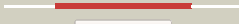



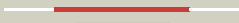

















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3299c_(atsB)_3683048_3685960
Date	Thu Aug 8 16:20:50 BST 2019
Unique Job ID	483bb8492a81566f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1hdha_</a>	 Alignment		100.0	33	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> Arylsulfatase
2	<a href="#">c4upiA_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfatase family protein; <b>PDBTitle:</b> dimeric sulfatase spas1 from silicibacter pomeroyi
3	<a href="#">c4uplC_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> sulfatase family protein; <b>PDBTitle:</b> dimeric sulfatase spas2 from silicibacter pomeroyi
4	<a href="#">d1p49a_</a>	 Alignment		100.0	23	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> Arylsulfatase
5	<a href="#">c3ed4A_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arylsulfatase; <b>PDBTitle:</b> crystal structure of putative arylsulfatase from escherichia coli
6	<a href="#">c4fdiA_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylgalactosamine-6-sulfatase; <b>PDBTitle:</b> the molecular basis of mucopolysaccharidosis iv a
7	<a href="#">c4ug4H_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> choline sulfatase; <b>PDBTitle:</b> crystal structure of a choline sulfatase from sinorhizobium2 melliloti
8	<a href="#">c4uphA_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfatase (sulfuric ester hydrolase) protein; <b>PDBTitle:</b> crystal structure of phosphonate monoester hydrolase of agrobacterium2 radiobacter
9	<a href="#">d1fsua_</a>	 Alignment		100.0	26	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> Arylsulfatase
10	<a href="#">c6b1vB_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> iota-carrageenan sulfatase; <b>PDBTitle:</b> crystal structure of ps i-cgsb c78s in complex with i-neocarratetraose
11	<a href="#">d1lauka_</a>	 Alignment		100.0	27	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> Arylsulfatase

12	<a href="#">c2qzuA_</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative sulfatase yidj; <b>PDBTitle:</b> crystal structure of the putative sulfatase yidj from bacteroides2 fragilis. northeast structural genomics consortium target bfr123
13	<a href="#">c4upkC_</a>	Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphonate monoester hydrolase; <b>PDBTitle:</b> phosphonate monoester hydrolase sppmh from silicibacter pomeroyi
14	<a href="#">c5fqIA_</a>	Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> iduronate-2-sulfatase; <b>PDBTitle:</b> insights into hunter syndrome from the structure of iduronate-2-2 sulfatase
15	<a href="#">c2vqrA_</a>	Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative sulfatase; <b>PDBTitle:</b> crystal structure of a phosphonate monoester hydrolase from rhizobium2 leguminosarum: a new member of the alkaline phosphatase superfamily
16	<a href="#">c4mivB_</a>	Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> n-sulphoglucosamine sulphohydrolase; <b>PDBTitle:</b> crystal structure of sulfamidase, crystal form I
17	<a href="#">c6j66B_</a>	Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> chondroitin sulfate/dermatan sulfate 4-o-endosulfatase <b>PDBTitle:</b> chondroitin sulfate/dermatan sulfate endolytic 4-o-sulfatase
18	<a href="#">c6hhmA_</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> arylsulfatase; <b>PDBTitle:</b> crystal structure of the family s1_7 ulvan-specific sulfatase fa220702 from formosa agariphila
19	<a href="#">c3b5qB_</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative sulfatase yidj; <b>PDBTitle:</b> crystal structure of a putative sulfatase (np_810509.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.40 a resolution
20	<a href="#">c5g2vA_</a>	Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylglucosamine-6-sulfatase; <b>PDBTitle:</b> structure of bt4656 in complex with its substrate d-glucosamine-2-n,2 6-o-disulfate.
21	<a href="#">c6hr5A_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-l-rhamnosidase/sulfatase (gh78); <b>PDBTitle:</b> structure of the s1_25 family sulfatase module of the rhamnosidase2 fa22250 from formosa agariphila
22	<a href="#">c4uopB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lipoteichoic acid primase; <b>PDBTitle:</b> crystal structure of the lipoteichoic acid synthase ltap from listeria2 monocytogenes
23	<a href="#">c3lxqB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein vp1736; <b>PDBTitle:</b> the crystal structure of a protein in the alkaline phosphatase2 superfamily from vibrio parahaemolyticus to 1.95a
24	<a href="#">c2w8dB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> processed glycerol phosphate lipoteichoic acid synthase 2; <b>PDBTitle:</b> distinct and essential morphogenic functions for wall-and2 lipo-teichoic acids in bacillus subtilis
25	<a href="#">c4uorK_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> K: <b>PDB Molecule:</b> lipoteichoic acid synthase; <b>PDBTitle:</b> structure of lipoteichoic acid synthase ltas from listeria2 monocytogenes in complex with glycerol phosphate
26	<a href="#">c2w5tA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> processed glycerol phosphate lipoteichoic acid <b>PDBTitle:</b> structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.
