of ph1500
31	c1rkjA_	Alignment	not modelled	59.8	39	PDB header: transcription/rna Chain: A: PDB Molecule: nucleolin; PDBTitle: solution structure of the complex formed by the two n-2 terminal rna-binding domains of nucleolin and a pre-rrna3 target
32	d1wsaa_	Alignment	not modelled	58.7	12	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
33	c5lc5D_	Alignment	not modelled	58.1	15	PDB header: oxidoreductase Chain: D: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 2, PDBTitle: structure of mammalian respiratory complex i, class2
34	d2et1a1	Alignment	not modelled	57.8	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
35	c2hwgA_	Alignment	not modelled	56.4	13	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
36	c3c8oB_	Alignment	not modelled	55.0	24	PDB header: hydrolase regulator Chain: B: PDB Molecule: regulator of ribonuclease activity a; PDBTitle: the crystal structure of rraa from pao1
37	d1pl8a1	Alignment	not modelled	52.1	25	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
38	d1nxja_	Alignment	not modelled	51.0	21	Fold: The "swivelling" beta/beta/alpha domain Superfamily: RraA-like Family: RraA-like
39	c1nxjA_	Alignment	not modelled	51.0	21	PDB header: unknown function Chain: A: PDB Molecule: probable s-adenosylmethionine:2- PDBTitle: structure of rv3853 from mycobacterium tuberculosis
40	c1ezaA_	Alignment	not modelled	50.8	14	PDB header: phosphotransferase Chain: A: PDB Molecule: enzyme i; PDBTitle: amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
41	d1od5a2	Alignment	not modelled	50.3	24	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
42	d1wl8a1	Alignment	not modelled	50.1	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
43	d1od5a1	Alignment	not modelled	49.3	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
44	c2q8kA_	Alignment	not modelled	49.1	18	PDB header: transcription Chain: A: PDB Molecule: proliferation-associated protein 2g4; PDBTitle: the crystal structure of ebp1
45	d1l9xa_	Alignment	not modelled	48.1	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
46	c1l9xA_	Alignment	not modelled	48.1	16	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: structure of gamma-glutamyl hydrolase
47	c4yn7A_	Alignment	not modelled	47.6	25	PDB header: transcription Chain: A: PDB Molecule: yfir; PDBTitle: non-oxidized yfir
48	d2hi6a1	Alignment	not modelled	47.0	16	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: AF0055-like
49	c5uz5A_	Alignment	not modelled	46.3	26	PDB header: nuclear protein/rna Chain: A: PDB Molecule: u1 small nuclear ribonucleoprotein 70 kda homolog; PDBTitle: s. cerevisiae u1 snrnp
50	c3l83A_	Alignment	not modelled	45.5	20	PDB header: transferase Chain: A: PDB Molecule: glutamine amido transferase; PDBTitle: crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
51	d1o1ya_	Alignment	not modelled	45.1	22	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
52	d2cqga1	Alignment	not modelled	44.9	10	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
53	c2v6cA_	Alignment	not modelled	43.1	23	PDB header: transcription regulator Chain: A: PDB Molecule: proliferation-associated protein 2g4; PDBTitle: crystal structure of erbb3 binding protein 1 (ebp1)
54	c2e9qA_	Alignment	not modelled	43.0	19	PDB header: plant protein Chain: A: PDB Molecule: 11s globulin subunit beta; PDBTitle: recombinant pro-11s globulin of pumpkin
55	d1j3la_	Alignment	not modelled	43.0	19	Fold: The "swivelling" beta/beta/alpha domain Superfamily: RraA-like

						Family: RraA-like
56	c5g2rA_	Alignment	not modelled	42.9	18	PDB header: transferase Chain: A: PDB Molecule: molybdopterin biosynthesis protein cnx1; PDBTitle: crystal structure of the mo-insertase domain cnx1e from2 arabidopsis thaliana
57	c5mp4C_	Alignment	not modelled	42.1	16	PDB header: oxidoreductase Chain: C: PDB Molecule: protoplast secreted protein 2; PDBTitle: the structure of pst2p from saccharomyces cerevisiae
58	d1gtta2	Alignment	not modelled	42.1	27	Fold: FAH Superfamily: FAH Family: FAH
59	c1uz5A_	Alignment	not modelled	41.8	26	PDB header: molybdopterin biosynthesis Chain: A: PDB Molecule: 402aa long hypothetical molybdopterin PDBTitle: the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
60	d1fxza2	Alignment	not modelled	41.0	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
61	c5ereA_	Alignment	not modelled	41.0	21	PDB header: signaling protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: extracellular ligand binding receptor from desulfohalobium retbaense2 dsm5692
62	c5ir2A_	Alignment	not modelled	40.9	18	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: crystal structure of novel cellulases from microbes associated with2 the gut ecosystem
63	c2nqgA_	Alignment	not modelled	40.1	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin biosynthesis protein moea; PDBTitle: moea r137q
64	c3kscD_	Alignment	not modelled	39.5	21	PDB header: plant protein Chain: D: PDB Molecule: lega class; PDBTitle: crystal structure of pea prolegumin, an 11s seed globulin from pisum2 sativum l.
