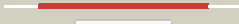



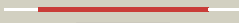






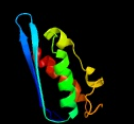
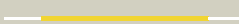

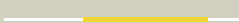


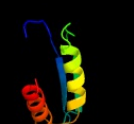






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3284 (-) _3665815_3666246
Date	Thu Aug 8 16:20:49 BST 2019
Unique Job ID	7ac440a932a55171

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1mzga_</a>	 Alignment		100.0	17	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> SufE-like
2	<a href="#">d1ni7a_</a>	 Alignment		100.0	25	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> SufE-like
3	<a href="#">c1wloA_</a>	 Alignment		100.0	39	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sufe protein; <b>PDBTitle:</b> solution structure of the hypothetical protein from thermus2 thermophilus hb8
4	<a href="#">d1r9pa_</a>	 Alignment		94.7	15	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> NifU/IscU domain
5	<a href="#">c4eb5C_</a>	 Alignment		93.2	14	<b>PDB header:</b> transferase/metal binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> nifu protein (nifu-1); <b>PDBTitle:</b> a. fulgidus iscs-iscu complex structure
6	<a href="#">d1wfa_</a>	 Alignment		87.5	15	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> NifU/IscU domain
7	<a href="#">c2qq4A_</a>	 Alignment		74.4	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> iron-sulfur cluster biosynthesis protein iscu; <b>PDBTitle:</b> crystal structure of iron-sulfur cluster biosynthesis protein iscu2 (ttha1736) from thermus thermophilus hb8
8	<a href="#">c2z7eB_</a>	 Alignment		73.1	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> nifu-like protein; <b>PDBTitle:</b> crystal structure of aquifex aeolicus iscu with bound [2Fe-2 S <sub>2</sub> ] cluster
9	<a href="#">d1su0b_</a>	 Alignment		73.0	15	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> NifU/IscU domain
10	<a href="#">c5uftA_</a>	 Alignment		68.2	12	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen-fixing nifu-like, n-terminal; <b>PDBTitle:</b> crystal structure of a nitrogen-fixing nifu-like protein (n-terminal)2 from brucella abortus
11	<a href="#">d1xjsa_</a>	 Alignment		67.4	13	<b>Fold:</b> SufE/NifU <b>Superfamily:</b> SufE/NifU <b>Family:</b> NifU/IscU domain

12	<a href="#">c4dztA</a>	Alignment		65.5	16	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> aqualysin-1; <b>PDBTitle:</b> aqualysin I: the crystal structure of a serine protease from an2 extreme thermophile, thermus aquaticus yt-1
13	<a href="#">c4mzdA</a>	Alignment		65.0	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nisin leader peptide-processing serine protease nisp; <b>PDBTitle:</b> high resolution crystal structure of the nisin leader peptidase nisp2 from lactococcus lactis