27	<a href="#">c2zktB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent phosphoglycerate <b>PDBTitle:</b> structure of ph0037 protein from pyrococcus horikoshii
28	<a href="#">c5i5fA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> inner membrane protein yejm; <b>PDBTitle:</b> salmonella global domain 191

29	<a href="#">c3m8yC_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphopentomutase; <b>PDBTitle:</b> phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
30	<a href="#">c5k4pA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable phosphatidylethanolamine transferase mcr-1; <b>PDBTitle:</b> catalytic domain of mcr-1 phosphoethanolamine transferase
31	<a href="#">c6bneA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoethanolamine transferase; <b>PDBTitle:</b> crystal structure of the intrinsic colistin resistance enzyme icr(mc)2 from moraxella catarrhalis, catalytic domain, phosphate-bound complex
32	<a href="#">c5tj3A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alkaline phosphatase pafa; <b>PDBTitle:</b> crystal structure of wild type alkaline phosphatase pafa to 1.7a2 resolution
33	<a href="#">c4kayA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> yhbxb/yhjw/yjip/yjdb family protein; <b>PDBTitle:</b> structure of the soluble domain of lipooligosaccharide2 phosphoethanolamine transferase a from neisseria meningitidis -3 complex with zn
34	<a href="#">c3q3qA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alkaline phosphatase; <b>PDBTitle:</b> crystal structure of spap: an novel alkaline phosphatase from2 bacterium sphingomonas sp. strain bsar-1
35	<a href="#">c2i09A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphopentomutase; <b>PDBTitle:</b> crystal structure of putative phosphopentomutase from streptococcus2 mutans
36	<a href="#">c6a82A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoethanolamine transferase eptc; <b>PDBTitle:</b> crystal structure of the c-terminal periplasmic domain of eceptc from2 escherichia coli
37	<a href="#">c4lqvA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bis(5'-adenosyl)-triphosphatase enpp4; <b>PDBTitle:</b> crystal structure of human enpp4 with amp
38	<a href="#">c5udyA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> human alkaline sphingomyelinase (alk-smase, enpp7, npp7)
39	<a href="#">c4tn0C_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> upf0141 protein yjdb; <b>PDBTitle:</b> crystal structure of the c-terminal periplasmic domain of2 phosphoethanolamine transferase eptc from campylobacter jejuni
40	<a href="#">c2gsoB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphodiesterase-nucleotide pyrophosphatase; <b>PDBTitle:</b> structure of xac nucleotide pyrophosphatase/phosphodiesterase in2 complex with vanadate
41	<a href="#">c5vemA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> human ectonucleotide pyrophosphatase / phosphodiesterase 5 (enpp5,2 npp5)
42	<a href="#">c5egeD_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> structure of enpp6, a choline-specific glycerophosphodiester-2 phosphodiesterase
43	<a href="#">d1o98a2</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
44	<a href="#">c5u9zB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoglycerol transferase; <b>PDBTitle:</b> phosphoglycerol transferase gach from streptococcus pyogenes
45	<a href="#">c3szzA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphonoacetate hydrolase; <b>PDBTitle:</b> crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
46	<a href="#">d2i09a1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> DeoB catalytic domain-like
47	<a href="#">d1ei6a_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> Phosphonoacetate hydrolase
48	<a href="#">c6c02B_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> human ectonucleotide pyrophosphatase / phosphodiesterase 3 (enpp3,2 npp3, cd203c), inactive (t205a), n594s, with alpha,beta-methylene-atp3 (ampcpp)
49	<a href="#">c5fgnA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase,hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipooligosaccharide phosphoethanolamine transferase a; <b>PDBTitle:</b> integral membrane protein lipooligosaccharide phosphoethanolamine2 transferase a (epta) from neisseria meningitidis
50	<a href="#">c5gz4A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> snake venom phosphodiesterase (pde); <b>PDBTitle:</b> crystal structure of snake venom phosphodiesterase (pde) from taiwan2 cobra (naja atra atra)
51	<a href="#">c2xrgA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor

52	<a href="#">c2xr9A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> crystal structure of autotaxin (enpp2)
53	<a href="#">c5gz5A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> snake venom phosphodiesterase (pde); <b>PDBTitle:</b> crystal structure of snake venom phosphodiesterase (pde) from taiwan2 cobra (naja atra atra) in complex with amp
54	<a href="#">c4b56A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> structure of ectonucleotide pyrophosphatase-phosphodiesterase-12 (npp1)
55	<a href="#">c1o98A_</a>	Alignment	not modelled	99.8	28	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent <b>PDBTitle:</b> 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
56	<a href="#">c5kgmA_</a>	Alignment	not modelled	99.8	27	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent phosphoglycerate <b>PDBTitle:</b> 2.95a resolution structure of apo independent phosphoglycerate mutase2 from c. elegans (monoclinic form)
57	<a href="#">c3igzB_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> cofactor-independent phosphoglycerate mutase; <b>PDBTitle:</b> crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
58	<a href="#">c4my4A_</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent phosphoglycerate <b>PDBTitle:</b> crystal structure of phosphoglycerate mutase from staphylococcus2 aureus.
