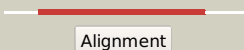

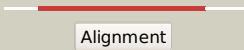

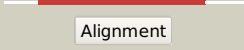
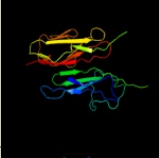

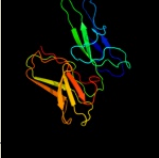


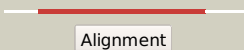


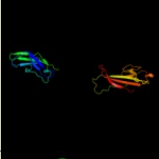



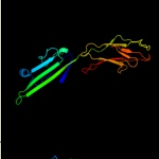

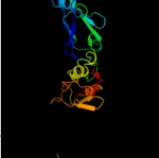
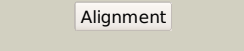
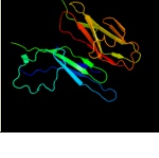
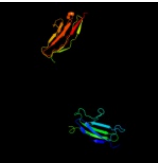
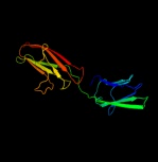
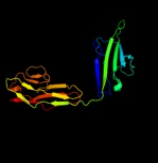


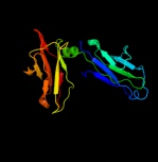





Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A1YIY0
Date	Tue Jul 30 13:19:15 BST 2013
Unique Job ID	1035bc4b501530df

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dmkA_	 Alignment		100.0	14	PDB header: cell adhesion Chain: A: PDB Molecule: down syndrome cell adhesion molecule (dscam) isoform PDBTitle: crystal structure of down syndrome cell adhesion molecule (dscam)2 isoform 1.30.30, n-terminal eight ig domains
2	c2om5A_	 Alignment		100.0	20	PDB header: cell adhesion Chain: A: PDB Molecule: contactin 2; PDBTitle: n-terminal fragment of human tax1
3	c3jxaA_	 Alignment		100.0	21	PDB header: cell adhesion Chain: A: PDB Molecule: contactin 4; PDBTitle: immunoglobulin domains 1-4 of mouse cntn4
4	c4k0vA_	 Alignment		100.0	12	PDB header: signaling protein/transferase Chain: A: PDB Molecule: tek tyrosine kinase variant; PDBTitle: structural basis for angiopoietin-1 mediated signaling initiation
5	c1p6fA_	 Alignment		100.0	9	PDB header: immune system Chain: A: PDB Molecule: natural cytotoxicity triggering receptor 1; PDBTitle: structure of the human natural cytotoxicity receptor nkp46
6	c1ollA_	 Alignment		99.9	9	PDB header: immune system/receptor Chain: A: PDB Molecule: nk receptor; PDBTitle: extracellular region of the human receptor nkp46
7	c3shsA_	 Alignment		99.9	18	PDB header: viral protein Chain: A: PDB Molecule: hoc head outer capsid protein; PDBTitle: three n-terminal domains of the bacteriophage rb49 highly immunogenic2 outer capsid protein (hoc)
8	c1efxE_	 Alignment		99.9	14	PDB header: immune system Chain: E: PDB Molecule: natural killer cell receptor kir2dl2; PDBTitle: structure of a complex between the human natural killer2 cell receptor kir2dl2 and a class i mhc ligand hla-cw3
9	c3o3uN_	 Alignment		99.9	16	PDB header: transport protein, signaling protein Chain: N: PDB Molecule: maltose-binding periplasmic protein, advanced glycosylation PDBTitle: crystal structure of human receptor for advanced glycation endproducts2 (rage)
10	c1e4jA_	 Alignment		99.9	16	PDB header: immune system Chain: A: PDB Molecule: low affinity immunoglobulin gamma fc receptor PDBTitle: crystal structure of the soluble human fc-gamma2 receptor iii
11	c3p3yA_	 Alignment		99.9	19	PDB header: cell adhesion Chain: A: PDB Molecule: neurofascin; PDBTitle: crystal structure of neurofascin homophilic adhesion complex in space2 group p6522

