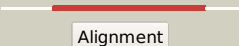



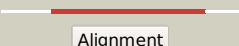
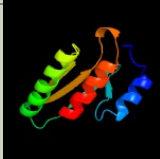




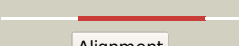



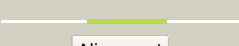


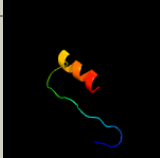

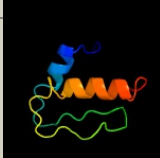

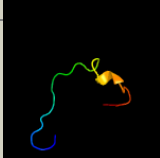
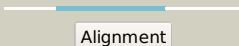

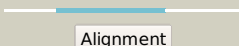



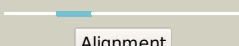

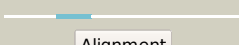

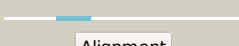

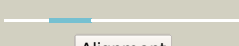





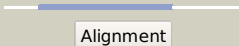

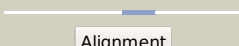
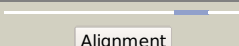
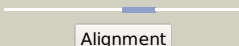




# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3110\_(moaB1)\_3478776\_3479171  
 Date Thu Aug 8 16:20:29 BST 2019  
 Unique Job ID 9acb610d870109ab

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2ebbA_</a>	 Alignment		100.0	29	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> pterin-4-alpha-carbinolamine dehydratase; <b>PDBTitle:</b> crystal structure of pterin-4-alpha-carbinolamine2 dehydratase (pterin carbinolamine dehydratase) from3 geobacillus kaustophilus hta426
2	<a href="#">d1ru0a_</a>	 Alignment		100.0	32	<b>Fold:</b> DCoH-like <b>Superfamily:</b> PCD-like <b>Family:</b> PCD-like
3	<a href="#">c3jstA_</a>	 Alignment		100.0	30	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative pterin-4-alpha-carbinolamine dehydratase; <b>PDBTitle:</b> crystal structure of transcriptional coactivator/pterin dehydratase2 from brucella melitensis
4	<a href="#">d1dcpa_</a>	 Alignment		100.0	28	<b>Fold:</b> DCoH-like <b>Superfamily:</b> PCD-like <b>Family:</b> PCD-like
5	<a href="#">c2v6uB_</a>	 Alignment		100.0	30	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> pterin-4a-carbinolamine dehydratase; <b>PDBTitle:</b> high resolution crystal structure of pterin-4a-2 carbinolamine dehydratase from toxoplasma gondii
6	<a href="#">d1usma_</a>	 Alignment		99.9	34	<b>Fold:</b> DCoH-like <b>Superfamily:</b> PCD-like <b>Family:</b> PCD-like
7	<a href="#">c4lowA_</a>	 Alignment		99.9	21	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> acraf; <b>PDBTitle:</b> structure and identification of a pterin dehydratase-like protein as a2 rubisco assembly factor in the alpha-carboxysome
8	<a href="#">d1a8ya3</a>	 Alignment		64.2	23	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Calsequestrin
9	<a href="#">c1z9bA_</a>	 Alignment		62.8	31	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> solution structure of the c1-subdomain of bacillus2 stearothermophilus translation initiation factor if2
10	<a href="#">d1svdm1</a>	 Alignment		48.7	15	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
11	<a href="#">d1prtc2</a>	 Alignment		39.5	36	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> Aerolysin/Pertussis toxin (APT) domain