59	<a href="#">c5vpuA_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent phosphoglycerate <b>PDBTitle:</b> crystal structure of 2,3-bisphosphoglycerate-independent2 phosphoglycerate mutase bound to 3-phosphoglycerate, from3 acinetobacter baumannii
60	<a href="#">c2d1gB_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acid phosphatase; <b>PDBTitle:</b> structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
61	<a href="#">c1ew2A_</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatase; <b>PDBTitle:</b> crystal structure of a human phosphatase
62	<a href="#">d1k7ha_</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> Alkaline phosphatase
63	<a href="#">d1zeda1</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> Alkaline phosphatase
64	<a href="#">c2iucB_</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alkaline phosphatase; <b>PDBTitle:</b> structure of alkaline phosphatase from the antarctic bacterium tab5
65	<a href="#">d1y6va1</a>	Alignment	not modelled	99.1	21	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> Alkaline phosphatase
66	<a href="#">c3a52A_</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cold-active alkaline phosphatase; <b>PDBTitle:</b> crystal structure of cold-active alkaline phosphatase from2 psychrophile shewanella sp.
67	<a href="#">c3wbbB_</a>	Alignment	not modelled	98.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alkaline phosphatase; <b>PDBTitle:</b> structural characteristics of alkaline phosphatase from a moderately2 halophilic bacteria halomonas sp.593
68	<a href="#">c2w0yB_</a>	Alignment	not modelled	98.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alkaline phosphatase; <b>PDBTitle:</b> h.salinarum alkaline phosphatase
69	<a href="#">c3e2dB_</a>	Alignment	not modelled	98.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alkaline phosphatase; <b>PDBTitle:</b> the 1.4 a crystal structure of the large and cold-active vibrio sp.2 alkaline phosphatase
70	<a href="#">c2x98A_</a>	Alignment	not modelled	98.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alkaline phosphatase; <b>PDBTitle:</b> h.salinarum alkaline phosphatase
71	<a href="#">c2jkbA_</a>	Alignment	not modelled	98.3	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> sialidase b; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae nanb in2 complex with 2,7-anhydro-neu5ac
72	<a href="#">c4yw5A_</a>	Alignment	not modelled	98.3	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> neuraminidase c; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae nanc, complex with2 oseltamivir carboxylate
73	<a href="#">c2r1dF_</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> cell adhesion, splicing <b>Chain:</b> F: <b>PDB Molecule:</b> neurexin-1-beta; <b>PDBTitle:</b> crystal structure of rat neurexin 1beta in the ca2+ containing form
74	<a href="#">c3poyA_</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> neurexin-1-alpha; <b>PDBTitle:</b> crystal structure of the alpha-neurexin-1 ectodomain, Ins 2-6
75	<a href="#">c3qcwB_</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> neurexin-1-alpha; <b>PDBTitle:</b> structure of neurexin 1 alpha (domains Ins1-Ins6), no splice inserts
76	<a href="#">c2v73B_</a>	Alignment	not modelled	98.0	14	<b>PDB header:</b> sugar-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative exo-alpha-sialidase; <b>PDBTitle:</b> the structure of the family 40 cbm from c. perfringens

						nanj2 in complex with a sialic acid containing molecule
77	<a href="#">c3asiA_</a>	Alignment	not modelled	97.9	21	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> neurexin-1-alpha; <b>PDBTitle:</b> alpha-neurexin-1 ectodomain fragment; lns5-egf3-Ins6
78	<a href="#">c3v65A_</a>	Alignment	not modelled	97.8	13	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> agrin; <b>PDBTitle:</b> crystal structure of agrin and lrp4 complex
79	<a href="#">c6er3B_</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> bnr/asp-box repeat protein; <b>PDBTitle:</b> ruminococcus gnavus it-sialidase cbm40 bound to alpha2,3 sialyllactose