12	c2y25C_	Alignment		99.9	20	PDB header: structural protein Chain: C: PDB Molecule: myomesin; PDBTitle: crystal structure of the myomesin domains my11-my13
13	c1e07A_	Alignment		99.9	12	PDB header: glycoprotein Chain: A: PDB Molecule: carcinoembryonic antigen; PDBTitle: model of human carcinoembryonic antigen by homology2 modelling and curve-fitting to experimental solution3 scattering data
14	c3oq3B_	Alignment		99.9	19	PDB header: cytokine/viral protein Chain: B: PDB Molecule: ifn-alpha/beta binding protein c12r; PDBTitle: structural basis of type-i interferon sequestration by a poxvirus2 decoy receptor
15	c2gy7B_	Alignment		99.9	12	PDB header: signaling protein Chain: B: PDB Molecule: angiotensin-1 receptor; PDBTitle: angiotensin-2/tie2 complex crystal structure
16	c3lafA_	Alignment		99.9	15	PDB header: apoptosis Chain: A: PDB Molecule: deleted in colorectal cancer; PDBTitle: structure of dcc, a netrin-1 receptor
17	c3sqjC_	Alignment		99.9	17	PDB header: immune system Chain: C: PDB Molecule: human fcg3a receptor; PDBTitle: unique carbohydrate-carbohydrate interactions are required for high2 affinity binding between fcgiii and antibodies lacking core fucose
18	c1g0xA_	Alignment		99.9	17	PDB header: immune system Chain: A: PDB Molecule: leucocyte immunoglobulin-like receptor-1; PDBTitle: crystal structure of the ligand binding domain of lir-12 (iit2)
19	c1im9D_	Alignment		99.9	15	PDB header: immune system Chain: D: PDB Molecule: killer cell immunoglobulin-like receptor 2d11; PDBTitle: crystal structure of the human natural killer cell2 inhibitory receptor kir2d11 bound to its mhc ligand hla-cw4
20	c3qs7F_	Alignment		99.9	12	PDB header: cytokine/signaling protein Chain: F: PDB Molecule: fl cytokine receptor; PDBTitle: crystal structure of a human fit3 ligand-receptor ternary complex
21	c1sy6A_	Alignment	not modelled	99.9	16	PDB header: signaling protein/antibiotic Chain: A: PDB Molecule: t-cell surface glycoprotein cd3 gamma/epsilon PDBTitle: crystal structure of cd3gammaepsilon heterodimer in complex2 with okt3 fab fragment
22	c3p2tA_	Alignment	not modelled	99.9	16	PDB header: immune system Chain: A: PDB Molecule: leukocyte immunoglobulin-like receptor subfamily b member PDBTitle: crystal structure of leukocyte ig-like receptor liirb4 (iit3/lir-2 5/cd85k)
23	c3rjdA_	Alignment	not modelled	99.9	19	PDB header: immune system Chain: A: PDB Molecule: high affinity immunoglobulin gamma fc receptor i; PDBTitle: crystal structure of fc ri and its implication to high affinity2 immunoglobulin g binding
24	c3dmkB_	Alignment	not modelled	99.9	19	PDB header: cell adhesion Chain: B: PDB Molecule: down syndrome cell adhesion molecule (dscam) isoform PDBTitle: crystal structure of down syndrome cell adhesion molecule (dscam)2 isoform 1.30.30, n-terminal eight ig domains
25	c3vh8H_	Alignment	not modelled	99.9	15	PDB header: immune system Chain: H: PDB Molecule: killer cell immunoglobulin-like receptor 3d11; PDBTitle: kir3d11 in complex with hla-b*5701
26	c3rbsA_	Alignment	not modelled	99.9	11	PDB header: contractile protein Chain: A: PDB Molecule: myomesin-1; PDBTitle: crystal structure of the myomesin domains 10 and 11
27	c2qi7B_	Alignment	not modelled	99.9	17	PDB header: blood clotting, cell adhesion Chain: B: PDB Molecule: gpvi protein; PDBTitle: crystal structure of human platelet glycoprotein vi (gpvi)
						PDB header: killer cell inhibitory receptor