12	<a href="#">d1rbli_</a>	 Alignment		39.2	12	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
13	<a href="#">d1uzhc1</a>	 Alignment		38.2	22	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
14	<a href="#">d1bwvs_</a>	 Alignment		38.0	14	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
15	<a href="#">c5mz2l_</a>	 Alignment		37.7	19	<b>PDB header:</b> photosynthesis <b>Chain:</b> I; <b>PDB Molecule:</b> rubisco small subunit; <b>PDBTitle:</b> rubisco from thalassiosira antarctica
16	<a href="#">d1bxni_</a>	 Alignment		32.2	33	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
17	<a href="#">c2ybvN_</a>	 Alignment		30.7	24	<b>PDB header:</b> lyase <b>Chain:</b> N; <b>PDB Molecule:</b> ribulose bisphosphate carboxylase small subunit; <b>PDBTitle:</b> structure of rubisco from thermosynechococcus elongatus
18	<a href="#">d1prt2</a>	 Alignment		30.0	32	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> Aerolysin/Pertussis toxin (APT) domain
19	<a href="#">c4gicB_</a>	 Alignment		28.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> histidinol dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative histidinol dehydrogenase (target psi-2 014034) from methylococcus capsulatus
20	<a href="#">c5nv3P_</a>	 Alignment		28.2	33	<b>PDB header:</b> lyase <b>Chain:</b> P; <b>PDB Molecule:</b> ribulose bisphosphate carboxylase small chain 1; <b>PDBTitle:</b> structure of rubisco from rhodobacter sphaeroides in complex with cabp
21	<a href="#">c1drwA_</a>	 Alignment	not modelled	27.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> escherichia coli dhpr/nhdh complex
22	<a href="#">c4n3gA_</a>	 Alignment	not modelled	24.4	9	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b-like protein, <b>PDBTitle:</b> crystal structure of eukaryotic translation initiation factor eif5b2 (870-1116) from chaetomium thermophilum, domains iii and iv
23	<a href="#">d1mv8a1</a>	 Alignment	not modelled	23.5	27	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
24	<a href="#">d1g7sa3</a>	 Alignment	not modelled	22.8	19	<b>Fold:</b> Initiation factor IF2/eIF5b, domain 3 <b>Superfamily:</b> Initiation factor IF2/eIF5b, domain 3 <b>Family:</b> Initiation factor IF2/eIF5b, domain 3
25	<a href="#">d1dlja1</a>	 Alignment	not modelled	21.4	13	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
26	<a href="#">c3j4jA_</a>	 Alignment	not modelled	21.2	24	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> model of full-length t. thermophilus translation initiation factor 22 refined against its cryo-em density from a 30s initiation complex map
27	<a href="#">c3ns6B_</a>	 Alignment	not modelled	21.0	6	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 subunit b; <b>PDBTitle:</b> crystal structure of hte rna recognition motif of yeast