65	d1a9xb2	Alignment	not modelled	39.3	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
66	c3k4iC_	Alignment	not modelled	38.8	20	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000
67	c2dqxA_	Alignment	not modelled	38.7	15	PDB header: rna binding protein Chain: A: PDB Molecule: kiaa0430 protein; PDBTitle: solution structure of the rna recognition motif in kiaa04302 protein
68	c5x15C_	Alignment	not modelled	38.0	26	PDB header: transferase inhibitor Chain: C: PDB Molecule: putative transferase; PDBTitle: crystal structure of streptomyces coelicolor rraas2, an unusual member2 of the rnase es inhibitor rraa protein family
69	c5wxuD_	Alignment	not modelled	37.6	21	PDB header: plant protein Chain: D: PDB Molecule: 11s globulin; PDBTitle: 11s globulin from wrightia tinctoria reveals auxin binding site
70	c1fxzC_	Alignment	not modelled	36.3	17	PDB header: plant protein Chain: C: PDB Molecule: glycinin g1; PDBTitle: crystal structure of soybean proglycinin a1ab1b homotrimer
71	c2zkiH_	Alignment	not modelled	35.9	22	PDB header: transcription Chain: H: PDB Molecule: 199aa long hypothetical trp repressor PDBTitle: crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
72	c5frhA_	Alignment	not modelled	35.8	9	PDB header: transcription Chain: A: PDB Molecule: anti-sigma factor rsra; PDBTitle: solution structure of oxidised rsra
73	c5wppwA_	Alignment	not modelled	35.7	18	PDB header: allergen Chain: A: PDB Molecule: 11s globulin isoform 1; PDBTitle: crystal structure of coconut allergen cocosin
74	c3ex7B_	Alignment	not modelled	35.4	21	PDB header: hydrolase/rna binding protein/rna Chain: B: PDB Molecule: rna-binding protein 8a; PDBTitle: the crystal structure of ejc in its transition state
75	c5e1rC_	Alignment	not modelled	35.2	21	PDB header: allergen Chain: C: PDB Molecule: 7s vicilin; PDBTitle: crystal structure of pecan (carya illinoensis) vicilin, a new food2 allergen
76	c2d5fB_	Alignment	not modelled	35.1	24	PDB header: plant protein Chain: B: PDB Molecule: glycinin a3b4 subunit; PDBTitle: crystal structure of recombinant soybean proglycinin a3b4 subunit, its2 comparison with mature glycinin a3b4 subunit, responsible for hexamer3 assembly
77	c2jvrA_	Alignment	not modelled	35.1	22	PDB header: rna binding protein Chain: A: PDB Molecule: nucleolar protein 3; PDBTitle: segmental isotope labeling of npl3p
78	c3qacA_	Alignment	not modelled	34.9	16	PDB header: plant protein Chain: A: PDB Molecule: 11s globulin seed storage protein; PDBTitle: structure of amaranth 11s proglobulin seed storage protein from2 amaranthus hypochondriacus l.