28	c1b6uA	Alignment	not modelled	99.9	15	Chain: A: PDB Molecule: p58 killer cell inhibitory receptor; PDBTitle: crystal structure of the human killer cell inhibitory2 receptor (kir2dl3) specific for hla-cw3 related alleles
29	c1o0vA	Alignment	not modelled	99.9	17	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin heavy chain epsilon-1; PDBTitle: the crystal structure of ige fc reveals an asymmetrically bent2 conformation
30	c3f8uB	Alignment	not modelled	99.9	12	PDB header: immune system/isomerase Chain: B: PDB Molecule: tapasin; PDBTitle: tapasin/erp57 heterodimer
31	c1iamA	Alignment	not modelled	99.9	12	PDB header: viral protein receptor Chain: A: PDB Molecule: intercellular adhesion molecule-1; PDBTitle: structure of the two amino-terminal domains of human intercellular2 adhesion molecule-1, icam-1
32	c1ovzB	Alignment	not modelled	99.9	15	PDB header: immune system Chain: B: PDB Molecule: immunoglobulin alpha fc receptor; PDBTitle: crystal structure of human fcari
33	c3alpB	Alignment	not modelled	99.9	13	PDB header: cell adhesion Chain: B: PDB Molecule: poliovirus receptor-related protein 1; PDBTitle: cell adhesion protein
34	c1fcgA	Alignment	not modelled	99.9	16	PDB header: immune system, membrane protein Chain: A: PDB Molecule: protein (fc receptor fc(gamma)riia); PDBTitle: ectodomain of human fc gamma receptor, fcgr1ia
35	c2d3vA	Alignment	not modelled	99.9	16	PDB header: immune system Chain: A: PDB Molecule: leukocyte immunoglobulin-like receptor subfamily PDBTitle: crystal structure of leukocyte ig-like receptor a52 (lilra5/lir9/ilt11)
36	c2yd7A	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: ptprd protein; PDBTitle: crystal structure of the n-terminal ig1-2 module of human receptor2 protein tyrosine phosphatase delta
37	c1p53A	Alignment	not modelled	99.9	11	PDB header: cell adhesion Chain: A: PDB Molecule: intercellular adhesion molecule-1; PDBTitle: the crystal structure of icam-1 d3-d5 fragment
38	c1j89D	Alignment	not modelled	99.9	17	PDB header: immune system Chain: D: PDB Molecule: high affinity immunoglobulin epsilon receptor alpha- PDBTitle: human high affinity fc receptor fc(epsilon)ri(alpha), tetragonal2 crystal form 2
39	c2y23A	Alignment	not modelled	99.9	11	PDB header: structural protein Chain: A: PDB Molecule: myomesin; PDBTitle: crystal structure of the myomesin domains my9-my11
40	c1mq8C	Alignment	not modelled	99.9	12	PDB header: immune system Chain: C: PDB Molecule: intercellular adhesion molecule-1; PDBTitle: crystal structure of alpha1 i domain in complex with icam-1
41	c3b43A	Alignment	not modelled	99.9	16	PDB header: structural protein Chain: A: PDB Molecule: titin; PDBTitle: i-band fragment i65-i70 from titin
42	c3mjgX	Alignment	not modelled	99.9	13	PDB header: hormone/transferase Chain: X: PDB Molecule: beta-type platelet-derived growth factor receptor; PDBTitle: the structure of a platelet derived growth factor receptor complex
43	c2o26X	Alignment	not modelled	99.9	13	PDB header: cytokine/signaling protein Chain: X: PDB Molecule: mast/stem cell growth factor receptor; PDBTitle: structure of a class iii rtk signaling assembly
44	c1bihA	Alignment	not modelled	99.9	15	PDB header: insect immunity Chain: A: PDB Molecule: hemolin; PDBTitle: crystal structure of the insect immune protein hemolin: a2 new domain arrangement with implications for homophilic3 adhesion
45	c3chnD	Alignment	not modelled	99.9	12	PDB header: immune system Chain: D: PDB Molecule: ig alpha-1 chain c region; PDBTitle: solution structure of human secretory iga1
46	c1zvoC	Alignment	not modelled	99.9	16	PDB header: immune system Chain: C: PDB Molecule: myeloma immunoglobulin d delta; PDBTitle: semi-extended solution structure of human myeloma2 immunoglobulin d determined by constrained x-ray scattering
47	c1dgiR	Alignment	not modelled	99.9	17	PDB header: virus/viral protein, receptor Chain: R: PDB Molecule: poliovirus receptor; PDBTitle:
48	c2yd3A	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: receptor-type tyrosine-protein phosphatase s; PDBTitle: crystal structure of the n-terminal ig1-2 module of human2 receptor protein tyrosine phosphatase sigma
49	c2v9gA	Alignment	not modelled	99.9	19	PDB header: receptor Chain: A: PDB Molecule: roundabout homolog 1; PDBTitle: first and second ig domains from human robo1
50	c3chnS	Alignment	not modelled	99.9	10	PDB header: immune system Chain: S: PDB Molecule: secretory component; PDBTitle: solution structure of human secretory iga1
51	c4hjjH	Alignment	not modelled	99.9	16	PDB header: immune system Chain: H: PDB Molecule: anti-il12 anti-il18 dfab heavy chain; PDBTitle: structure reveals function of the dual variable domain immunoglobulin2 (dvd-ig) molecule
52	c3bn3B	Alignment	not modelled	99.9	13	PDB header: cell adhesion, immune system Chain: B: PDB Molecule: intercellular adhesion molecule 5; PDBTitle: crystal structure of icam-5 in complex with al i domain
53	c2v5mA	Alignment	not modelled	99.9	16	PDB header: cell adhesion Chain: A: PDB Molecule: dscam; PDBTitle: structural basis for dscam isoform specificity

