Supporting Information

Sok et al. 10.1073/pnas.1415789111

SI Materials and Methods

Antibody Nomenclature. The previously isolated PGT antibodies from the Protocol G cohort were isolated through Theraclone screening, and thus were named "PGT." To distinguish between antibodies isolated from Theraclone (by B-cell culture) and antibodies isolated by investigators of this study (by antigen selection), we have named the newly isolated variants "PGDM." We start the series with "14" to indicate that they are related to the PGT140 series, but we have added an extra digit to the end of the name because we have >10 antibodies. The somatic variants therefore are named PGDM1400–1412.

Human Specimens. PBMCs were obtained from donor 84, an HIV-1-infected donor from the IAVI Protocol G cohort (1). All human samples were collected with written informed consent under clinical protocols approved by the Republic of Rwanda National Ethics Committee, the Emory University Institutional Review Board, the University of Zambia Research Ethics Committee, the Charing Cross Research Ethics Committee, the Uganda Virus Research Institute Science and Ethics Committee, the University of New South Wales Research Ethics Committee, St. Vincent's Hospital and Eastern Sydney Area Health Service, Kenyatta National Hospital Ethics and Research Committee, University of Cape Town Research Ethics Committee, the International Institutional Review Board, the Mahidol University Ethics Committee, the Walter Reed Army Institute of Research Institutional Review Board, and the Ivory Coast Comité National d'Éthique des Sciences de la Vie et de la Santé.

Data and Materials Availability. Gene sequences of the reported antibodies have been deposited in GenBank under the accession numbers KP006370–KP006382 for heavy-chain sequences and KP006383–KP006395 for kappa-chain sequences.

Construct Design. For this study, a variant of the recombinant envelope protein BG505 SOSIP.664 gp140 trimer (2) bearing an avi tag at the C terminus of the gp41 ectodomain (gp41ECTO) was made by adding the amino acid sequence GSGLNDI-FEAQKIEWHE after residue 664 in gp41ECTO and preceding the stop codon. This protein is designated "SOSIP.664-Avi gp140." A monomeric BG505 gp120 with a sequence identical to the gp120 components of the gp140 trimer also was constructed with an avi tag, designated "BG505-avi" and includes the L111A substitution to decrease gp120 dimer formation (3, 4). BG505 SOSIP.664 containing a polyhistidine tag (BG505 SOSIP.664-His gp140) was used as described previously (2).

Recombinant Env Trimer Expression. The recombinant envelope proteins BG505 SOSIP.664-avi gp140, BG505 SOSIP.664-His gp140, and BG505-avi gp120 were expressed in HEK293F cells (Invitrogen) as described previously (2). Briefly, HEK293F cells were maintained in FreeStyle medium (Invitrogen). For gp140 trimer production, HEK293F cells were seeded at a density of 0.5×10^6 /mL. After 24 h, cells were transfected with 1 mg of 293Fectin (Invitrogen) with 300 µg of Env plasmid and 75 µg of furin plasmid in Opti-MEM (Life Technologies) according to the manufacturer's protocol. Kifunensine-treated proteins were produced by adding kifunensine (Tocris) to HEK293F cells at a final concentration of 25 µM on the day of transfection. Culture supernatants were harvested 6–7 d after transfection. SDS/ PAGE and Blue Native-PAGE were performed as described previously (2). Recombinant Env Trimer Purification. BG505 SOSIP.664-avi gp140 and BG505 SOSIP.664-His gp140 were purified by affinity chromatography using a 2G12 column as described previously (2). BG505-avi gp120 proteins were purified using a Galanthus nivalis lectin (Vector Labs) column (2). Briefly, transfection supernatants were vacuum-filtered through 0.2-µm filters and then passed over the column at a 0.5-1 mL/min flow rate. The 2G12 column was made from cyanogen bromide-activated Sepharose 4B beads (GE Healthcare) coupled to the bnAb 2G12 (Polymun Sciences). Purification using this column was performed as follows: The beads were washed with two column volumes of buffer [0.5 M NaCl, 20 mM Tris (pH 8.0)] before eluting bound Env proteins using one column volume of 3 M MgCl₂ into one column volume of 75 mM NaCl, 10 mM Tris (pH 8.0). The eluted Env proteins were concentrated using Vivaspin columns with a 100-kDa cut off (GE Healthcare). The affinity-purified Env proteins were purified further to size homogeneity using sizeexclusion chromatography on a Superose 6 10/300 GL column (GE Healthcare) in PBS. The trimer fractions were collected and pooled, and protein concentrations were determined using either a bicinchonic acid-based assay (Thermo Scientific) or UV280 absorbance using theoretical extinction coefficients (5). The Env proteins were biotinylated in vitro using the BirA enzyme (Aviditiy) according to the manufacturer's protocol.

ELISA for Monomeric and Trimeric BG505 Env Proteins. ELISAs were performed as described previously (2) with minor modifications. Microlon 96-well plates (Corning) were coated overnight with streptavidin (Thermo Scientific), anti-biotin antibody (Roche), or anti-His antibody (Thermo Scientific) at 2.5 µg/mL in PBS (50 µL per well). After washing and blocking with 3% BSA for 1 h at room temperature, biotinylated BG505 SOSIP.664-Avi gp140, BG505 SOSIP.664-His gp140, or BG505-avi gp120 proteins were added at 1 µg/mL in PBS/1% BSA for 2 h at 37 °C. Unbound Env proteins were washed away, and serially diluted mAbs in PBS/1% BSA then were added for 2 h at room temperature. Unbound mAbs were washed away, and alkaline phosphataselabeled goat anti-human IgG (Jackson ImmunoResearch) was added for 1 h at a 1:1,000 dilution (final concentration 0.33 µg/mL) in PBS/1% BSA at room temperature. After washing, absorption was measured at 405 nm. For binding to gp120 extracted from lysed virions, plates were coated with 5 ng/uL of sheep D7324 anti-gp120 antibody (Aalto Bioreagents). Virus supernatants were lysed using a final concentration of 1% Nonidet P-40 and incubated on coated plates for 2 h at 37 °C. Detection was measured using goat anti-human IgG $F(ab')_2$ conjugated to alkaline phosphatase (Pierce). Antibody concentration was calculated by linear regression using a standard concentration curve of purified IgG protein.

Competition ELISA. For competition ELISA experiments, competing antibodies were biotinylated using an antibody biotinylation kit (Thermo Scientific). Plates were coated with an anti-His antibody (Roche) at 5 µg/mL overnight. After washing, plates were blocked with 3% BSA for 1 h at room temperature. BG505 SOSIP.664-His gp120 then was captured at 2.5 µg/mL in PBS (50 µL per well) for 2 h at 37 °C. After washing, serially diluted antibodies in PBS/1% BSA were added for 30 min. The biotinylated antibody was added at a constant EC₇₀ concentration for 1 h. Plates were washed, and detection was measured using alkaline phosphatase-conjugated streptavidin (Pierce) at

1:1,000 for 1 h at room temperature. Absorption was measured at 405 nm.