80	<a href="#">c2jd4B_</a>	Alignment	not modelled	97.7	12	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> laminin subunit alpha-1; <b>PDBTitle:</b> mouse laminin alpha1 chain, domains lg4-5
81	<a href="#">c1okqA_</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> laminin alpha 2 chain; <b>PDBTitle:</b> laminin alpha 2 chain lg4-5 domain pair, ca1 site mutant
82	<a href="#">c2c5dA_</a>	Alignment	not modelled	97.6	10	<b>PDB header:</b> signaling protein/receptor <b>Chain:</b> A: <b>PDB Molecule:</b> growth-arrest-specific protein 6 precursor; <b>PDBTitle:</b> structure of a minimal gas6-axl complex
83	<a href="#">c3vkfC_</a>	Alignment	not modelled	97.6	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> C: <b>PDB Molecule:</b> neurexin-1-beta; <b>PDBTitle:</b> crystal structure of neurexin 1beta/neuroigin 1 complex
84	<a href="#">c3vkfD_</a>	Alignment	not modelled	97.6	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> D: <b>PDB Molecule:</b> neurexin-1-beta; <b>PDBTitle:</b> crystal structure of neurexin 1beta/neuroigin 1 complex
85	<a href="#">d2r1da1</a>	Alignment	not modelled	97.6	20	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Laminin G-like module
86	<a href="#">c2wjsA_</a>	Alignment	not modelled	97.5	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> laminin subunit alpha-2; <b>PDBTitle:</b> crystal structure of the lg1-3 region of the laminin alpha22 chain
87	<a href="#">d1dyka1</a>	Alignment	not modelled	97.5	12	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Laminin G-like module
88	<a href="#">c5fraD_</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> sugar binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> sialidase; <b>PDBTitle:</b> cbm40_cpf0721-6'sl
89	<a href="#">d2erfa1</a>	Alignment	not modelled	97.4	15	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Laminin G-like module
90	<a href="#">c5mc9A_</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> laminin subunit alpha-1; <b>PDBTitle:</b> crystal structure of the heterotrimeric integrin-binding region of2 laminin-111
91	<a href="#">c2sliA_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> intramolecular trans-sialidase; <b>PDBTitle:</b> leech intramolecular trans-sialidase complexed with 2,7-2 anhydro-neu5ac, the reaction product
92	<a href="#">c1za4A_</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> thrombospondin 1; <b>PDBTitle:</b> crystal structure of the thrombospondin-1 n-terminal domain2 in complex with arixtra
93	<a href="#">c2r16A_</a>	Alignment	not modelled	97.3	18	<b>PDB header:</b> cell adhesion, splicing <b>Chain:</b> A: <b>PDB Molecule:</b> neurexin-1-alpha; <b>PDBTitle:</b> crystal structure of bovine neurexin 1 alpha lns/ig domain 4 (with no2 splice insert)
94	<a href="#">c1qu0D_</a>	Alignment	not modelled	97.2	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> laminin alpha2 chain; <b>PDBTitle:</b> crystal structure of the fifth laminin g-like module of the2 mouse laminin alpha2 chain
95	<a href="#">c1qu0A_</a>	Alignment	not modelled	97.2	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> laminin alpha2 chain; <b>PDBTitle:</b> crystal structure of the fifth laminin g-like module of the2 mouse laminin alpha2 chain
96	<a href="#">c3fpj_</a>	Alignment	not modelled	97.2	14	<b>PDB header:</b> sugar binding protein <b>Chain:</b> J: <b>PDB Molecule:</b> sap-like pentraxin; <b>PDBTitle:</b> crystal structure of native heptameric sap-like pentraxin2 from limulus polyphemus
97	<a href="#">c4dqaA_</a>	Alignment	not modelled	97.1	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative carbohydrate binding protein2 (bacova_03559) from bacteroides ovatus atcc 8483 at 1.50 a resolution
98	<a href="#">c5ho0A_</a>	Alignment	not modelled	97.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular arabinanase; <b>PDBTitle:</b> crystal structure of abna (closed conformation), a gh43 extracellular2 arabinanase from geobacillus stearothermophilus
99	<a href="#">c3mw3A_</a>	Alignment	not modelled	97.1	18	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> neurexin-2-beta; <b>PDBTitle:</b> crystal structure of beta-neurexin 2 with the splice insert 4
100	<a href="#">d2sli1</a>	Alignment	not modelled	96.8	10	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Leech intramolecular trans-sialidase, N-terminal domain