54	c2yd9A	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: receptor-type tyrosine-protein phosphatase s; PDBTitle: crystal structure of the n-terminal ig1-3 module of human receptor2 protein tyrosine phosphatase sigma
55	c1hzhK	Alignment	not modelled	99.9	10	PDB header: immune system Chain: K: PDB Molecule: immunoglobulin heavy chain; PDBTitle: crystal structure of the intact human igg b12 with broad and potent2 activity against primary hiv-1 isolates: a template for hiv vaccine3 design
56	c4hjlL	Alignment	not modelled	99.9	14	PDB header: immune system Chain: L: PDB Molecule: anti-il12 anti-il18 dfab light chain; PDBTitle: structure reveals function of the dual variable domain immunoglobulin2 (dvd-ig) molecule
57	c2rcjD	Alignment	not modelled	99.9	10	PDB header: immune system Chain: D: PDB Molecule: light chain; PDBTitle: solution structure of human immunoglobulin m
58	c3sgjA	Alignment	not modelled	99.9	11	PDB header: immune system Chain: A: PDB Molecule: human fc fragment; PDBTitle: unique carbohydrate-carbohydrate interactions are required for high2 affinity binding between fcgiii and antibodies lacking core fucose
59	c2yd4A	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase crypalha1 isoform; PDBTitle: crystal structure of the n-terminal ig1-2 module of chicken receptor2 protein tyrosine phosphatase sigma
60	c2yd2A	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: receptor-type tyrosine-protein phosphatase s; PDBTitle: crystal structure of the n-terminal ig1-2 module of human2 receptor protein tyrosine phosphatase sigma
61	c1qgc4	Alignment	not modelled	99.9	12	PDB header: virus/immune system Chain: 4: PDB Molecule: protein (immunoglobulin); PDBTitle: structure of the complex of an fab fragment of a neutralizing antibody2 with foot and mouth disease virus
62	c2ec8A	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: mast/stem cell growth factor receptor; PDBTitle: crystal structure of the extracellular domain of the receptor2 tyrosine kinase, kit
63	c4fomA	Alignment	not modelled	99.9	16	PDB header: cell adhesion Chain: A: PDB Molecule: poliovirus receptor-related protein 3; PDBTitle: crystal structure of human nectin-3 full ectodomain (d1-d3)
64	c1vcaA	Alignment	not modelled	99.9	14	PDB header: cell adhesion protein Chain: A: PDB Molecule: human vascular cell adhesion molecule-1; PDBTitle: crystal structure of an integrin-binding fragment of2 vascular cell adhesion molecule-1 at 1.8 angstroms3 resolution
65	c1l6zA	Alignment	not modelled	99.9	20	PDB header: cell adhesion Chain: A: PDB Molecule: biliary glycoprotein c; PDBTitle: crystal structure of murine ceacam1a[1,4]: a coronavirus receptor and2 cell adhesion molecule in the cea family
66	c3pxjD	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: D: PDB Molecule: tyrosine-protein phosphatase lar; PDBTitle: tandem ig repeats of dlar
67	c3nl4L	Alignment	not modelled	99.9	13	PDB header: immune system Chain: L: PDB Molecule: antigen binding fragment, immunoglobulin igg - light chain; PDBTitle: crystal structure of amyloid prefibrillar oligomer-specific rabbit fab
68	c3qs9F	Alignment	not modelled	99.9	13	PDB header: cytokine/signaling protein Chain: F: PDB Molecule: fl cytokine receptor; PDBTitle: crystal structure of a human fit3 ligand-receptor ternary complex
69	c2wimA	Alignment	not modelled	99.9	18	PDB header: cell adhesion Chain: A: PDB Molecule: neural cell adhesion molecule 2; PDBTitle: crystal structure of ncam2 ig1-3
70	c3do3A	Alignment	not modelled	99.9	12	PDB header: immune system Chain: A: PDB Molecule: ig gamma-1 chain c region; PDBTitle: human 1gg1 fc fragment, 2.5 angstrom structure
71	c3v2aR	Alignment	not modelled	99.9	13	PDB header: hormone/signaling protein Chain: R: PDB Molecule: vascular endothelial growth factor receptor 2; PDBTitle: vegfr-2/vegfr-a complex structure
72	c2r15A	Alignment	not modelled	99.9	17	PDB header: contractile protein Chain: A: PDB Molecule: myomesin-1; PDBTitle: crystal structure of the myomesin domains 12 and 13
73	c1zxqA	Alignment	not modelled	99.9	16	PDB header: cell adhesion Chain: A: PDB Molecule: intercellular adhesion molecule-2; PDBTitle: the crystal structure of icam-2
74	c3v6bR	Alignment	not modelled	99.9	13	PDB header: hormone/signaling protein Chain: R: PDB Molecule: vascular endothelial growth factor receptor 2; PDBTitle: vegfr-2/vegfr-e complex structure
75	c2rikA	Alignment	not modelled	99.9	16	PDB header: structural protein Chain: A: PDB Molecule: titin; PDBTitle: i-band fragment i67-i69 from titin
76	c2v5rB	Alignment	not modelled	99.9	13	PDB header: cell adhesion Chain: B: PDB Molecule: dscam; PDBTitle: structural basis for dscam isoform specificity
77	c2x1xR	Alignment	not modelled	99.9	13	PDB header: hormone/signaling protein Chain: R: PDB Molecule: vascular endothelial growth factor receptor 2; PDBTitle: crystal structure of vegf-c in complex with domains 2 and 32 of vegfr2 in a tetragonal crystal form
78	c1ilcB	Alianment	not modelled	99.9	14	PDB header: immune system Chain: B: PDB Molecule: ig gamma-2a chain c region;

						PDBTitle: non-fcrrn binding fc fragment of rat igg2a
79	c1igyB_	Alignment	not modelled	99.9	13	PDB header: immunoglobulin Chain: B: PDB Molecule: igg1 intact antibody mab61.1.3; PDBTitle: structure of immunoglobulin
80	c2wahA_	Alignment	not modelled	99.9	13	PDB header: immune system Chain: A: PDB Molecule: sig gamma-1 chain c region; PDBTitle: crystal structure of an igg1 fc glycoform (man9glcnac2)
81	c2ql1A_	Alignment	not modelled	99.9	14	PDB header: immune system Chain: A: PDB Molecule: ighm protein; PDBTitle: structural characterization of a mutated, adcc-enhanced human fc2 fragment
82	c1djsA_	Alignment	not modelled	99.9	19	PDB header: hormone/growth factor/receptor Chain: A: PDB Molecule: protein (fibroblast growth factor receptor 2); PDBTitle: ligand-binding portion of fibroblast growth factor receptor 2 in2 complex with fgf1
83	c3ejjX_	Alignment	not modelled	99.9	15	PDB header: cytokine/signaling protein Chain: X: PDB Molecule: macrophage colony-stimulating factor 1 receptor; PDBTitle: structure of m-csf bound to the first three domains of fms
84	c2j6eA_	Alignment	not modelled	99.9	12	PDB header: immune system Chain: A: PDB Molecule: sig gamma-1 chain c region; PDBTitle: crystal structure of an autoimmune complex between a human2 igm rheumatoid factor and igg1 fc reveals a novel fc3 epitope and evidence for affinity maturation
85	c2wngA_	Alignment	not modelled	99.9	12	PDB header: cell adhesion Chain: A: PDB Molecule: tyrosine-protein phosphatase non-receptor type PDBTitle: complete extracellular structure of human signal regulatory2 protein (sirp) alpha
86	c3qs9E_	Alignment	not modelled	99.9	12	PDB header: cytokine/signaling protein Chain: E: PDB Molecule: fl cytokine receptor; PDBTitle: crystal structure of a human fit3 ligand-receptor ternary complex
87	c3dnkA_	Alignment	not modelled	99.9	12	PDB header: immune system Chain: A: PDB Molecule: ighm protein; PDBTitle: enzyme deglycosylated human igg1 fc fragment
88	c4dz8B_	Alignment	not modelled	99.9	11	PDB header: immune system Chain: B: PDB Molecule: sig gamma-1 chain c region; PDBTitle: human igg1 fc fragment heterodimer
89	c2druA_	Alignment	not modelled	99.9	17	PDB header: immune system Chain: A: PDB Molecule: chimera of cd48 antigen and t-cell surface antigen cd2; PDBTitle: crystal structure and binding properties of the cd2 and cd244 (2b4)2 binding protein, cd48
90	c4fn0B_	Alignment	not modelled	99.9	15	PDB header: cell adhesion Chain: B: PDB Molecule: poliovirus receptor-related protein 2; PDBTitle: crystal structure of mouse nectin-2 extracellular fragment d1-d2, 2nd2 crystal form
91	c1za6H_	Alignment	not modelled	99.9	14	PDB header: immune system Chain: H: PDB Molecule: igg heavy chain; PDBTitle: the structure of an antitumor ch2-domain-deleted humanized2 antibody
92	c1z7zl_	Alignment	not modelled	99.9	13	PDB header: virus/receptor Chain: I: PDB Molecule: intercellular adhesion molecule-1; PDBTitle: cryo-em structure of human coxsackievirus a21 complexed with five2 domain icam-1kilifi
93	c1iraY_	Alignment	not modelled	99.9	18	PDB header: complex (cytokine receptor/antagonist) Chain: Y: PDB Molecule: interleukin-1 receptor; PDBTitle: complex of the interleukin-1 receptor with the interleukin-1 receptor2 antagonist (il1ra)
94	c1w72L_	Alignment	not modelled	99.9	12	PDB header: immune system Chain: L: PDB Molecule: hyb3 light chain; PDBTitle: crystal structure of hla-a1:mage-a1 in complex with fab-2 hyb3
95	c1igtB_	Alignment	not modelled	99.9	13	PDB header: immunoglobulin Chain: B: PDB Molecule: igg2a intact antibody - mab231; PDBTitle: structure of immunoglobulin
96	c1hezD_	Alignment	not modelled	99.9	10	PDB header: antibody Chain: D: PDB Molecule: heavy chain of ig; PDBTitle: antibody-antigen complex
97	c3ftjB_	Alignment	not modelled	99.9	11	PDB header: immune system Chain: B: PDB Molecule: sig gamma-1 chain c region; PDBTitle: crystal structure of a human fc fragment engineered for extended serum2 half-life
98	c2pf6A_	Alignment	not modelled	99.9	21	PDB header: cell adhesion Chain: A: PDB Molecule: lutheran blood group glycoprotein; PDBTitle: lutheran glycoprotein, n-terminal domains 1 and 2
99	c4iiqC_	Alignment	not modelled	99.9	22	PDB header: immune system Chain: C: PDB Molecule: beta-2-microglobulin, mhc class i-related protein; PDBTitle: crystal structure of a human mait tcr in complex with bovine mr1
100	c3sgjB_	Alignment	not modelled	99.8	10	PDB header: immune system Chain: B: PDB Molecule: human fc fragment; PDBTitle: unique carbohydrate-carbohydrate interactions are required for high2 affinity binding between fcgiii and antibodies lacking core fucose
101	c3pxhA_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: receptor-type tyrosine-protein phosphatase f; PDBTitle: tandem ig domains of tyrosine phosphatase lar
102	c1hngB_	Alignment	not modelled	99.8	13	PDB header: lymphocyte adhesion glycoprotein Chain: B: PDB Molecule: cd2; PDBTitle: crystal structure at 2.8 angstroms resolution of a soluble2 form of the cell adhesion molecule cd2
						PDB header: immune system