Flow Cytometry Staining of WEHI B-Cell Lines. Previously described mouse B-cell WEHI cell lines (6), which express cell-surface bnAbs, were used in flow cytometric binding assays to evaluate the antigenicity of BG505 SOSIP-AviB trimers. The bnAbexpressing cells were induced by overnight incubation with doxycycline (1 μ g/mL) as described previously (6). Cells (1 × 10⁶) were stained simultaneously with 50 nM of BG505 SOSIP-AviB conjugated to streptavidin-PE (Invitrogen) and 50 nM of JR-CSF gp120-AviB conjugated to streptavidin-APC (Invitrogen). Staining was performed in a final volume of 100 μ L at 4 °C in 1× PBS with 1 mM EDTA and 1% FBS, before washing and was analyzed on a BD LSR II FACS machine.

Single B-Cell RT-PCR, Gene Amplification, and Cloning. Reverse transcription and subsequent PCR amplification of heavy- and light-chain variable genes were performed according to previous protocols (7, 8). All PCR reactions were performed in a 25-µL volume with 2.5 µL of cDNA transcript using HotStar Taq DNA polymerase master mix (Qiagen). Previous primer mixes were supplemented with additional specific V_H 1-8 primers and V_K 2-28 primers: heavy-chain PCR 1 (ATGGACTGGATTTGGAG-GAT), heavy-chain PCR 2 (ATGGACTGGATTTGGAGGATC-CTCTTCTTGG), kappa-chain PCR 1 (ATGAGGCTCCCTGCT-GCCATCCTGGGGGCTGCTAATGC), and kappa-chain PCR 2 (GCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGG). Amplified IgG heavy- and light-chain variable regions were sequenced and analyzed using the international ImMunoGeneTics information system (IMGT) V-quest webserver (www.IMGT.org) (9). Wells for which heavy-chain (V_H 1-8 gene) and light-chain (V_K 2-28) sequences were deemed productive rearrangements by IMGT analysis were selected for cloning into corresponding Igy1, Igk, and Ig λ expression vectors as previously described (7).

Antibody Production. Heavy- and light-chain plasmids were cotransfected (1:1 ratio) in either HEK 293T or 293 FreeStyle cells using Fugene 6 (Promega) or 293fectin (Invitrogen), respectively. Transfections were performed according to the manufacturer's protocol, and antibody supernatants were harvested 4 d after transfection. Antibodies produced in 293T cells were quantified by ELISA and used directly in neutralization assays. Antibodies produced in 293 freestyle cells were purified over a protein A column as described previously (10).

Cell Surface-Binding Assays. Titrating amounts of mAbs were added to HIV-1 Env-transfected 293T cells and were incubated for 1 h at 4 °C in 1× PBS. After washing, cells were fixed with 2% paraformaldehyde (PolySciences) for 20 min at room temperature. The cells then were washed and stained with a 1:200 dilution of PE-conjugated goat anti-human IgG F(ab')₂ (Jackson) for 1 h at room temperature. Binding was analyzed using flow cytometry. Binding competitions were performed by titrating amounts of competitor mAbs before adding biotinylated antibody at the concentration required to achieve IC₇₀ and then measuring binding with PE-labeled streptavidin (Invitrogen). FlowJo software was used for data interpretation.

Autoreactivity Assays. Antibodies were assayed at 100 μ g/mL for autoreactivity to HEp-2 cells (Aesku Diagnostics) by immuno-fluorescence according to the manufacturer's instructions. Briefly, 2.5 μ g or 25 μ L of 100 μ g/mL mAb was incubated on HEP-2 slides in a moist chamber at room temperature for

30 min. The slides then were placed in staining dishes and washed with PBS. FITC-conjugated goat anti-human IgG (20 µL) was applied to each well, and slides were incubated for another 30 min. After washing, slides were photographed on an EVOS f1 fluorescence microscope at a 250-ms exposure with 70% intensity. Reactivity to HIV-1⁻ human epithelial HEp-2 cells was interpreted by the staining patterns. Positive and negative control sera were provided by the vendor. ELISAs were performed as described previously (11). Briefly, human placental dsDNA (Sigma) and ganglioside GD1a (Sigma) in 96% ethanol were coated at 37 °C overnight onto ELISA wells. BSA (Sigma), ovalbumin (Sigma), apo transferrin, and histone (Sigma) were resuspended in PBS and coated overnight at 4 °C. All antigens were coated at 50 ng per well. Then the wells were washed and blocked for 1 h at room temperature with 3% BSA. Serial dilutions of antibodies were added for 1 h at room temperature. After washing, bound antibody was detected by using an alkaline phosphatase-conjugated goat anti-human IgG F(ab')₂ antibody (Pierce) diluted 1:1,000 in 1% BSA/PBS.

Octet Measurements. Binding curves were determined by bio-layer interferometry using an Octet RED instrument (ForteBio, Inc.) as previously described (12, 13). Briefly, IgG antibodies were immobilized onto anti-human IgG Fc biosensors. Varying concentrations of BG505-SOSIP.664-AviB were flowed as analyte in solution. Binding-affinity constants (K_D ; on-rate, k_a ; off-rate, k_d) were determined using Octet Analysis version 7 software (ForteBio; Pall Life Sciences).

Determination of PGDM1400 Fab Crystal Structure. Expression and purification of the PGDM1400 Fab was executed following a protocol similar to that previously described (14). Briefly, the Fab was produced by cotransfection of the heavy- and light-chain genes into HEK 293F cells. Six days after transfection, the supernatant was recovered and flowed over an anti-human kappa light-chain affinity matrix (CaptureSelect Fab K; BAC). The eluted fraction containing the Fab was purified further by MonoS cation exchange chromatography (GE Healthcare). PGDM1400 Fab at a concentration of 6 mg/mL in 20 mM sodium acetate (pH 5.6) was crystallized from nonbuffered mother liquor containing 0.04 M potassium dihydrogen phosphate, 16% (wt/vol) polyethylene glycol 8000, and 20% (vol/vol) glycerol. Crystals were flash cooled in liquid nitrogen, and data were collected at the Stanford Synchrotron Radiation Lightsource (SSRL) beamline 11-1. Statistics for data collection and data processing in XDS (15) are summarized in Table S1. The monoclinic space group $P2_1$ and the structure was solved by molecular replacement using the program Phaser (16) with the PGT145 Fab structure (PDB ID code 3U1S) as a search model. Refinement of three Fab copies in the asymmetric unit was performed using a combination of Phenix (17) and Coot (18). Final refinement statistics are reported in Table S1.

Electron Microscopy. Sample grids were prepared as described previously (19). Data were collected on an FEI Tecnai T12 electron microscope operating at 120 keV coupled with a 4×4 k Tietz TemCam-F416 camera. Images were taken using the LEGINON interface (20). The imaging magnification was 52,000× with a pixel size of 2.05 Å at the specimen plane. The data were collected using an electron dose of ~30 e⁻/Å². Particles were picked using DoG picker in the Appion interface (21, 22), and class averages were generated using the SPARX software package (23).