						eif3b residues2 76-170
28	<a href="#">d1ir1s_</a>	Alignment	not modelled	20.8	24	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
29	<a href="#">d1k75a_</a>	Alignment	not modelled	20.0	24	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> L-histidinol dehydrogenase HisD
30	<a href="#">c1bcpH_</a>	Alignment	not modelled	17.1	36	<b>PDB header:</b> toxin <b>Chain:</b> H: <b>PDB Molecule:</b> pertussis toxin; <b>PDBTitle:</b> binary complex of pertussis toxin and atp
31	<a href="#">c2l8kA_</a>	Alignment	not modelled	16.6	23	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein 7; <b>PDBTitle:</b> nmr structure of the arterivirus nonstructural protein 7 alpha (nsp72 alpha)
32	<a href="#">c3wbkB_</a>	Alignment	not modelled	16.0	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b; <b>PDBTitle:</b> crystal structure analysis of eukaryotic translation initiation factor2 5b and 1a complex
33	<a href="#">c6an0A_</a>	Alignment	not modelled	15.4	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> histidinol dehydrogenase; <b>PDBTitle:</b> crystal structure of histidinol dehydrogenase from elizabethkingia2 anophelis
34	<a href="#">c2k4vA_</a>	Alignment	not modelled	14.5	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pa1076; <b>PDBTitle:</b> solution structure of uncharacterized protein pa1076 from pseudomonas2 aeruginosa. northeast structural genomics consortium (nesg) target3 pat3, ontario center for structural proteomics target pa1076 .
35	<a href="#">c5vldC_</a>	Alignment	not modelled	14.3	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> histidinol dehydrogenase, chloroplastic; <b>PDBTitle:</b> crystal structure of medicago truncatula l-histidinol dehydrogenase in2 complex with l-histidine and nad+
36	<a href="#">c4b0zA_</a>	Alignment	not modelled	13.1	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> 26s proteasome regulatory subunit rpn12; <b>PDBTitle:</b> crystal structure of s. pombe rpn12
37	<a href="#">c3s6eB_</a>	Alignment	not modelled	12.3	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> rna-binding protein 39; <b>PDBTitle:</b> crystal structure of a rna binding motif protein 39 (rbm39) from mus2 musculus at 0.95 a resolution
38	<a href="#">c3b09A_</a>	Alignment	not modelled	12.2	11	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-prolyl cis-trans isomerase; <b>PDBTitle:</b> crystal structure of the n-domain of fkbp22 from shewanella sp. sib1
39	<a href="#">d1ej7s_</a>	Alignment	not modelled	12.1	22	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
40	<a href="#">d1wdds_</a>	Alignment	not modelled	12.0	22	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
41	<a href="#">d2idaa1</a>	Alignment	not modelled	11.7	21	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> Zf-UBP
42	<a href="#">c3izyP_</a>	Alignment	not modelled	10.5	16	<b>PDB header:</b> rna, ribosomal protein <b>Chain:</b> P: <b>PDB Molecule:</b> translation initiation factor if-2, mitochondrial; <b>PDBTitle:</b> mammalian mitochondrial translation initiation factor 2
43	<a href="#">c5zojE_</a>	Alignment	not modelled	10.3	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> inner nuclear membrane protein man1; <b>PDBTitle:</b> crystal structure of human smad2-man1 complex
44	<a href="#">c5h3jB_</a>	Alignment	not modelled	9.9	64	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> golgin-45; <b>PDBTitle:</b> crystal structure of grasg domain of grasg55 complexed with the2 golgin45 c-terminus
45	<a href="#">d1g47a1</a>	Alignment	not modelled	9.9	16	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
46	<a href="#">c2fhoA_</a>	Alignment	not modelled	9.8	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> spliceosomal protein sf3b155; <b>PDBTitle:</b> nmr solution structure of the human spliceosomal protein2 complex p14-sf3b155
47	<a href="#">c2jvfA_</a>	Alignment	not modelled	9.4	14	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo protein m7; <b>PDBTitle:</b> solution structure of m7, a computationally-designed2 artificial protein
48	<a href="#">c4v06A_</a>	Alignment	not modelled	9.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan 5-hydroxylase 2; <b>PDBTitle:</b> crystal structure of human tryptophan hydroxylase 2 (tph2), catalytic2 domain
49	<a href="#">c4kzD_</a>	Alignment	not modelled	8.9	36	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> crystal structure of thermus thermophilus if2, apo and gdp-bound forms2 (2-474)
50	<a href="#">c4ky3A_</a>	Alignment	not modelled	8.7	16	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> designed protein or327; <b>PDBTitle:</b> three-dimensional structure of the orthorhombic crystal of2 computationally designed insertion domain , northeast structural3 genomics consortium (nesg) target or327
51	<a href="#">c5z5mB_</a>	Alignment	not modelled	8.6	27	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted protein; <b>PDBTitle:</b> crystal structure of (s)-allantoin synthase
52	<a href="#">d1gk8i_</a>	Alignment	not modelled	8.5	24	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
						<b>Fold:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains

53	<a href="#">d1phza2</a>	Alignment	not modelled	8.3	23	<b>Superfamily:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Family:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
54	<a href="#">d1mlwa_</a>	Alignment	not modelled	8.3	17	<b>Fold:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Superfamily:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Family:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
55	<a href="#">c1qysA_</a>	Alignment	not modelled	7.9	16	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> stop7; <b>PDBTitle:</b> crystal structure of top7: a computationally designed2 protein with a novel fold
56	<a href="#">d1toha_</a>	Alignment	not modelled	7.8	27	<b>Fold:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Superfamily:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Family:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
57	<a href="#">d1o0pa_</a>	Alignment	not modelled	7.5	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
58	<a href="#">c4n3nA_</a>	Alignment	not modelled	7.3	8	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b-like protein, <b>PDBTitle:</b> crystal structure of eukaryotic translation initiation factor eif5b2 (517-1116) from chaetomium thermophilum, apo form
59	<a href="#">c5i87A_</a>	Alignment	not modelled	7.1	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> peroxin 14; <b>PDBTitle:</b> targeting the pex14-pex5 interaction by small molecules provides novel2 therapeutic routes to treat trypanosomiases.
60	<a href="#">c4x82A_</a>	Alignment	not modelled	7.0	23	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> zinc transporter zip4; <b>PDBTitle:</b> crystal structure of the extracellular domain of zip4
61	<a href="#">c3gj6B_</a>	Alignment	not modelled	7.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear pore complex protein nup153; <b>PDBTitle:</b> crystal structure of human rangdp-nup153znf1 complex
62	<a href="#">c4b4tT_</a>	Alignment	not modelled	6.9	5	<b>PDB header:</b> hydrolase <b>Chain:</b> T: <b>PDB Molecule:</b> 26s proteasome regulatory subunit rpn12; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
63	<a href="#">c2f9jP_</a>	Alignment	not modelled	6.9	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> P: <b>PDB Molecule:</b> splicing factor 3b subunit 1; <b>PDBTitle:</b> 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
64	<a href="#">d2v6ai1</a>	Alignment	not modelled	6.8	24	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
65	<a href="#">d8rucj_</a>	Alignment	not modelled	6.7	24	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
66	<a href="#">d1uzdc1</a>	Alignment	not modelled	6.6	24	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
67	<a href="#">d2cmua1</a>	Alignment	not modelled	6.6	13	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Porphyromonas-type peptidylarginine deiminase
68	<a href="#">d1j8ua_</a>	Alignment	not modelled	6.6	23	<b>Fold:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Superfamily:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Family:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
69	<a href="#">c2phmA_</a>	Alignment	not modelled	6.5	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (phenylalanine-4-hydroxylase); <b>PDBTitle:</b> structure of phenylalanine hydroxylase dephosphorylated
70	<a href="#">c2yfwC_</a>	Alignment	not modelled	6.5	25	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> histone h3-like centromeric protein cse4; <b>PDBTitle:</b> heterotetramer structure of kluyveromyces lactis cse4,h4
71	<a href="#">c4d10H_</a>	Alignment	not modelled	6.4	20	<b>PDB header:</b> signaling protein <b>Chain:</b> H: <b>PDB Molecule:</b> cop9 signalosome complex subunit 8; <b>PDBTitle:</b> crystal structure of the cop9 signalosome
72	<a href="#">c4ljiA_</a>	Alignment	not modelled	6.3	22	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c-550-like protein; <b>PDBTitle:</b> crystal structure at 1.5 angstrom resolution of the psbv2 cytochrome2 from the cyanobacterium thermosynechococcus elongatus
73	<a href="#">c2hueB_</a>	Alignment	not modelled	6.3	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> histone h3; <b>PDBTitle:</b> structure of the h3-h4 chaperone asf1 bound to histones h3 and h4
74	<a href="#">c1t8jA_</a>	Alignment	not modelled	6.2	33	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> bba5; <b>PDBTitle:</b> nmr structure of bba5, a compact, independently folded bba2 motif
75	<a href="#">c5fg3A_</a>	Alignment	not modelled	6.2	23	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> probable translation initiation factor if-2; <b>PDBTitle:</b> crystal structure of gdp-bound aif5b from aeropyrum pernix
76	<a href="#">c2l1aA_</a>	Alignment	not modelled	6.2	60	<b>PDB header:</b> actin binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> formin-c; <b>PDBTitle:</b> solution nmr structure of the n-terminal gtpase-like domain of2 dictyostelium discoideum formin c
77	<a href="#">c3e2tA_</a>	Alignment	not modelled	6.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan 5-hydroxylase 1;