79	c1dm9A_	Alignment	not modelled	34.8	10	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical 15.5 kd protein in mrca-pcka intergenic PDBTitle: heat shock protein 15 kd
80	d1dm9a_	Alignment	not modelled	34.8	10	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Heat shock protein 15 kd
81	d1kola2	Alianment	not modelled	34.8	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

						Family: Alcohol dehydrogenase-like, C-terminal domain
82	d1v7la_	Alignment	not modelled	34.8	17	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: LeuD-like
83	c4ht7G_	Alignment	not modelled	34.7	28	PDB header: protein binding Chain: G: PDB Molecule: co2 concentrating mechanism protein p; PDBTitle: co2 concentrating mechanism protein p, ccmp form 2
84	c3wklA_	Alignment	not modelled	34.5	25	PDB header: hydrolase Chain: A: PDB Molecule: putative zinc metalloprotease aq_1964; PDBTitle: the periplasmic pdz tandem fragment of the rsep homologue from aquifex2 aeolicus
85	d1r61a_	Alignment	not modelled	34.4	20	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Putative cyclase Family: Putative cyclase
86	c3kglB_	Alignment	not modelled	34.3	25	PDB header: plant protein Chain: B: PDB Molecule: cruciferin; PDBTitle: crystal structure of procruciferin, 11s globulin from brassica napus
87	c3egnA_	Alignment	not modelled	34.3	30	PDB header: splicing Chain: A: PDB Molecule: rna-binding protein 40; PDBTitle: c-terminal rna recognition motif of the u11/u12 65k protein
88	c6b4sB_	Alignment	not modelled	34.0	21	PDB header: allergen Chain: B: PDB Molecule: 11s globulin; PDBTitle: crystal structure of brazil nut (bertholletia excelsa) allergen ber e2 2
89	c2e44A_	Alignment	not modelled	34.0	20	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
90	c3vdoB_	Alignment	not modelled	33.3	17	PDB header: dna binding protein/protein binding Chain: B: PDB Molecule: anti-sigma-k factor rskA; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rskA from mycobacterium3 tuberculosis
91	d1fuia2	Alignment	not modelled	33.2	9	Fold: Fucl/AraA N-terminal and middle domains Superfamily: Fucl/AraA N-terminal and middle domains Family: L-fucose isomerase, N-terminal and second domains
92	c2jrsA_	Alignment	not modelled	33.1	12	PDB header: rna binding protein Chain: A: PDB Molecule: rna-binding protein 39; PDBTitle: solution nmr structure of caper rrm2 domain. northeast2 structural genomics target hr4730a
93	c3c3vA_	Alignment	not modelled	32.2	20	PDB header: allergen Chain: A: PDB Molecule: arachin arah3 isoform; PDBTitle: crystal structure of peanut major allergen ara h 3
94	d1k78a1	Alignment	not modelled	32.1	44	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
95	c3nojA_	Alignment	not modelled	32.0	19	PDB header: lyase Chain: A: PDB Molecule: 4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate PDBTitle: the structure of hmg/cha aldolase from the protocatechuate degradation2 pathway of pseudomonas putida
96	c4bs2A_	Alignment	not modelled	31.8	26	PDB header: transcription Chain: A: PDB Molecule: star dna-binding protein 43; PDBTitle: nmr structure of human tdp-43 tandem rrms in complex with ug-rich rna
97	c4cvhA_	Alignment	not modelled	31.8	15	PDB header: transferase Chain: A: PDB Molecule: isoprenoid synthase domain-containing protein; PDBTitle: crystal structure of human isoprenoid synthase domain-containing2 protein
98	c2jz7A_	Alignment	not modelled	31.5	26	PDB header: selenium-binding protein Chain: A: PDB Molecule: selenium binding protein; PDBTitle: solution nmr structure of selenium-binding protein from2 methanococcus vannielii