^{1.} Simek MD, et al. (2009) Human immunodeficiency virus type 1 elite neutralizers: Individuals with broad and potent neutralizing activity identified by using a high-

throughput neutralization assay together with an analytical selection algorithm. J Virol 83(14):7337-7348.

- Sanders RW, et al. (2013) A next-generation cleaved, soluble HIV-1 Env Trimer, BG505 SOSIP.664 gp140, expresses multiple epitopes for broadly neutralizing but not nonneutralizing antibodies. *PLoS Pathog* 9(9):e1003618.
- Hoffenberg S, et al. (2013) Identification of an HIV-1 clade A envelope that exhibits broad antigenicity and neutralization sensitivity and elicits antibodies targeting three distinct epitopes. J Virol 87(10):5372–5383.
- Finzi A, et al. (2010) Conformational characterization of aberrant disulfide-linked HIV-1 gp120 dimers secreted from overexpressing cells. J Virol Methods 168(1-2):155–161.
- 5. Gasteiger J (2006) Chemoinformatics: A new field with a long tradition. *Anal Bioanal Chem* 384(1):57–64.
- Ota T, et al. (2012) Anti-HIV B Cell lines as candidate vaccine biosensors. J Immunol 189(10):4816–4824.
- Wu X, et al. (2010) Rational design of envelope identifies broadly neutralizing human monoclonal antibodies to HIV-1. *Science* 329(5993):856–861.
- Tiller T, et al. (2008) Efficient generation of monoclonal antibodies from single human B cells by single cell RT-PCR and expression vector cloning. J Immunol Methods 329(1-2):112–124.
- Lefranc M-P, et al. (2009) IMGT, the international ImMunoGeneTics information system. Nucleic Acids Res 37(Database issue):D1006–D1012.
- Sok D, et al. (2013) The effects of somatic hypermutation on neutralization and binding in the PGT121 family of broadly neutralizing HIV antibodies. *PLoS Pathog* 9(11):e1003754.
- Walker LM, et al.; Protocol G Principal Investigators (2009) Broad and potent neutralizing antibodies from an African donor reveal a new HIV-1 vaccine target. Science 326(5950):285–289.

- Ekiert DC, et al. (2011) A highly conserved neutralizing epitope on group 2 influenza A viruses. Science 333(6044):843–850.
- Tran K, et al. (2014) Vaccine-elicited primate antibodies use a distinct approach to the HIV-1 primary receptor binding site informing vaccine redesign. Proc Natl Acad Sci USA 111(7):E738–E747.
- Pejchal R, et al. (2010) Structure and function of broadly reactive antibody PG16 reveal an H3 subdomain that mediates potent neutralization of HIV-1. Proc Natl Acad Sci USA 107(25):11483–11488.
- 15. Kabsch W (2010) Xds. Acta Crystallogr D Biol Crystallogr 66(Pt 2):125-132.
- McCoy AJ, et al. (2007) Phaser crystallographic software. J Appl Cryst 40(Pt 4):658–674.
 Adams PD, et al. (2010) PHENIX: A comprehensive Python-based system for macro-
- molecular structure solution. Acta Crystallogr D Biol Crystallogr 66(Pt 2):213–221. 18. Emsley P, Cowtan K (2004) Coot: Model-building tools for molecular graphics. Acta
- Crystallogr D Biol Crystallogr 60(Pt 12 Pt 1):2126–2132.
 Julien J-P, et al. (2013) Asymmetric recognition of the HIV-1 trimer by broadly neutralizing antibody PG9. Proc Natl Acad Sci USA 110(11):4351–4356.
- Suloway C, et al. (2005) Automated molecular microscopy: The new Leginon system. J Struct Biol 151(1):41–60.
- Voss NR, Yoshioka CK, Radermacher M, Potter CS, Carragher B (2009) DoG Picker and TiltPicker: Software tools to facilitate particle selection in single particle electron microscopy. J Struct Biol 166(2):205–213.
- Lander GC, et al. (2009) Appion: An integrated, database-driven pipeline to facilitate EM image processing. J Struct Biol 166(1):95–102.
- Hohn M, et al. (2007) SPARX, a new environment for Cryo-EM image processing. J Struct Biol 157(1):47–55.



Fig. S1. BG505 SOSIP.664-AviB is an appropriate probe for bnAbs. (*A*–C) Biotinylated BG505 SOSIP.664-Avi (BG505 SOSIP.664-AviB) was tested in a streptavidin-capture ELISA against trimer-dependent bnAbs (*A*); CD4bs, CD4i, and V3/V4-glycan bnAbs (*B*); and MPER and non-bnAbs (*C*). (*D*) Binding of BG505 SOSIP.664-AviB and JR-CSF gp120-AviB to PGT128 and PGT145 WEHI mouse B-cell lines (1) was detected via flow cytometry using streptavidin-PE and streptavidin-Alexa 488, respectively. Values are presented in mean fluorescence intensity (MFI). (*E*) PBMCs from HIV-seronegative donors were isolated by Ficoll gradient, and IgG⁺ memory B cells were stained with BG505 SOSIP.664-AviB and streptavidin-PE to evaluate the extent of nonspecific trimer binding.

1. Ota T, et al. (2012) Anti-HIV B Cell lines as candidate vaccine biosensors. J Immunol 189(10):4816-4824.

	mAb	V-GENE	J-GENE	CDRH3 Length (aa)	CDRH3 Sequence (aa)	V _H J _H % mut (nt)	Insertion/Deletions
	PGDM1400			34	CAKGSKHRLRDYALYDDDGALNWAVDVDYLSNLEFW	73%	
	PGDM1401			34	CARGSKHRLRDYVMYDDYGALQWAVYVDYLSNLDVW	73%	
	PGDM1402			34	CAKGSKHRLRDYALYDDIGALQWAVDVDYLSTLEFW	73%	
	PGDM1403			33	CVKGSKFRLREWADYNEWGLVSAQHGDYVTQLGIW	74%	
	PGDM1404			34	CVRGAKFRLRHDATYDYWNDLLWADDRDYVTQLDLW	77%	
	PGDM1405			34	CVRGAKFRLRHDATYDYYNDLLWADDRDYVTQLDLW	76%	
Z	PGDM1406			33	CVKGQKFRLTEWADYNEFGLVAAQKGDYVTQLDVW	76%	
₹	PGDM1407			33	CVKGQKFRLTEWADYNEFGLVAAEKGDYVTQLDVW	75%	
さ	PGDM1408			34	CARGSKHKLRDYVMYDDYGALQWAVYVDYLSNLDVW	73%	
≻	PGDM1409	IGHV1-8	IGHJ6	34	CVRGAKFRLRHDATYDYWNDLLWADDRDYVTQLDLW	75%	
₹	PGDM1410			34	CVRGSKFRLRNDAIYDYWNDLLWADDGDYVTKLDLW	75%	
뿌	PGDM1411			33	CARRTEKQLRAEYVLDQEDGFYREEAIYITVLDVW	78%	
-	PGDM1412			33	CVKGLKFRLREWSDYNEFGLVAAQHGDYVTQMEVW	78%	
	PGT141			34	CTRGSKHRLRDYVLYDDYGLINYQEWNDYLEFLDVW	82%	
	PGT142			34	CTRGSKHRLRDYVLYDDYGLINYQEWNDYLEFLDVW	82%	
	PGT143			34	CTRGSKHRLRDYVLYDDYGLINYQEWNDYLEFLDVW	82%	
	PGT144			34	CTGGSKHRLRDYVLYDDYGLINQQEWNDYLEFLDVW	82%	
	PGT145			33	CLTGSKHRLRDYFLYNEYGPNYEEWGDYLATLDVW	77%	
	PGDM1400			9	CMQGRESPWTF	89%	
	PGDM1401			9	CMOGRESPWTF	88%	
	PGDM1402			9	CMQGRESPWTF	89%	
	PGDM1403			9	CMQGLQSPTTF	88%	+7 (CDR1)
	PGDM1404			9	CMQGRHIPLTF	85%	+3 (CDR1)
	PGDM1405			9	CMQGRHIPLTF	84%	+3 (CDR1)
z	PGDM1406			9	CMQGLRTPMTF	84%	+7 (CDR1)
Ā	PGDM1407			9	CMQGLRTPMTF	82%	+7 (CDR1)
H H	PGDM1408			9	CMQGRESPWTF	88%	
Ĕ	PGDM1409	IGKV2-28	IGKJ1	9	CMQGRHIPLTF	85%	+3 (CDR1)
Ϋ́	PGDM1410			9	CFQGRHTPLTF	86%	+3 (CDR1)
Ĕ	PGDM1411			9	CMDTLRPPYAF	78%	-1 (CDR1)
—	PGDM1412			9	CMQGLQVPMTF	88%	+7 (CDR1)
	PGT141			9	CMQGLNRPWTF	86%	. ,
	PGT142			9	CMQGLNRPWTF	86%	
	PGT143			9	CMQGLNRPWTF	86%	
	PGT144			9	CMQGLNRPWTF	87%	
	PGT145			9	CMQGLHSPWTF	84%	

Fig. S2. Summary of mutation frequency and gene family of newly isolated somatic variants. PGDM1400–1412 were analyzed for germline gene, CDRH3 length, CDRH3 sequence, percent identity (in nucleotides), and possible insertions or deletions. Genetic analyses were performed using the IMGT system (1).

1. Lefranc M-P, et al. (2009) IMGT, the international ImMunoGeneTics information system. Nucleic Acids Res 37(Database issue):D1006–D1012.