77	<a href="#">c6zta_</a>	Alignment	not modelled	6.1	47	<b>PDBTitle:</b> the catalytic domain of chicken tryptophan hydroxylase 12 with bound tryptophan
78	<a href="#">d1s5qb_</a>	Alignment	not modelled	6.1	25	<b>Fold:</b> PAH2 domain <b>Superfamily:</b> PAH2 domain <b>Family:</b> PAH2 domain
79	<a href="#">c5ugjC_</a>	Alignment	not modelled	6.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of htpa reductase from neisseria meningitidis
80	<a href="#">c5knwA_</a>	Alignment	not modelled	5.9	11	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> la-related protein 7; <b>PDBTitle:</b> solution nmr structure of human larp7 xrrm2
81	<a href="#">c5denA_</a>	Alignment	not modelled	5.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanine-4-hydroxylase; <b>PDBTitle:</b> the first structure of a full-length mammalian phenylalanine2 hydroxylase reveals the architecture of an auto-inhibited tetramer
82	<a href="#">c3ff5B_</a>	Alignment	not modelled	5.8	17	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal biogenesis factor 14; <b>PDBTitle:</b> crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
83	<a href="#">d2dita1_</a>	Alignment	not modelled	5.7	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
84	<a href="#">c6f0fB_</a>	Alignment	not modelled	5.6	31	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> ip2_s; <b>PDBTitle:</b> crystal structure asf1-ip2_s
85	<a href="#">d1zbra1_</a>	Alignment	not modelled	5.6	20	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Porphyromonas-type peptidylarginine deiminase
86	<a href="#">c2lzeA_</a>	Alignment	not modelled	5.6	7	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> a primordial catalytic fold generated by in vitro <b>PDBTitle:</b> ligase 10c
87	<a href="#">c3gj8D_</a>	Alignment	not modelled	5.5	16	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> nuclear pore complex protein nup153; <b>PDBTitle:</b> crystal structure of human rangdp-nup153znf34 complex
88	<a href="#">c3gj5B_</a>	Alignment	not modelled	5.5	20	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear pore complex protein nup153; <b>PDBTitle:</b> crystal structure of human rangdp-nup153znf4 complex
89	<a href="#">c3gj5D_</a>	Alignment	not modelled	5.5	20	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> nuclear pore complex protein nup153; <b>PDBTitle:</b> crystal structure of human rangdp-nup153znf4 complex
90	<a href="#">c2nlwA_</a>	Alignment	not modelled	5.5	19	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 3 <b>PDBTitle:</b> solution structure of the rrm domain of human eukaryotic2 initiation factor 3b
91	<a href="#">c2mztA_</a>	Alignment	not modelled	5.5	7	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein hrb1; <b>PDBTitle:</b> nmr structure of the rrm3 domain of hrb1
92	<a href="#">c6b2wB_</a>	Alignment	not modelled	5.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative peptidyl-arginine deiminase family protein; <b>PDBTitle:</b> c. jejuni c315s agmatine deiminase with substrate bound
93	<a href="#">c5aonB_</a>	Alignment	not modelled	5.4	15	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> peroxin 14; <b>PDBTitle:</b> crystal structure of the conserved n-terminal domain of2 pex14 from trypanosoma brucei
94	<a href="#">c5jk5A_</a>	Alignment	not modelled	5.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanine-4-hydroxylase; <b>PDBTitle:</b> phenylalanine hydroxylase from dictyostelium - bh2 complex
95	<a href="#">c1h2mS_</a>	Alignment	not modelled	5.3	18	<b>PDB header:</b> transcription activator/inhibitor <b>Chain:</b> S: <b>PDB Molecule:</b> hypoxia-inducible factor 1 alpha; <b>PDBTitle:</b> factor inhibiting hif-1 alpha in complex with hif-1 alpha fragment2 peptide
96	<a href="#">d2j0sd1_</a>	Alignment	not modelled	5.3	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Canonical RBD
97	<a href="#">d2ewoa1_</a>	Alignment	not modelled	5.2	13	<b>Fold:</b> Pentain, beta/alpha-propeller <b>Superfamily:</b> Pentain <b>Family:</b> Porphyromonas-type peptidylarginine deiminase
98	<a href="#">c1tmxA_</a>	Alignment	not modelled	5.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxyquinol 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure of hydroxyquinol 1,2-dioxygenase from nocardiooides2 simplex 3e
99	<a href="#">c2q37A_</a>	Alignment	not modelled	5.1	14	<b>PDB header:</b> plant protein, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> ohcu decarboxylase; <b>PDBTitle:</b> crystal structure of ohcu decarboxylase in the presence of2 (s)-allantoin