103	c1ypzE_	Alignment	not modelled	99.8	16	Chain: E: PDB Molecule: t cell receptor delta; PDBTitle: immune receptor
104	c1cczA_	Alignment	not modelled	99.8	17	PDB header: glycoprotein Chain: A: PDB Molecule: protein (cd58); PDBTitle: crystal structure of the cd2-binding domain of cd58 (lymphocyte2 function-associated antigen 3) at 1.8-a resolution
105	c2gj7A_	Alignment	not modelled	99.8	12	PDB header: immune system/virus/viral protein Chain: A: PDB Molecule: ig gamma-1 chain c region; PDBTitle: crystal structure of a ge-gi/fc complex
106	c2gj7B_	Alignment	not modelled	99.8	12	PDB header: immune system/virus/viral protein Chain: B: PDB Molecule: ig gamma-1 chain c region; PDBTitle: crystal structure of a ge-gi/fc complex
107	c3dnkB_	Alignment	not modelled	99.8	12	PDB header: immune system Chain: B: PDB Molecule: ighm protein; PDBTitle: enzyme deglycosylated human igg1 fc fragment
108	c3mlwL_	Alignment	not modelled	99.8	13	PDB header: immune system Chain: L: PDB Molecule: human monoclonal anti-hiv-1 gp120 v3 antibody 1006-15d fab PDBTitle: crystal structure of anti-hiv-1 v3 fab 1006-15d in complex with an mn2 v3 peptide
109	c1pkqF_	Alignment	not modelled	99.8	12	PDB header: immune system Chain: F: PDB Molecule: (8-18c5) chimeric fab, light chain; PDBTitle: myelin oligodendrocyte glycoprotein-(8-18c5) fab-complex
110	c2e9wB_	Alignment	not modelled	99.8	15	PDB header: transferase/hormone Chain: B: PDB Molecule: mast/stem cell growth factor receptor; PDBTitle: crystal structure of the extracellular domain of kit in complex with2 stem cell factor (scf)
111	c3s7gD_	Alignment	not modelled	99.8	13	PDB header: immune system Chain: D: PDB Molecule: ig gamma-1 chain c region; PDBTitle: aglycosylated human igg1 fc fragment
112	c3o4oB_	Alignment	not modelled	99.8	14	PDB header: immune system Chain: B: PDB Molecule: interleukin-1 receptor accessory protein; PDBTitle: crystal structure of an interleukin-1 receptor complex
113	c1qokA_	Alignment	not modelled	99.8	20	PDB header: immunoglobulin Chain: A: PDB Molecule: mfe-23 recombinant antibody fragment; PDBTitle: mfe-23 an anti-carcinoembryonic antigen single-chain fv2 antibody
114	c2vu0B_	Alignment	not modelled	99.8	13	PDB header: immune system Chain: B: PDB Molecule: ig gamma chain c region; PDBTitle: crystal structure of the rabbit igg fc fragment
115	c4acpA_	Alignment	not modelled	99.8	14	PDB header: immune system Chain: A: PDB Molecule: ig gamma-1 chain c region; PDBTitle: deactivation of human igg1 fc by endoglycosidase treatment
116	c1qseD_	Alignment	not modelled	99.8	11	PDB header: immune system Chain: D: PDB Molecule: protein (hman t-cell receptor); PDBTitle: structure of human a6-tcr bound to hla-a2 complexed with2 altered htlv-1 tax peptide v7r
117	c1hnfA_	Alignment	not modelled	99.8	14	PDB header: t lymphocyte adhesion glycoprotein Chain: A: PDB Molecule: cd2; PDBTitle: crystal structure of the extracellular region of the human cell2 adhesion molecule cd2 at 2.5 angstroms resolution
118	c3ay4A_	Alignment	not modelled	99.8	13	PDB header: immune system Chain: A: PDB Molecule: ig gamma-1 chain c region; PDBTitle: crystal structure of nonfucosylated fc complexed with bis-glycosylated2 soluble form of fc gamma receptor iiiia
119	c1aakL_	Alignment	not modelled	99.8	15	PDB header: immunoglobulin Chain: L: PDB Molecule: fab b7-15a2; PDBTitle: three-dimensional structure of a human fab with high2 affinity for tetanus toxoid
120	c3b5hB_	Alignment	not modelled	99.8	12	PDB header: cell invasion Chain: B: PDB Molecule: cervical emmprin; PDBTitle: crystal structure of the extracellular portion of hab18g/cd147