| Α | % Sequence
identity
(nucleotide) | oGDM1400 | GDM1401 | PGDM1402
 | -GDM1403 | PGDM1404 | PGDM1405 | -GDM1406
 | -GDM1407 | -GDM1408 | oGDM1409 | PGDM1410 | PGDM1411
 | oGDM1412 | PGT141 | PGT142
 | PGT143 | PGT144 | PGT145
 | %
sequence
identity
scale |
|---------------------------|--|---|--
--
---	--	--	---
--	---		
--	--		
---	--	--	---
1	PGDM1400	100	88
 | 67 | 66 | 66 | 66
 | 64 | 87 | 66 | 70 | 66
 | 67 | 75 | 75
 | 74 | 74 | 73
 | 100 |
| | PGDM1401 | 88 | 100 | 90
 | 66 | 67 | 68 | 65
 | 65 | 97 | 67 | 70 | 66
 | 66 | 75 | 74
 | 74 | 74 | 73
 | 90 |
| | PGDM1402 | 94 | 90 | 100
 | 67 | 67 | 66 | 66
 | 65 | 88 | 66 | 69 | 66
 | 67 | 74 | 74
 | 74 | 73 | 72
 | 80 |
| | PGDM1403 | 67 | 66 | 67
 | 100 | 74 | 74 | 83
 | 82 | 65 | 74 | 76 | 65
 | 84 | 69 | 68
 | 69 | 69 | 72
 | 70 |
| | PGDM1404 | 66 | 67 | 67
 | 74 | 100 | 92 | 71
 | 72 | 67 | 93 | 91 | 63
 | 74 | 71 | 71
 | 71 | 70 | 72
 | 60 |
| | PGDM1405 | 66 | 68 | 66
 | 74 | 92 | 100 | 71
 | 72 | 67 | 98 | 91 | 62
 | 72 | 70 | 70
 | 70 | 69 | 70
 | 50 |
| Z, | PGDM1406 | 66 | 65 | 66
 | 83 | 71 | 71 | 100
 | 91 | 65 | 70 | 72 | 67
 | 88 | 68 | 68
 | 68 | 68 | 70
 | 40 |
| H | PGDM1407 | 64 | 65 | 65
 | 82 | 12 | 12 | 91
 | 100 | 64 | 12 | 73 | 66
 | 87 | 69 | 69
 | 70 | 69 | /1
 | |
| XC | PGDM1408 | 66 | 67 | 00
 | 74 | 03 | 07 | 70
 | 72 | 67 | 100 | 01 | 61
 | 73 | 74 | 70
 | 70 | 60 | 73
 | |
| A | PGDM1409 | 70 | 70 | 69
 | 76 | 91 | 91 | 72
 | 73 | 70 | 91 | 100 | 65
 | 74 | 72 | 72
 | 72 | 71 | 73
 | |
| 뽀 | PGDM1411 | 66 | 66 | 66
 | 65 | 63 | 62 | 67
 | 66 | 66 | 61 | 65 | 100
 | 67 | 68 | 68
 | 68 | 67 | 67
 | |
| | PGDM1412 | 67 | 66 | 67
 | 84 | 74 | 72 | 88
 | 87 | 66 | 73 | 74 | 67
 | 100 | 70 | 70
 | 71 | 70 | 71
 | |
| | PGT141 | 75 | 75 | 74
 | 69 | 71 | 70 | 68
 | 69 | 74 | 70 | 72 | 68
 | 70 | 100 | 99
 | 98 | 96 | 86
 | |
| | PGT142 | 75 | 74 | 74
 | 68 | 71 | 70 | 68
 | 69 | 74 | 70 | 72 | 68
 | 70 | 99 | 100
 | 98 | 96 | 86
 | |
| | PGT143 | 74 | 74 | 74
 | 69 | 71 | 70 | 68
 | 70 | 74 | 70 | 72 | 68
 | 71 | 98 | 98
 | 100 | 96 | 87
 | |
| | PGT144 | 74 | 74 | 73
 | 69 | 70 | 69 | 68
 | 69 | 73 | 69 | 71 | 67
 | 70 | 96 | 96
 | 96 | 100 | 86
 | |
| | PGT145 | 73 | 73 | 72
 | 72 | 72 | 70 | 70
 | 71 | 73 | 71 | 73 | 67
 | 71 | 86 | 86
 | 87 | 86 | 100
 | |
| | DODMA | 400 | 04 | 00
 | 00 | 70 | 70 | 70
 | 70 | 00 | 00 | 00 | 70
 | 00 | 00 | 00
 | 04 | 04 | 04
 | |
| | PGDW1400 | 01 | 100 | 98
 | 82 | 79 | 80 | 79
 | 70 | 90 | 81 | 81 | 70
 | 81 | 82 | 82
 | 82 | 82 | 80
 | |
| | PGDM1407 | 98 | 91 | 100
 | 83 | 80 | 80 | 79
 | 78 | 91 | 81 | 82 | 76
 | 82 | 80 | 80
 | 81 | 81 | 81
 | |
| | PGDM1403 | 82 | 82 | 83
 | 100 | 81 | 80 | 86
 | 84 | 82 | 81 | 82 | 75
 | 91 | 80 | 80
 | 80 | 81 | 80
 | |
| | PGDM1404 | 79 | 79 | 80
 | 81 | 100 | 90 | 78
 | 75 | 79 | 91 | 92 | 72
 | 82 | 78 | 78
 | 77 | 78 | 76
 | |
| | PGDM1405 | 79 | 80 | 80
 | 80 | 90 | 100 | 79
 | 76 | 80 | 97 | 90 | 71
 | 82 | 78 | 78
 | 77 | 78 | 76
 | |
| z | PGDM1406 | 79 | 78 | 79
 | 86 | 78 | 79 | 100
 | 95 | 78 | 79 | 80 | 76
 | 86 | 77 | 77
 | 76 | 78 | 76
 | |
| ΙĮ | PGDM1407 | 78 | 79 | 78
 | 84 | 75 | 76 | 95
 | 100 | 78 | 76 | 77 | 74
 | 83 | 75 | 75
 | 74 | 75 | 74
 | |
| Ċ | PGDM1408 | 90 | 99 | 91
 | 82 | 79 | 80 | 78
 | 78 | 100 | 80 | 80 | 73
 | 80 | 81 | 81
 | 81 | 81 | 80
 | |
| H | PGDM1409 | 80 | 81 | 81
 | 81 | 91 | 97 | 79
 | 76 | 80 | 100 | 90 | 72
 | 82 | 79 | 79
 | 79 | 80 | 78
 | |
| 9 | PGDM1410 | 82 | 81 | 82
 | 82 | 92 | 90 | 80
 | 77 | 80 | 90 | 100 | 75
 | 83 | 79 | 79
 | 78 | 79 | 79
 | |
| _ | PGDM1411 | 10 | /4
01 | 10
 | 75 | 12 | /1 | 10
 | 74 | 73 | 12 | /5 | 100
 | 100 | 75 | 75
 | 75 | 75 | 75
 | |
| | PGDW1412 | 80 | 82 | 80
 | 80 | 78 | 78 | 77
 | 75 | 81 | 70 | 79 | 75
 | 79 | 100 | 100
 | 08 | 98 | 84
 | |
| | PGT141 | 80 | 82 | 80
 | 80 | 78 | 78 | 77
 | 75 | 81 | 79 | 79 | 75
 | 79 | 100 | 100
 | 98 | 98 | 84
 | |
| | PGT143 | 81 | 82 | 81
 | 80 | 77 | 77 | 76
 | 74 | 81 | 79 | 78 | 75
 | 79 | 98 | 98
 | 100 | 98 | 85
 | |
| | PGT144 | 81 | 82 | 81
 | 81 | 78 | 78 | 78
 | 75 | 81 | 80 | 79 | 75
 | 80 | 98 | 98
 | 98 | 100 | 85
 | |
| | PGT145 | 81 | 80 | 81
 | 80 | 76 | 76 | 76
 | 74 | 80 | 78 | 79 | 75
 | 79 | 84 | 84
 | 85 | 85 | 100
 | |
 | | | |
 | | | | |
 | | |
 | | |
 | |
-			
 | | | |
 | | | | |
 | | |
 | | |
 | |
| B | | 0 | - | N
 | 3 | 4 | 5 | Ś
 | | 80 | Ø | 0 | -
 | N | |
 | | |
 | |
| в | % Sequence | 400 | 401 | 402
 | 403 | 404 | 405 | 406
 | 407 | 408 | 409 | 410 | 411
 | 412 | 41 | 42
 | 43 | 44 | 45
 | % |
| в | % Sequence identity | M1400 | M1401 | M1402
 | M1403 | M1404 | M1405 | M1406
 | M1407 | M1408 | M1409 | M1410 | M1411
 | M1412 | T141 | T142
 | T143 | T144 | T145
 | %
sequence |
| в | % Sequence
identity
(amino acid) | GDM1400 | GDM1401 | GDM1402
 | GDM1403 | GDM1404 | GDM1405 | GDM1406