99	c4lejA_	Alignment	not modelled	31.2	22	PDB header: allergen, plant protein Chain: A: PDB Molecule: vicilin; PDBTitle: crystal structure of the korean pine (pinus koraiensis) vicilin
100	d1a8ya3	Alignment	not modelled	31.0	50	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Calsequestrin
101	c3tasC_	Alignment	not modelled	31.0	25	PDB header: oxidoreductase Chain: C: PDB Molecule: small laccase, multi-copper oxidase; PDBTitle: small laccase from streptomyces viridosporus t7a
102	d1qdlb_	Alignment	not modelled	30.9	28	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
103	c4jj0B_	Alignment	not modelled	30.9	17	PDB header: electron transport Chain: B: PDB Molecule: mamp; PDBTitle: crystal structure of mamp
104	c4ex8A_	Alignment	not modelled	30.9	24	PDB header: ligase Chain: A: PDB Molecule: alna; PDBTitle: crystal structure of the prealuminum c-glycosynthase alna
105	c6mvtA_	Alignment	not modelled	30.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of a bacterial aldH16 complexed with nadh
106	c4gjjC_	Alignment	not modelled	30.7	20	PDB header: hydrolase Chain: C: PDB Molecule: pseudouridine-5'-phosphate glycosidase; PDBTitle: crystal structure of pseudouridine monophosphate glycosidase complexed2 with sulfate
107	c1cauB_	Alignment	not modelled	30.6	22	PDB header: seed storage protein Chain: B: PDB Molecule: canavalin;

107	c1caub_	Alignment	not modelled	30.8	42	PDBTitle: determination of three crystal structures of canavalin by molecular2 replacement
108	c1sddA_	Alignment	not modelled	30.6	21	PDB header: blood clotting Chain: A; PDB Molecule: coagulation factor v; PDBTitle: crystal structure of bovine factor vai
109	c2qq1A_	Alignment	not modelled	30.5	16	PDB header: structural protein Chain: A; PDB Molecule: molybdenum cofactor biosynthesis mog; PDBTitle: crystal structure of molybdenum cofactor biosynthesis2 (aq_061) other form from aquifex aeolicus vf5
110	c4g9gA_	Alignment	not modelled	30.4	19	PDB header: lyase Chain: A; PDB Molecule: 4-carboxymuconolactone decarboxylase; PDBTitle: crystal structure of a 4-carboxymuconolactone decarboxylase
111	d1r31a1	Alignment	not modelled	30.1	41	Fold: Ferredoxin-like Superfamily: NAD-binding domain of HMG-CoA reductase Family: NAD-binding domain of HMG-CoA reductase
112	c5cadA_	Alignment	not modelled	30.0	27	PDB header: plant protein Chain: A; PDB Molecule: sm80.1 vicilin; PDBTitle: crystal structure of the vicilin from solanum melongena revealed2 existence of different anionic ligands in structurally similar3 pockets
113	c5suhB_	Alignment	not modelled	30.0	20	PDB header: structural protein Chain: B; PDB Molecule: msm0271 protein; PDBTitle: the structure of double ringed trimeric shell protein msm0271 from the2 rmm microcompartment
114	c3vbaE_	Alignment	not modelled	29.9	14	PDB header: lyase Chain: E; PDB Molecule: isopropylmalate/citramalate isomerase small subunit; PDBTitle: crystal structure of methanogen 3-isopropylmalate isomerase small2 subunit
115	d6paxa1	Alignment	not modelled	29.6	44	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
116	c2f3jA_	Alignment	not modelled	29.5	30	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).
117	d2a9va1	Alignment	not modelled	29.3	26	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
118	c4j0nA_	Alignment	not modelled	29.2	30	PDB header: hydrolase Chain: A; PDB Molecule: isatin hydrolase b; PDBTitle: crystal structure of a manganese dependent isatin hydrolase
119	c5yjsB_	Alignment	not modelled	29.1	18	PDB header: plant protein Chain: B; PDB Molecule: vicilin-like antimicrobial peptides 2-2; PDBTitle: structure of vicilin from capsicum annum
120	d2npta1	Alignment	not modelled	29.0	38	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain