


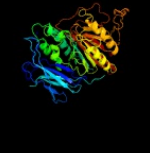
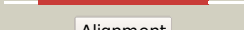
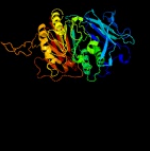
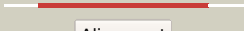




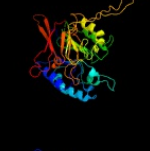




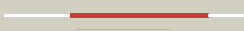









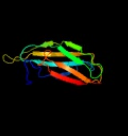






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2577 (-) _2900928_2902517
Date	Wed Aug 7 12:50:21 BST 2019
Unique Job ID	6f29b4aa308a0e69

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3zk4A_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> diphosphonucleotide phosphatase 1; <b>PDBTitle:</b> structure of purple acid phosphatase ppd1 isolated from2 yellow lupin (lupinus luteus) seeds
2	<a href="#">c1kbpB_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase (phosphoric monoester) <b>Chain:</b> B; <b>PDB Molecule:</b> purple acid phosphatase; <b>PDBTitle:</b> kidney bean purple acid phosphatase
3	<a href="#">c1xzwB_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> purple acid phosphatase; <b>PDBTitle:</b> sweet potato purple acid phosphatase/phosphate complex
4	<a href="#">c2yeqA_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> alkaline phosphatase d; <b>PDBTitle:</b> structure of phod
5	<a href="#">d2qfra2</a>	 Alignment		100.0	25	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> Purple acid phosphatase-like
6	<a href="#">d1xwzA2</a>	 Alignment		100.0	26	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> Purple acid phosphatase-like
7	<a href="#">c3tghA_</a>	 Alignment		100.0	19	<b>PDB header:</b> cell invasion <b>Chain:</b> A; <b>PDB Molecule:</b> glideosome-associated protein 50; <b>PDBTitle:</b> gap50 the anchor in the inner membrane complex of plasmodium
8	<a href="#">d1lutea_</a>	 Alignment		100.0	23	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> Purple acid phosphatase-like
9	<a href="#">d1qhwa_</a>	 Alignment		100.0	23	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> Purple acid phosphatase-like
10	<a href="#">c1qhwa_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> protein (purple acid phosphatase); <b>PDBTitle:</b> purple acid phosphatase from rat bone
11	<a href="#">c2xmoB_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> lmo2642 protein; <b>PDBTitle:</b> the crystal structure of lmo2642

12	<a href="#">d2nxfA1</a>	Alignment		99.9	19	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> ADPRibase-Mn-like
13	<a href="#">c5ebbA_</a>	Alignment		99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acid sphingomyelinase-like phosphodiesterase 3a; <b>PDBTitle:</b> structure of human sphingomyelinase phosphodiesterase like 3a2 (smpd3a) with zn2+
14	<a href="#">c5karA_</a>	Alignment		99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acid sphingomyelinase-like phosphodiesterase 3b; <b>PDBTitle:</b> murine acid sphingomyelinase-like phosphodiesterase 3b (smpd3b)
15	<a href="#">c3ib7A_</a>	Alignment		99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> icc protein; <b>PDBTitle:</b> crystal structure of full length rv0805
16	<a href="#">d2qfra1</a>	Alignment		99.9	21	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Purple acid phosphatase, N-terminal domain <b>Family:</b> Purple acid phosphatase, N-terminal domain
17	<a href="#">d3d03a1</a>	Alignment		99.9	15	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> GpdQ-like
18	<a href="#">c5ficD_</a>	Alignment		99.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> sphingomyelin phosphodiesterase; <b>PDBTitle:</b> open form of murine acid sphingomyelinase in presence of lipid
19	<a href="#">d1xzwa1</a>	Alignment		99.8	21	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Purple acid phosphatase, N-terminal domain <b>Family:</b> Purple acid phosphatase, N-terminal domain
20	<a href="#">c2hy1A_</a>	Alignment		99.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rv0805; <b>PDBTitle:</b> crystal structure of rv0805
21	<a href="#">d2hy1a1</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> GpdQ-like
22	<a href="#">d1uf3a_</a>	Alignment	not modelled	99.6	10	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> TT1561-like
23	<a href="#">c3av0A_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna double-strand break repair protein mre11; <b>PDBTitle:</b> crystal structure of mre11-rad50 bound to atp s
24	<a href="#">d2yvta1</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> TT1561-like
25	<a href="#">c1oidA_</a>	Alignment	not modelled	99.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein usha; <b>PDBTitle:</b> 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
26	<a href="#">c3rl4A_</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metallophosphoesterase mpped2; <b>PDBTitle:</b> rat metallophosphodiesterase mpped2 g252h mutant
27	<a href="#">c3auzA_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna double-strand break repair protein mre11; <b>PDBTitle:</b> crystal structure of mre11 with manganese
28	<a href="#">c5k8kA_</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-2,3-diacetylglucosamine hydrolase; <b>PDBTitle:</b> structure of the haemophilus influenzae lpxh-lipid x complex
						<b>Fold:</b> Metallo-dependent phosphatases

29	<a href="#">d1ii7a_</a>	Alignment	not modelled	99.3	14	<b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> DNA double-strand break repair nuclease
30	<a href="#">c2q8uA_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exonuclease, putative; <b>PDBTitle:</b> crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
31	<a href="#">c3qfnA_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
32	<a href="#">c5b4bB_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-2,3-diacylglucosamine hydrolase; <b>PDBTitle:</b> crystal structure of lpxh with lipid x in spacegroup c2
33	<a href="#">c3jvdA_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotidase; <b>PDBTitle:</b> putative 5'-nucleotidase (c4898) from escherichia coli in complex with2 uridine
34	<a href="#">d1usha2</a>	Alignment	not modelled	99.2	14	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
35	<a href="#">c4fcxB_</a>	Alignment	not modelled	99.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair protein rad32; <b>PDBTitle:</b> s.pombe mre11 apoenzym
36	<a href="#">d3c9fa2</a>	Alignment	not modelled	99.1	19	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
37	<a href="#">c4ltyD_</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> exonuclease subunit sbcd; <b>PDBTitle:</b> crystal structure of e.coli sbcd at 1.8 a resolution
38	<a href="#">c5wlyA_</a>	Alignment	not modelled	99.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-2,3-diacylglucosamine hydrolase; <b>PDBTitle:</b> e. coli lpxh- 8 mutations
39	<a href="#">d2z1aa2</a>	Alignment	not modelled	99.0	17	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
40	<a href="#">d1z2wa1</a>	Alignment	not modelled	99.0	22	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> YfcE-like
41	<a href="#">c3qg5D_</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> mre11; <b>PDBTitle:</b> the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
42	<a href="#">c4ykeA_</a>	Alignment	not modelled	99.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mre11; <b>PDBTitle:</b> crystal structure of eukaryotic mre11 catalytic domain from chaetomium2 thermophilum
43	<a href="#">c3qfkA_</a>	Alignment	not modelled	99.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> 2.05 angstrom crystal structure of putative 5'-nucleotidase from2 staphylococcus aureus in complex with alpha-ketoglutarate
44	<a href="#">c3rqzC_</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> metallophosphoesterase; <b>PDBTitle:</b> crystal structure of metallophosphoesterase from sphaerobacter2 thermophilus
45	<a href="#">d1s3la_</a>	Alignment	not modelled	98.9	16	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> YfcE-like
46	<a href="#">c1s3mA_</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> phosphodiesterase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein mj0936; <b>PDBTitle:</b> structural and functional characterization of a novel2 archaeal phosphodiesterase
47	<a href="#">c3t1iC_</a>	Alignment	not modelled	98.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> double-strand break repair protein mre11a; <b>PDBTitle:</b> crystal structure of human mre11: understanding tumorigenic mutations
48	<a href="#">c5w8mD_</a>	Alignment	not modelled	98.9	18	<b>PDB header:</b> endocytosis <b>Chain:</b> D: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 29; <b>PDBTitle:</b> crystal structure of chaetomium thermophilum vps29
49	<a href="#">c2z1aA_</a>	Alignment	not modelled	98.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 5'-nucleotidase; <b>PDBTitle:</b> crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8
50	<a href="#">d1nnwa_</a>	Alignment	not modelled	98.8	18	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> Phosphoesterase-related
51	<a href="#">c5xceB_</a>	Alignment	not modelled	98.8	21	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 29; <b>PDBTitle:</b> crystal structure of wild type vps29 from entamoeba histolytica
52	<a href="#">c5h7wB_</a>	Alignment	not modelled	98.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> venom 5'-nucleotidase; <b>PDBTitle:</b> crystal structure of 5'-nucleotidase from venom of naja atra
53	<a href="#">c4h1sB_</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 5'-nucleotidase; <b>PDBTitle:</b> crystal structure of a truncated soluble form of human cd73 with ecto-2 5'-nucleotidase activity
54	<a href="#">c4fbkB_</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> hydrolase, protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair and telomere maintenance protein nbs1,dna repair

						<b>PDBTitle:</b> crystal structure of a covalently fused nbs1-mre11 complex with one2 manganese ion per active site
55	<a href="#">d2a22a1</a>	Alignment	not modelled	98.7	20	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> YfcE-like
56	<a href="#">d3ck2a1</a>	Alignment	not modelled	98.7	21	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> YfcE-like
57	<a href="#">c3c9fB</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 5'-nucleotidase; <b>PDBTitle:</b> crystal structure of 5'-nucleotidase from candida albicans sc5314
58	<a href="#">c3jyfB</a>	Alignment	not modelled	98.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 2',3'-cyclic nucleotide 2'-phosphodiesterase/3'- <b>PDBTitle:</b> the crystal structure of a 2,3-cyclic nucleotide 2-2 phosphodiesterase/3-nucleotidase bifunctional periplasmic precursor3 protein from klebsiella pneumoniae subsp. pneumoniae mgh 78578
59	<a href="#">c3zu0A</a>	Alignment	not modelled	98.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nad nucleotidase; <b>PDBTitle:</b> structure of haemophilus influenzae nad nucleotidase (nadm)
60	<a href="#">c3gveB</a>	Alignment	not modelled	98.6	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> yfkn protein; <b>PDBTitle:</b> crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
61	<a href="#">c5iheB</a>	Alignment	not modelled	98.4	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase ii small subunit; <b>PDBTitle:</b> d-family dna polymerase - dp1 subunit (3'-5' proof-reading2 exonuclease)
62	<a href="#">c4b2oB</a>	Alignment	not modelled	98.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ymdb phosphodiesterase; <b>PDBTitle:</b> crystal structure of bacillus subtilis ymdb, a global2 regulator of late adaptive responses.
63	<a href="#">d1xm7a</a>	Alignment	not modelled	98.3	11	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> Hypothetical protein aq 1666
64	<a href="#">d1t71a</a>	Alignment	not modelled	98.3	11	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> DR1281-like
65	<a href="#">d2z06a1</a>	Alignment	not modelled	98.3	21	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> TTHA0625-like
66	<a href="#">c2kknA</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of themotoga maritima protein tm1076:2 northeast structural genomics consortium target vt57
67	<a href="#">c2wdfA</a>	Alignment	not modelled	98.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfur oxidation protein soxb; <b>PDBTitle:</b> termus thermophilus sulfate thiohydrolase soxb
68	<a href="#">d1su1a</a>	Alignment	not modelled	97.9	20	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> YfcE-like
69	<a href="#">c1su1A</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yfce; <b>PDBTitle:</b> structural and biochemical characterization of yfce, a phosphoesterase2 from e. coli
70	<a href="#">d1t70a</a>	Alignment	not modelled	97.7	12	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> DR1281-like
71	<a href="#">c6nvoA</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclease mpe; <b>PDBTitle:</b> crystal structure of pseudomonas putida nuclease mpe
72	<a href="#">d1x5aa1</a>	Alignment	not modelled	97.3	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
73	<a href="#">c4zxbE</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> hormone receptor/immune system <b>Chain:</b> E: <b>PDB Molecule:</b> insulin receptor; <b>PDBTitle:</b> structure of the human insulin receptor ectodomain, irdeltabeta2 construct, in complex with four fab molecules
74	<a href="#">d1x4xa1</a>	Alignment	not modelled	97.1	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
75	<a href="#">c4bk4A</a>	Alignment	not modelled	97.0	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 4; <b>PDBTitle:</b> crystal structure of the human epha4 ectodomain
76	<a href="#">c2dm4A</a>	Alignment	not modelled	97.0	19	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> sortilin-related receptor; <b>PDBTitle:</b> solution structure of the second fn3 domain of human2 sorla/lr11
77	<a href="#">d2haza1</a>	Alignment	not modelled	96.9	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
78	<a href="#">c2ed7A</a>	Alignment	not modelled	96.8	15	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> netrin receptor dcc; <b>PDBTitle:</b> solution structure of the first fibronectin type iii domain2 of human netrin receptor dcc
79	<a href="#">c2dkmA</a>	Alignment	not modelled	96.7	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen alpha-1(xx) chain; <b>PDBTitle:</b> solution structures of the fn3 domain of human collagen2 alpha-1(xx) chain
						<b>Fold:</b> Immunoglobulin-like beta-sandwich

80	<a href="#">d1x3da1</a>	Alignment	not modelled	96.7	9	<b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
81	<a href="#">d2b5ib2</a>	Alignment	not modelled	96.7	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
82	<a href="#">d1cd9b2</a>	Alignment	not modelled	96.6	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
83	<a href="#">c2ed8A_</a>	Alignment	not modelled	96.6	16	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> netrin receptor dcc; <b>PDBTitle:</b> solution structure of the second fibronectin type iii2 domain of human netrin receptor dcc
84	<a href="#">d1x5ka1</a>	Alignment	not modelled	96.6	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
85	<a href="#">c2dlhA_</a>	Alignment	not modelled	96.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor-type tyrosine-protein phosphatase delta; <b>PDBTitle:</b> solution structure of the second fn3 domain of human2 receptor-type tyrosine-protein phosphatase delta
86	<a href="#">d2ibga1</a>	Alignment	not modelled	96.6	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
87	<a href="#">d1ujta_</a>	Alignment	not modelled	96.5	21	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
88	<a href="#">c6dg5B_</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> biosynthetic protein/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> interleukin-2 receptor subunit beta; <b>PDBTitle:</b> structure of a de novo designed interleukin-2/interleukin-15 mimetic2 complex with il-2rb and il-2rg
89	<a href="#">c4n68A_</a>	Alignment	not modelled	96.5	18	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> contactin-5; <b>PDBTitle:</b> crystal structure of an internal fn3 domain from human contactin-52 [psi-nysgrc-005804]
90	<a href="#">c2djuA_</a>	Alignment	not modelled	96.5	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> receptor-type tyrosine-protein phosphatase f; <b>PDBTitle:</b> solution structures of the fn3 domain of human receptor-2 type tyrosine-protein phosphatase f
91	<a href="#">c3fl7A_</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> transferase, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin receptor; <b>PDBTitle:</b> crystal structure of the human ephrin a2 ectodomain
92	<a href="#">d2crza1</a>	Alignment	not modelled	96.5	18	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
93	<a href="#">d2crma1</a>	Alignment	not modelled	96.5	12	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
94	<a href="#">d1x5fa1</a>	Alignment	not modelled	96.5	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
95	<a href="#">c2docA_</a>	Alignment	not modelled	96.4	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> neural cell adhesion molecule 2; <b>PDBTitle:</b> solution structure of the fibronectin type-iii domain of2 human neural cell adhesion molecule 2
96	<a href="#">d1g5ba_</a>	Alignment	not modelled	96.4	14	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> Protein serine/threonine phosphatase
97	<a href="#">d1x5xa1</a>	Alignment	not modelled	96.4	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
98	<a href="#">d1va9a1</a>	Alignment	not modelled	96.4	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
99	<a href="#">c4pehC_</a>	Alignment	not modelled	96.3	11	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> C: <b>PDB Molecule:</b> rna lariat debranching enzyme, putative; <b>PDBTitle:</b> dbr1 in complex with synthetic linear rna
100	<a href="#">c2dleA_</a>	Alignment	not modelled	96.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor-type tyrosine-protein phosphatase eta; <b>PDBTitle:</b> solution structure of the fourth fn3 domain of human2 receptor-type tyrosine-protein phosphatase eta
101	<a href="#">c2edeA_</a>	Alignment	not modelled	96.3	11	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> netrin receptor dcc; <b>PDBTitle:</b> solution structure of the sixth fibronectin type iii domain2 of human netrin receptor dcc
102	<a href="#">d1wf5a1</a>	Alignment	not modelled	96.2	11	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
103	<a href="#">d1x5la1</a>	Alignment	not modelled	96.2	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
104	<a href="#">d2djsa1</a>	Alignment	not modelled	96.2	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
105	<a href="#">c4lsdF_</a>	Alignment	not modelled	96.2	15	<b>PDB header:</b> hormone <b>Chain:</b> F: <b>PDB Molecule:</b> fibronectin type iii domain-containing protein 5; <b>PDBTitle:</b> myokine structure
106	<a href="#">d1x5ha1</a>	Alignment	not modelled	96.1	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III