101	<a href="#">d1q56a_</a>	Alignment	not modelled	96.8	17	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Laminin G-like module
102	<a href="#">c2h0bC_</a>	Alignment	not modelled	96.8	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> C: <b>PDB Molecule:</b> neurexin-1-alpha; <b>PDBTitle:</b> crystal structure of the second lns/ig domain from neurexin 1 alpha <b>PDB header:</b> transcription

103	<a href="#">c3pveA</a>	Alignment	not modelled	96.7	21	<b>Chain:</b> A: <b>PDB Molecule:</b> agrin, agrin protein; <b>PDBTitle:</b> crystal structure of the g2 domain of agrin from mus musculus
104	<a href="#">c4qvsA</a>	Alignment	not modelled	96.7	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> s-layer domain-containing protein; <b>PDBTitle:</b> 2.1 angstrom resolution crystal structure of s-layer domain-containing2 protein (residues 221-444) from clostridium thermocellum atcc 27405
105	<a href="#">c1qu0C</a>	Alignment	not modelled	96.6	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> laminin alpha2 chain; <b>PDBTitle:</b> crystal structure of the fifth laminin g-like module of the2 mouse laminin alpha2 chain
106	<a href="#">c1z0hB</a>	Alignment	not modelled	96.6	7	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> botulinum neurotoxin type b; <b>PDBTitle:</b> n-terminal helix reorients in recombinant c-fragment of2 clostridium botulinum type b
107	<a href="#">d1pz7a</a>	Alignment	not modelled	96.6	15	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Laminin G-like module
108	<a href="#">c3sh5A</a>	Alignment	not modelled	96.4	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lg3 peptide; <b>PDBTitle:</b> calcium-bound laminin g like domain 3 from human perlecan
109	<a href="#">c5oltA</a>	Alignment	not modelled	96.4	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose biosynthesis protein bcsq; <b>PDBTitle:</b> crystal structure of the extramembrane domain of the cellulose2 biosynthetic protein bcsq from salmonella typhimurium
110	<a href="#">c1yynA</a>	Alignment	not modelled	96.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tetanus toxin; <b>PDBTitle:</b> a common binding site for disialyllactose and a tri-peptide2 in the c-fragment of tetanus neurotoxin
111	<a href="#">d1epwa1</a>	Alignment	not modelled	96.3	6	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Clostridium neurotoxins, the second last domain
112	<a href="#">d1n1ta1</a>	Alignment	not modelled	96.2	12	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Trypanosoma sialidase, C-terminal domain
113	<a href="#">c2vu9A</a>	Alignment	not modelled	96.2	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> botulinum neurotoxin a heavy chain; <b>PDBTitle:</b> crystal structure of botulinum neurotoxin serotype a2 binding domain in complex with gt1b
114	<a href="#">c4c1wA</a>	Alignment	not modelled	96.1	9	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> neuraminidase; <b>PDBTitle:</b> carbohydrate binding domain from streptococcus pneumoniae2 hana sialidase complexed with 3'-sialyllactose
115	<a href="#">d2ah2a1</a>	Alignment	not modelled	96.0	12	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Trypanosoma sialidase, C-terminal domain
116	<a href="#">d1h30a2</a>	Alignment	not modelled	96.0	13	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Laminin G-like module
117	<a href="#">d1h30a1</a>	Alignment	not modelled	95.7	14	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Laminin G-like module
118	<a href="#">c3iddA</a>	Alignment	not modelled	95.4	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent <b>PDBTitle:</b> cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
119	<a href="#">d1pz8a</a>	Alignment	not modelled	95.4	16	<b>Fold:</b> Concanavalin A-like lectins/glucanases <b>Superfamily:</b> Concanavalin A-like lectins/glucanases <b>Family:</b> Laminin G-like module
120	<a href="#">c4pboA</a>	Alignment	not modelled	95.2	12	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> c-reactive protein; <b>PDBTitle:</b> crystal structure of zebrafish short-chain pentraxin protein without2 calcium ions