14	<a href="#">c3whiA</a>	Alignment		64.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> subtilisin e; <b>PDBTitle:</b> crystal structure of unautoprocessed form of is1-inserted pro-2 subtilisin e
15	<a href="#">c2pmwB</a>	Alignment		63.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> proprotein convertase subtilisin/kexin type 9; <b>PDBTitle:</b> the crystal structure of proprotein convertase subtilisin2 kexin type 9 (pcsk9)
16	<a href="#">c5vliA</a>	Alignment		62.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proprotein convertase subtilisin/kexin type 9; <b>PDBTitle:</b> short pcsk9 delta-p' complex with peptide pep3
17	<a href="#">c1s2nB</a>	Alignment		59.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> extracellular subtilisin-like serine proteinase; <b>PDBTitle:</b> crystal structure of a cold adapted subtilisin-like serine proteinase
18	<a href="#">c3f7oB</a>	Alignment		59.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> serine protease; <b>PDBTitle:</b> crystal structure of cuticle-degrading protease from paecilomyces2 lilacinus (pl646)
19	<a href="#">c2b6nA</a>	Alignment		58.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proteinase k; <b>PDBTitle:</b> the 1.8 a crystal structure of a proteinase k like enzyme from a2 psychrotroph serratia species
20	<a href="#">c5z6oA</a>	Alignment		57.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease; <b>PDBTitle:</b> crystal structure of penicillium cyclopium protease
21	<a href="#">c4tr2A</a>	Alignment	not modelled	56.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> subtilisin-like 1 serine protease; <b>PDBTitle:</b> crystal structure of pvsb1
22	<a href="#">c2w2qA</a>	Alignment	not modelled	55.6	20	<b>PDB header:</b> hydrolase/receptor <b>Chain:</b> A: <b>PDB Molecule:</b> proprotein convertase subtilisin/kexin type 9; <b>PDBTitle:</b> pcsk9-deltac d374h mutant bound to wt egf-a of ldlr
23	<a href="#">c5vlpA</a>	Alignment	not modelled	54.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proprotein convertase subtilisin/kexin type 9; <b>PDBTitle:</b> pcsk9 complex with ldlr antagonist peptide and fab7g7
24	<a href="#">d1gcia</a>	Alignment	not modelled	54.8	16	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
25	<a href="#">d1pdaa2</a>	Alignment	not modelled	53.5	19	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain <b>Family:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
26	<a href="#">c2iy9A</a>	Alignment	not modelled	53.4	8	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> suba; <b>PDBTitle:</b> crystal structure of the a-subunit of the ab5 toxin from e.2 coli
27	<a href="#">d1gnsa</a>	Alignment	not modelled	52.9	11	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
28	<a href="#">c2oxaA</a>	Alignment	not modelled	51.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular serine protease; <b>PDBTitle:</b> crystal structure of serine protease of aeromonas sobria