					<b>Family:</b> Fibronectin type III
107	<a href="#">d2d9qb2</a>	Alignment	not modelled	96.0	17 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
108	<a href="#">d2ic2a1</a>	Alignment	not modelled	96.0	14 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
109	<a href="#">d2b5ic1</a>	Alignment	not modelled	95.9	10 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
110	<a href="#">c3tesD_</a>	Alignment	not modelled	95.9	18 <b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> tencon; <b>PDBTitle:</b> crystal structure of tencon
111	<a href="#">d1wk0a_</a>	Alignment	not modelled	95.9	19 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
112	<a href="#">c2dmkA_</a>	Alignment	not modelled	95.9	14 <b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> midline 2 isoform 2; <b>PDBTitle:</b> the solution structure of the fn3 domain of human midline 22 protein
113	<a href="#">d1p9ma3</a>	Alignment	not modelled	95.9	13 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
114	<a href="#">c6hn5F_</a>	Alignment	not modelled	95.8	14 <b>PDB header:</b> signaling protein <b>Chain:</b> F: <b>PDB Molecule:</b> insulin receptor,general control protein gcn4; <b>PDBTitle:</b> leucine-zippered human insulin receptor ectodomain with single bound2 insulin - "upper" membrane-distal part
115	<a href="#">d1bqua2</a>	Alignment	not modelled	95.8	12 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
116	<a href="#">c3s98A_</a>	Alignment	not modelled	95.8	12 <b>PDB header:</b> signaling protein receptor <b>Chain:</b> A: <b>PDB Molecule:</b> interferon alpha/beta receptor 1; <b>PDBTitle:</b> human ifnar1
117	<a href="#">c5u8qA_</a>	Alignment	not modelled	95.7	18 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> insulin-like growth factor 1 receptor; <b>PDBTitle:</b> structure of the ectodomain of the human type 1 insulin-like growth2 factor receptor in complex with igf-i
118	<a href="#">d2vkwa2</a>	Alignment	not modelled	95.7	18 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
119	<a href="#">d1wfu_</a>	Alignment	not modelled	95.7	12 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Fibronectin type III <b>Family:</b> Fibronectin type III
120	<a href="#">c2q7nA_</a>	Alignment	not modelled	95.6	16 <b>PDB header:</b> cytokine receptor/cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> leukemia inhibitory factor receptor; <b>PDBTitle:</b> crystal structure of leukemia inhibitory factor in complex with lif2 receptor (domains 1-5)