 | GDM1407 | GDM1408 | GDM1409 | GDM1410 | GDM1411
 | GDM1412 | PGT141 | PGT142
 | PGT143 | PGT144 | PGT145
 | %
sequence
identity |
| В | % Sequence
identity
(amino acid) | PGDM1400 | PGDM1401 | BGDM1402
 | PGDM1403 | PGDM1404 | PGDM1405 | PGDM1406
 | PGDM1407 | PGDM1408 | PGDM1409 | BGDM1410 | PGDM1411
 | BGDM1412 | PGT141 | PGT142
 | PGT143 | PGT144 | 9 PGT145
 | %
sequence
identity
scale |
| В | % Sequence
identity
(amino acid)
PGDM1400 | 3 00 PGDM1400 | 8 PGDM1401 | 6 PGDM1402
 | 5 15 PGDM1403 | 1 8 PGDM1404 | 3 & PGDM1405 | 6 PGDM1406
 | 6 6 PGDM1407 | 6 PGDM1408 | 1 6 PGDM1409 | 8 PGDM1410 | 4 PGDM1411
 | 5 5 PGDM1412 | 2 9 PGT141 | 9 9 PGT142
 | 3 9 PGT143 | 9 PGT144 | 8 9 PGT145
 | %
sequence
identity
scale |
| В | % Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402 | 6 PGDM1400 | 80 001 401 | 01 8 00 M1402
 | 1 0 1 PGDM1403 | 07 1404 BGDM1404 | 6 2 8 PGDM1405 | 5 6 6 PGDM1406
 | 5 & & PGDM1407 | 80 PGDM1408 | 60 H B B B B B B B B B B B B B B B B B B | 5 2 PGDM1410 | 5 2 4 PGDM1411
 | 25 PGDM1412 | 141141 | 0 0 0 PGT142
 | © 9 9 PGT143 | 9 9 9 PGT144 | 0 2 0 PGT145
 | %
sequence
identity
scale
100
90
80 |
| В | % Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402
PGDM1403 | 001400
28
93 | 82 BGDW1401 | 001 PGDM1402
 | 51 50 51 100 | 404 PGDM1404 | 405 PGDM1405 | 49 50 52 72
 | 407 PGDW1407 | 96 PGDM1408 | 6041409 | 014100 50 50 PGDM1410 | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
 | 21410001412 | 141141
5 5 2 9 PGT141 | 5 9 9 9 PGT142
 | 9 9 9 9 PGT143 | 4 6 5 6 4 5 4 5 4 5 4 5 4 5 5 4 5 5 5 5 | 8 0 5 0 PGT145
 | %
sequence
identity
scale
100
90
80
70 |
| В | % Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1403
PGDM1404 | 0071400
100
82
93
51
48 | 82 bGDW1401
84 50 51 | 93 84 100 51 50 M1405
 | 51 50 51 100 64 | 48 bCDW1404
50 64
100 | 9071402
8 5 8 PGDM1405 | 49
50
52
58
 | 49 48 50 74 60 74 60 | 79
96
81
50
51 | 6071409
49
50
66
94 | 014100 50 50 66 88 | 1141MD94 44 44 45 45
 | 5141MD94 52 52 54 77 62 | 141TPG 62 22 22 22 22 22 22 22 22 22 22 22 22 | C7142 65 66 4 55 57
 | 65 65 64 55 bGT143 | 741120 64 55 55 55 55 55 55 55 55 55 55 55 55 55 | 92 80 50 90 PGT145
 | %
sequence
identity
scale
100
90
80
70
60 |
В	% Sequence identity (amino acid) PGDM1400 PGDM1401 PGDM1403 PGDM1403 PGDM1405	100 100 82 93 51 48 48	82 100 84 50 51 52	93 84 100 51 50 49	51 50 50 51 50 50 51 50 50 50 50 50 50 50 50 50 50 50 50 50	48 50 64 100 92	48 52 49 64 92 100	49 50 52 58 59	49 48 50 74 60 63	79 96 81 50 51 52	6071WD9d 49 51 50 66 94 95	0141MD9d 50 50 66 88 87	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	52 52 54 77 62 62	14114 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	5 5 5 6 6 7 145 8 7 145 8 7 145 7 145 8 7 145 7 145 7 145 7 145 7 145 7 145 7 145 7 145 7 14	65 55 64 56 57 59 bella 5	4 5 5 5 5 below be	96 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	% sequence identity scale 100 90 80 70 60 50
B	% Sequence identity (amino acid) PGDM1400 PGDM1401 PGDM1402 PGDM1403 PGDM1405 PGDM1405	0071W09d 0071W09000000000000000000000000000000000	82 100 84 50 51 52 50	93 84 100 51 50 49 52	51 50 51 100 64 64 72	48 51 50 64 100 92 58	48 52 49 64 92 100 59	9041WD94 49 50 52 72 58 59 100	L0+1WQ9d 49 48 50 74 60 63 87	8071W09d 79 96 81 50 51 52 49	6071WQ9d 49 51 50 66 94 95 59	50 bCDW1410 50 52 50 66 88 87 58	1141MGD4 44 44 44 44 44 44 44 44 44 44 44 44 4	52 52 54 77 62 62 80	14110 65 55 57 58 53	C7142 65 66 45 57 58 53	65 55 64 56 57 59 53 50 bell	++112 6 5 5 5 5 5 5 5 5 5 5	97149 0 2 0 8 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	% sequence identity scale 100 90 80 70 60 50 50 40
B	% Sequence identity (amino acid) PGDM1400 PGDM1401 PGDM1402 PGDM1404 PGDM1405 PGDM1406 PGDM1407	0071W09d 0071W09000000000000000000000000000000000	82 100 84 50 51 52 50 48	93 84 100 51 50 49 52 50	51 50 51 100 64 64 72 74	48 51 50 64 100 92 58 60	48 bCDW1402 48 52 49 64 92 100 59 63	90+LWQ9d 49 50 52 72 58 59 100 87	49 48 50 74 60 63 87 100	79 96 81 50 51 52 49 47	6041WDDJ 49 51 50 66 94 95 59 63	50 52 50 66 88 87 58 61	1141MGD4 44 44 44 44 49	52 52 54 77 62 80 80 80 80 80 80 80 80 80 80 80 80 80	65 67 65 55 57 58 53 56	65 66 64 55 57 58 56 55 57 58 56	65 65 64 55 59 53 56 belta 43	##1120 64 65 54 55 51 54 55 55 55 55 54 55 54 55 54 55 54 55 54 55 54 55 55 54 55 55 54 55 55 54 55 55 54 55 55 54 54 55 55 54 55 55 54 55 55 54 55 54 55	971194 60 20 68 56 55 60	% sequence identity scale 100 90 80 70 60 50 40
CHAIN	% Sequence identity (amino acid) PGDM1400 PGDM1401 PGDM1402 PGDM1404 PGDM1405 PGDM1406 PGDM1406 PGDM1407	0071WGDd 0071WG0000000000000000000000000000000000	100 82 100 84 50 51 52 50 48 96	93 84 100 51 50 49 52 50 81	51 50 51 100 64 64 72 74 50	48 51 50 64 100 92 58 60 51	48 bCDW1402 48 52 49 64 92 100 59 63 52	9041WG9d 49 50 52 72 58 59 100 87 49	49 48 50 74 60 63 87 100 47	79 96 81 50 51 52 49 47 100	6041WGDJ 49 51 50 66 94 95 59 63 51	50 52 50 66 88 87 58 61 52	1141MGDJ 44 74 45 44 47 49 47	52 52 54 77 62 80 80 80 80 51	65 67 65 55 57 58 53 56 66	65 66 64 55 57 58 53 56 65	65 65 64 56 57 59 53 56 65	##119d 64 65 54 55 51 54 64	971194 60 20 85 56 55 60 61	% sequence identity scale 100 90 80 70 60 50 40