29	<a href="#">c5yl7A</a>	Alignment	not modelled	51.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pseudoalteromonas arctica pamc 21717; <b>PDBTitle:</b> proteases from pseudoalteromonas arctica pamc 21717 (pro21717)
30	<a href="#">d1gtka2</a>	Alignment	not modelled	50.6	24	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain <b>Family:</b> Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
31	<a href="#">c4j94A</a>	Alignment	not modelled	50.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> membrane-anchored mycosin mycp1; <b>PDBTitle:</b> crystal structure of mycp1 from the esx-1 type vii secretion system
32	<a href="#">d1p8ja2</a>	Alignment	not modelled	48.7	16	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
33	<a href="#">c3vv3B</a>	Alignment	not modelled	48.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> deseasin mcp-01; <b>PDBTitle:</b> crystal structure of deseasin mcp-01 from pseudoalteromonas sp. sm9913
34	<a href="#">d1r0re</a>	Alignment	not modelled	47.7	16	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
35	<a href="#">d1to2e</a>	Alignment	not modelled	45.7	12	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
36	<a href="#">c4kg7A</a>	Alignment	not modelled	45.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase s8 and s53, subtilisin, kexin, sedolisin; <b>PDBTitle:</b> structure of mycp3 protease from the type vii (esx-3) secretion2 system.
37	<a href="#">d2id4a2</a>	Alignment	not modelled	44.7	19	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
38	<a href="#">c4lvnA</a>	Alignment	not modelled	44.5	16	<b>PDB header:</b> hydrolase/inhibitor/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> subtilisin-like serine protease; <b>PDBTitle:</b> crystal structure of pfsb1-prodomain-nimp.m7 fab complex
39	<a href="#">d2ixta1</a>	Alignment	not modelled	44.5	16	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
40	<a href="#">d1v6ca</a>	Alignment	not modelled	44.5	23	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
41	<a href="#">c1r64A</a>	Alignment	not modelled	42.1	19	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> kexin; <b>PDBTitle:</b> the 2.2 a crystal structure of kex2 protease in complex with ac-arg-2 glu-lys-boroarg peptidyl boronic acid inhibitor
42	<a href="#">c1p8jB</a>	Alignment	not modelled	39.1	16	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> furin precursor; <b>PDBTitle:</b> crystal structure of the proprotein convertase furin
43	<a href="#">d1bh6a</a>	Alignment	not modelled	37.0	16	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
44	<a href="#">c4mlqA</a>	Alignment	not modelled	32.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> porphobilinogen deaminase; <b>PDBTitle:</b> crystal structure of bacillus megaterium porphobilinogen deaminase
45	<a href="#">c3bpsA</a>	Alignment	not modelled	31.8	20	<b>PDB header:</b> hydrolase/lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> proprotein convertase subtilisin/kexin type 9; <b>PDBTitle:</b> pcsk9:egf-a complex
46	<a href="#">d1nexa1</a>	Alignment	not modelled	31.3	4	<b>Fold:</b> Skp1 dimerisation domain-like <b>Superfamily:</b> Skp1 dimerisation domain-like <b>Family:</b> Skp1 dimerisation domain-like
47	<a href="#">c3lpcA</a>	Alignment	not modelled	29.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aprb2; <b>PDBTitle:</b> crystal structure of a subtilisin-like protease
48	<a href="#">c2ypnA</a>	Alignment	not modelled	29.3	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (hydroxymethylbilane synthase); <b>PDBTitle:</b> hydroxymethylbilane synthase
49	<a href="#">d1fs1b1</a>	Alignment	not modelled	27.2	9	<b>Fold:</b> Skp1 dimerisation domain-like <b>Superfamily:</b> Skp1 dimerisation domain-like <b>Family:</b> Skp1 dimerisation domain-like
50	<a href="#">c4htgA</a>	Alignment	not modelled	26.3	14	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> porphobilinogen deaminase, chloroplastic; <b>PDBTitle:</b> porphobilinogen deaminase from arabidopsis thaliana
51	<a href="#">d1fs2b1</a>	Alignment	not modelled	25.9	9	<b>Fold:</b> Skp1 dimerisation domain-like <b>Superfamily:</b> Skp1 dimerisation domain-like <b>Family:</b> Skp1 dimerisation domain-like
52	<a href="#">c3eq1A</a>	Alignment	not modelled	25.7	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> porphobilinogen deaminase; <b>PDBTitle:</b> the crystal structure of human porphobilinogen deaminase at 2.8a resolution
53	<a href="#">c3qfhE</a>	Alignment	not modelled	22.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> epidermin leader peptide processing serine protease epip; <b>PDBTitle:</b> 2.05 angstrom resolution crystal structure of epidermin leader peptide2 processing serine protease (epip) from staphylococcus aureus.
54	<a href="#">d2pwaa1</a>	Alignment	not modelled	21.7	19	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases

55	<a href="#">d2ovra1</a>	Alignment	not modelled	18.9	9	<b>Fold:</b> Skp1 dimerisation domain-like <b>Superfamily:</b> Skp1 dimerisation domain-like <b>Family:</b> Skp1 dimerisation domain-like
56	<a href="#">d1meeaa</a>	Alignment	not modelled	18.7	16	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
57	<a href="#">c3vtaB</a>	Alignment	not modelled	18.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cucumisin; <b>PDBTitle:</b> crystal structure of cucumisin, a subtilisin-like endoprotease from2 cucumis melo l
58	<a href="#">d1r6va</a>	Alignment	not modelled	18.4	20	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like <b>Family:</b> Subtilases
59	<a href="#">d1wwia1</a>	Alignment	not modelled	18.0	22	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Bacterial histone-fold protein
60	<a href="#">d1r4va</a>	Alignment	not modelled	17.7	19	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Bacterial histone-fold protein
61	<a href="#">c6mcjA</a>	Alignment	not modelled	17.1	21	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> orange carotenoid-binding protein; <b>PDBTitle:</b> structure of helical carotenoid protein 2 from fremyella diplosiphon
62	<a href="#">c4odaD</a>	Alignment	not modelled	16.7	29	<b>PDB header:</b> hydrolase/replication <b>Chain:</b> D: <b>PDB Molecule:</b> dna polymerase processivity factor component a20; <b>PDBTitle:</b> crystal structure of the vaccinia virus dna polymerase holoenzyme2 subunit d4 in complex with the a20 n-terminus
63	<a href="#">c4odaC</a>	Alignment	not modelled	16.7	29	<b>PDB header:</b> hydrolase/replication <b>Chain:</b> C: <b>PDB Molecule:</b> dna polymerase processivity factor component a20; <b>PDBTitle:</b> crystal structure of the vaccinia virus dna polymerase holoenzyme2 subunit d4 in complex with the a20 n-terminus
64	<a href="#">d1n83a</a>	Alignment	not modelled	14.7	9	<b>Fold:</b> Nuclear receptor ligand-binding domain <b>Superfamily:</b> Nuclear receptor ligand-binding domain <b>Family:</b> Nuclear receptor ligand-binding domain
65	<a href="#">c3t41B</a>	Alignment	not modelled	14.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> epidermin leader peptide processing serine protease epip; <b>PDBTitle:</b> 1.95 angstrom resolution crystal structure of epidermin leader peptide2 processing serine protease (epip) s393a mutant from staphylococcus3 aureus
66	<a href="#">c3wozA</a>	Alignment	not modelled	12.8	25	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> clip-associating protein 2; <b>PDBTitle:</b> crystal structure of clasp2 tog domain (tog3)
67	<a href="#">d1m98a1</a>	Alignment	not modelled	11.8	17	<b>Fold:</b> Orange carotenoid protein, N-terminal domain <b>Superfamily:</b> Orange carotenoid protein, N-terminal domain <b>Family:</b> Orange carotenoid protein, N-terminal domain
68	<a href="#">c2kvhA</a>	Alignment	not modelled	11.1	35	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger and btb domain-containing protein 32; <b>PDBTitle:</b> structure of the three-cys2his2 domain of mouse testis zinc2 finger protein
69	<a href="#">c3cuoB</a>	Alignment	not modelled	11.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator ygav; <b>PDBTitle:</b> crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
70	<a href="#">c4zoqM</a>	Alignment	not modelled	10.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> intracellular serine protease; <b>PDBTitle:</b> crystal structure of a lanthipeptide protease
71	<a href="#">d1pq9a</a>	Alignment	not modelled	10.0	14	<b>Fold:</b> Nuclear receptor ligand-binding domain <b>Superfamily:</b> Nuclear receptor ligand-binding domain <b>Family:</b> Nuclear receptor ligand-binding domain
72	<a href="#">c2hc4A</a>	Alignment	not modelled	9.8	15	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> vitamin d receptor; <b>PDBTitle:</b> crystal structure of the lbd of vdr of danio rerio in2 complex with calcitriol
73	<a href="#">c6cw3F</a>	Alignment	not modelled	9.7	33	<b>PDB header:</b> gene regulation <b>Chain:</b> F: <b>PDB Molecule:</b> histone acetyltransferase gcn5; <b>PDBTitle:</b> crystal structure of a yeast saga transcriptional coactivator2 ada2/gcn5 hat subcomplex, crystal form 2
74	<a href="#">c5o1mA</a>	Alignment	not modelled	9.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> rubber oxygenase; <b>PDBTitle:</b> structure of latex clearing protein lcp in the closed state
75	<a href="#">c4h08A</a>	Alignment	not modelled	9.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of a putative hydrolase (bt3161) from bacteroides2 thetaiotaomicron vpi-5482 at 1.80 a resolution
76	<a href="#">c3i74B</a>	Alignment	not modelled	9.6	32	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> subtilisin-like protease; <b>PDBTitle:</b> crystal structure of the plant subtilisin-like protease sbt3 in2 complex with a chloromethylketone inhibitor
77	<a href="#">c2hl7A</a>	Alignment	not modelled	9.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c-type biogenesis protein ccmh; <b>PDBTitle:</b> crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
78	<a href="#">c2mn4A</a>	Alignment	not modelled	8.1	25	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> computational designed protein based on structure template <b>PDBTitle:</b> nmr solution structure of a computational designed protein based on2 structure template 1cy5
79	<a href="#">d1dbia</a>	Alianment	not modelled	7.9	17	<b>Fold:</b> Subtilisin-like <b>Superfamily:</b> Subtilisin-like

				Family:Subtlases		
80	<a href="#">c2g84a1</a>	Alignment	not modelled	7.9	16	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
81	<a href="#">c3lbdA</a>	Alignment	not modelled	7.7	15	<b>PDB header:</b> nuclear receptor <b>Chain:</b> A; <b>PDB Molecule:</b> retinoic acid receptor gamma; <b>PDBTitle:</b> ligand-binding domain of the human retinoic acid receptor gamma bound to 9-cis retinoic acid
82	<a href="#">d1osva</a>	Alignment	not modelled	7.6	18	<b>Fold:</b> Nuclear receptor ligand-binding domain <b>Superfamily:</b> Nuclear receptor ligand-binding domain <b>Family:</b> Nuclear receptor ligand-binding domain
83	<a href="#">d1n46a</a>	Alignment	not modelled	7.6	15	<b>Fold:</b> Nuclear receptor ligand-binding domain <b>Superfamily:</b> Nuclear receptor ligand-binding domain <b>Family:</b> Nuclear receptor ligand-binding domain
84	<a href="#">c4ozrE</a>	Alignment	not modelled	7.3	29	<b>PDB header:</b> transcription <b>Chain:</b> E; <b>PDB Molecule:</b> ecdysone receptor; <b>PDBTitle:</b> crystal structure of the ligand binding domains of the bovicola ovis2 ecdysone receptor ecr/usp heterodimer (methylene lactam crystal)
85	<a href="#">d1ie9a</a>	Alignment	not modelled	7.1	12	<b>Fold:</b> Nuclear receptor ligand-binding domain <b>Superfamily:</b> Nuclear receptor ligand-binding domain <b>Family:</b> Nuclear receptor ligand-binding domain
86	<a href="#">c4nn7A</a>	Alignment	not modelled	7.0	50	<b>PDB header:</b> cytokine/cytokine receptor <b>Chain:</b> A; <b>PDB Molecule:</b> thymic stromal lymphopoietin; <b>PDBTitle:</b> cytokine receptor complex - crystal form 2
87	<a href="#">d2zmia1</a>	Alignment	not modelled	6.8	9	<b>Fold:</b> Nuclear receptor ligand-binding domain <b>Superfamily:</b> Nuclear receptor ligand-binding domain <b>Family:</b> Nuclear receptor ligand-binding domain
88	<a href="#">d1i36a1</a>	Alignment	not modelled	6.8	27	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> Conserved hypothetical protein MTH1747
89	<a href="#">c3l0jA</a>	Alignment	not modelled	6.6	15	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> nuclear receptor ror-gamma; <b>PDBTitle:</b> crystal structure of orphan nuclear receptor rorgamma in complex with 2 natural ligand
90	<a href="#">c3dm5A</a>	Alignment	not modelled	6.5	26	<b>PDB header:</b> rna binding protein, transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> structures of srp54 and srp19, the two proteins assembling the 2 ribonucleic core of the signal recognition particle from the archaeon 3 pyrococcus furiosus.
91	<a href="#">c6f9mA</a>	Alignment	not modelled	6.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> serine protease; <b>PDBTitle:</b> the lipyl-f-motif in an intracellular subtilisin protease is involved in inhibition
92	<a href="#">c2qw4D</a>	Alignment	not modelled	6.5	14	<b>PDB header:</b> hormone receptor <b>Chain:</b> D; <b>PDB Molecule:</b> orphan nuclear receptor nr4a1; <b>PDBTitle:</b> human nr4a1 ligand-binding domain
93	<a href="#">c2nogA</a>	Alignment	not modelled	6.4	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> iswi protein; <b>PDBTitle:</b> sant domain structure of xenopus remodeling factor iswi
94	<a href="#">c4j8cB</a>	Alignment	not modelled	6.3	8	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> hsc70-interacting protein; <b>PDBTitle:</b> crystal structure of the dimerization domain of hsc70-interacting 2 protein
95	<a href="#">c4j8cA</a>	Alignment	not modelled	6.3	8	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> hsc70-interacting protein; <b>PDBTitle:</b> crystal structure of the dimerization domain of hsc70-interacting 2 protein
96	<a href="#">c5j12A</a>	Alignment	not modelled	6.1	38	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> thymic stromal lymphopoietin; <b>PDBTitle:</b> structure of human tslp:tslpr in complex with mouse il-7ralpha
97	<a href="#">d2r40d1</a>	Alignment	not modelled	6.1	24	<b>Fold:</b> Nuclear receptor ligand-binding domain <b>Superfamily:</b> Nuclear receptor ligand-binding domain <b>Family:</b> Nuclear receptor ligand-binding domain
98	<a href="#">c4trkA</a>	Alignment	not modelled	5.8	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> c. elegans him-3; <b>PDBTitle:</b> structure of c. elegans him-3
99	<a href="#">c3bc5A</a>	Alignment	not modelled	5.8	20	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> peroxisome proliferator-activated receptor gamma; <b>PDBTitle:</b> x-ray crystal structure of human ppar gamma with 2-(5-(3-(2-(5-methyl-2-phenyloxazol-4-yl)ethoxy)benzyl)-2-phenyl-2h-1,2,3-triazol-4-yl)3 acetic acid