VY CHAIN	 % Sequence identity (amino acid) PGDM1400 PGDM1401 PGDM1402 PGDM1403 PGDM1405 PGDM1406 PGDM1407 PGDM1407 PGDM1408 PGDM1409 	0071W09d 100 82 93 51 48 49 49 79 49	Lop Lop 82 100 84 50 51 52 50 48 96 51	93 84 100 51 50 49 52 50 81 50																
 | 51
50
51
50
51
64
64
72
74
50
66 | *0*LWQDG 48 51 50 64 100 92 58 60 51 94 | 48
52
49
64
92
63
59
63
52
95 | 49
50
52
72
58
59
100
87
49
59
 | 49
48
50
74
60
63
87
100
47
63 | 8041W09J
966
811
500
511
522
499
477
1000
51 | 6041M05d
49
51
50
66
94
95
59
63
59
63
51
100 | 50
50
50
66
88
87
58
61
52
88 | 1171WD9d 44 77 44 45 44 44 47 49 47 44
 | 52
52
54
77
62
80
80
80
51
63 | 65 7 65 55 57 58 53 66 59 | CP112d 65 66 4 55 53 56 59
 | 65 65 64 56 57 59 53 56 65 60 | ##L19d 64 65 64 65 55 51 54 64 57 57 54 57 <th< td=""><td>60 2 0 8 6 6 5 6 6 1 5 6 1 4 5 6 1 4 5 6 1 4 5 6 6 1 5 6 1 1</td><td>%
sequence
identity
scale
100
90
80
70
60
60
50
40</td></th<> | 60 2 0 8 6 6 5 6 6 1 5 6 1 4 5 6 1 4 5 6 1 4 5 6 6 1 5 6 1
5 6 1 1 | %
sequence
identity
scale
100
90
80
70
60
60
50
40 |
| IEAVY CHAIN | * Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402
PGDM1405
PGDM1405
PGDM1405
PGDM1407
PGDM1409
PGDM1409
PGDM1409
PGDM1409 | 0041W09d 100
82
93
51
48
49
49
79
49
50 | 10014000000000000000000000000000000000 | 93
84
100
51
50
49
52
50
81
50
50
50
 | 51
50
51
100
64
64
72
74
50
66
66
66 | 48
51
50
64
100
92
58
60
51
94
88 | 48
52
49
64
92
100
59
63
52
95
87 | 9041M09d 49
50
52
72
58
59
100
87
49
59
59
59
 | 49
48
50
74
60
63
87
100
47
63
61 | 79
96
81
50
51
52
49
47
100
51
52 | 6041M09d 49
51
50
66
94
95
59
63
51
100
88 | 50
50
52
50
66
88
87
52
88
61
52
88
100 | 1171WD9d 44 47 44 44 44 44 44 44 44 44 44 44 44
 | 52 52 54 77 62 62 80 80 51 63 61 63 | 141129d 65 75 55 57 58 3 56 66 59 9 1 | C1142 666 64 55 758 356 598 100 100 100 100 100 100 100 100 100 10
 | 65 65 66 57 59 3 56 56 00 1 | ##LDd 64 55 51 44 57 56 57 56 57 56 57 56 57 56 57 56 57 56 57 57 56 57 56 57 57 56 56 57 56 56 57 56 56 56 56 56 56 56 56 56 56 56 56 56 57 56 <t< td=""><td>60 2 00 5 6 6 5 5 6 0 1 5 5 0 1 5 5 5 6 0 1 5 5 5 6 1 5 5 5 5 6 1 5 5 5 5 6 1 5 5 5 5</td><td>%
sequence
identity
scale
100
90
80
70
60
50
40</td></t<> | 60 2 00 5 6 6 5 5 6 0 1 5 5 0 1 5 5 5 6 0 1 5 5 5 6 1 5 5 5 5 6 1 5 5 5 5 6 1 5 5 5 5
 | %
sequence
identity
scale
100
90
80
70
60
50
40 |
| HEAVY CHAIN | * Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402
PGDM1403
PGDM1405
PGDM1405
PGDM1407
PGDM1407
PGDM1401
PGDM1411 | 00140000000000000000000000000000000000 | 100141000
82
1000
84
50
51
52
50
48
96
51
52
51
52
47 | 93
84
100
51
50
49
52
50
81
50
81
50
44
 | 51
50
51
100
64
64
72
74
50
66
66
66
45 | 48
51
50
64
100
92
58
60
51
94
88
44
88
44 | 48
52
49
64
92
100
59
63
52
95
87
44 |
9041M090
49
50
52
72
58
59
100
87
49
59
58
49
58
47 | 49
48
50
74
60
63
87
100
47
63
61
49 | 79
96
81
50
51
52
49
47
100
51
52
47 | 6041M05d 49
51
50
66
94
95
59
63
51
100
88
44 | 0141M09d
50
52
50
66
88
87
58
61
52
88
100
44 | 11711111111111111111111111111111111111
 | 52
52
54
77
62
62
80
80
51
63
61
47 | 141129d 65 67 65 55 57 58 3 56 66 59 51 141 | C1142 65 66 45 57 58 53 66 59 58 51 62 57 58 51 65 59 58 51 50 58 51 50 50 50 50 50 50 50 50 50 50 50 50 50
 | 65 65 66 65 60 60 51 60 50 50 50 50 50 50 50 50 50 50 50 50 50 | ##1129d 64 65 54 55 51 54 57 56 91 | 971192 00 20 00 56 55 50 01 58 59 11
 | %
sequence
identity
scale
100
90
80
70
60
50
40 |
| HEAVY CHAIN | * Sequence
identity
(amino acid)
PGDM1401
PGDM1401
PGDM1402
PGDM1405
PGDM1405
PGDM1405
PGDM1406
PGDM1409
PGDM1409
PGDM1411
PGDM1411
PGDM1411 | 0041W05d 00
82
93
51
48
49
49
79
49
50
49
50
44
50
44
50 | 100
82
100
84
50
51
52
50
48
96
51
52
47
52
47
52 | 93
84
100
51
50
49
52
50
81
50
50
44
50
44
50
 | 51
50
51
100
64
64
72
74
50
66
66
66
45
77 | 400 48 50 64 100 92 58 600 51 94 88 44 62 57 | 48
52
49
64
92
100
59
63
52
95
87
44
62 |
49
50
52
72
58
59
100
87
49
59
58
47
80
87
80
87 | 49
48
50
74
60
63
87
100
47
63
61
49
80
63 | 8041W09d
79
96
81
50
51
52
49
47
100
51
52
47
51
52 | 60+1W09d 49
51
50
66
94
95
59
63
51
100
88
44
63 | 0141M009d 500
522 500
666 888
877 588
611 52
888 1000
441 610 | 11710001 44 74 45 44 44 47 94 74 44 100 47 1
 | 52 52 54 77 62 62 80 80 51 63 61 47 100 56 | 17111111111111111111111111111111111111 | C1142 56 66 45 57 58 56 59 58 1 50 50 50 50 50 50 50 50 50 50 50 50 50
 | 65 65 64 65 57 59 53 66 50 60 51 57 60 60 51 57 60 60 51 57 60 50 51 57 60 50 50 50 50 50 50 50 50 50 50 50 50 50 | think think think <t< td=""><td>97149
60 2 60 8 66 55 60 61 58 9 51 58 20 51 58 20 51 58 20 50 50 50 50 50 50 50 50 50 50 50 50 50</td><td>%
sequence
identity
scale
100
90
80
70
60
50
50
40</td></t<> | 97149
60 2 60 8 66 55 60 61 58 9 51 58 20 51 58 20 51 58 20 50 50 50 50 50 50 50 50 50 50 50 50 50
 | %
sequence
identity
scale
100
90
80
70
60
50
50
40 |
| HEAVY CHAIN | Sequence
identity
(amino acid) PGDM1400 PGDM1401 PGDM1403 PGDM1403 PGDM1405 PGDM1405 PGDM1406 PGDM1407 PGDM1408 PGDM1409 PGDM1409 PGDM1401 PGDM1401 PGDM1410 PGDM1411 PGT141 PGT141 PGT141 PGT141 | 0071WG9d 00
82
93
51
48
49
49
79
49
50
44
52
56 | L00 WCD d 82 100 84 50 51 52 50 48 96 51 52 50 48 96 51 52 50 48 96 51 52 67 66 66 | 93
84
100
51
50
49
52
50
81
50
81
50
44
50
44
50
65
44
50
65
64
 | 51
50
51
50
64
64
72
74
50
66
66
66
66
55
55 | 400 48 48 51 50 64 100 92 58 60 51 94 88 44 62 57 | 48
48
52
49
64
92
63
59
63
52
95
87
44
62
87
87
87
87
87
87
87
87
87
87
87
87
87 |
901400
49
50
52
72
58
59
100
87
49
59
58
47
80
87
80
53
53 | L0ptIW0Dd 49
48
50
74
60
63
87
100
47
63
61
49
80
65
56 | 804LWG9d 79
96
81
50
51
52
49
47
100
51
52
47
51
52
47
51
52
66
65 | 604140
49
51
50
66
94
95
59
63
51
100
88
44
63
59 | 0141M09d 50
52
50
66
88
87
58
61
52
88
61
52
88
100
44
61
58 | 1141M0DJ 44 74 45 44 44 47 49 47 44 44 100 47 51 1
 | 21+1/WQ9d 52 52 54 77 62 62 80 80 51 63 61 470 56 | 17119d 65 67 65 55 57 58 53 56 66 59 51 56 100 88 | 65 66 4 55 57 58 53 56 59 8 50 58 50 50 50 50 50 50 50 50 50 50 50 50 50
 | 655575935655000000000000000000000000000000000 | ##L19d 64 55 55 55 55 55 55 55 55 55 55 55 55 55 | 941-154 60 2 60 8 56 55 60 1 58 59 51 58 83 1
 | %
sequence
identity
scale
100
90
80
70
60
60
50
40 |
| HEAVY CHAIN | * Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402
PGDM1402
PGDM1404
PGDM1405
PGDM1405
PGDM1407
PGDM1407
PGDM1407
PGDM1410
PGDM1411
PGDM1411
PGDM1411
PGTM141
PGT142
PGT142 | 0011W09d 100
82
93
51
48
49
49
49
50
44
52
65
55
55 | 1041M05d 82
100
84
50
51
52
50
48
96
51
52
47
52
67
66
65 | 93
84
100
51
50
81
50
81
50
81
50
44
54
65
44 | E001 MOD MOD <td>4014000 488 510 644 500 511 944 62 577 57</td> <td>S001 B 48 52 49 64 92 100 59 63 52 95 87 44 62 58 59 57</td> <td>9041M03d 49
50
52
58
59
100
87
49
59
58
47
80
53
53</td> <td>L041M020d 99
48
50
60
63
87
100
47
63
61
49
80
63
61
49
80
55
6
55
6</td> <td>804LWQ9d 79
96
81
50
51
52
49
47
100
51
52
47
51
52
47
51
52
66
55</td> <td>6071W059d 49
51
50
66
94
95
59
63
51
100
88
44
63
59
960</td> <td>0141M09d 50
52
50
66
88
87
58
61
52
88
100
44
61
55
86
0</td> <td>1141W09d 44
447
444
447
49
47
444
447
49
47
444
40
47
51
51</td> <td>CltptlW09d S2 S2</td> <td>141120 65 67 65 55 57 58 53 56 66 59 51 56 100 98 99</td> <td>Control Control <t< td=""><td>65 65 64 56 65 57 59 53 56 60 51 57 99 96 100</td><td>11 11 <th< td=""><td>Sector Sector Sector<</td><td>%
sequence
identity
scale
100
90
80
70
60
50
40</td></th<></td></t<></td> | 4014000 488 510 644 500 511 944 62 577 57 | S001 B 48 52 49 64 92 100 59 63 52 95 87 44 62 58 59 57 | 9041M03d 49
50
52
58
59
100
87
49
59
58
47
80
53
53 | L041M020d 99
48
50
60
63
87
100
47
63
61
49
80
63
61
49
80
55
6
55
6 | 804LWQ9d 79
96
81
50
51
52
49
47
100
51
52
47
51
52
47
51
52
66
55 | 6071W059d 49
51
50
66
94
95
59
63
51
100
88
44
63
59
960 | 0141M09d 50
52
50
66
88
87
58
61
52
88
100
44
61
55
86
0 | 1141W09d 44
447
444
447
49
47
444
447
49
47
444
40
47
51
51 | CltptlW09d S2 | 141120 65 67 65 55 57 58 53 56 66 59 51 56 100 98 99 | Control Control <t< td=""><td>65 65 64 56 65 57 59 53 56 60 51 57 99 96 100</td><td>11 11 <th< td=""><td>Sector Sector Sector<</td><td>%
sequence
identity
scale
100
90
80
70
60
50
40</td></th<></td></t<> | 65 65 64 56 65 57 59 53 56 60 51 57 99 96 100 | 11 11 <th< td=""><td>Sector Sector Sector<</td><td>%
sequence
identity
scale
100
90
80
70
60
50
40</td></th<> | Sector Sector< | %
sequence
identity
scale
100
90
80
70
60
50
40 |
| HEAVY CHAIN | * Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402
PGDM1403
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1409
PGDM1410
PGDM1411
PGDM1412
PGT141
PGT142
PGT142
PGT143
PGT144 | 00FIW09d 100
82
93
51
48
48
49
97
9
50
44
52
65
65
65
64 | 1041M05d 82
100
84
50
51
52
50
48
96
51
52
47
52
67
66
5
65 | COPLINGS 33 84 100 51 50 49 52 50 81 50 50 44 54 65 64 65 64 65 64 65 64 65 50 50 50 50 50 44 54 65 64 < | 8000000000000000000000000000000000000 | 4014000 488 510 644 500 511 944 62 577 575 555 555 555 555 555 555 555 55 | S001 S001 48 52 49 64 92 100 59 63 52 95 87 44 62 58 58 59 55 55 | 9041M09d 49
50
52
58
59
100
87
49
59
58
47
80
53
53
53
53 | L041M029d 9
49
48
50
63
87
100
47
63
61
49
80
56
56
56
56
56 | 8041MG9d 79
96
81
50
51
52
49
47
100
51
52
47
51
66
5
65
64 | 60+1WQ9d 49
51
50
66
94
95
59
63
51
100
88
44
63
59
960
57 | 0141W09d 50
50 66
888 87
58 61
52
88
100
44
61
59
860
56 | 117100 44 47 44 45 44 44 47 49 47 44 100 47 51 51 51 51 51 51 51 51 51 51 51 51 51 | Cl+LWQ9d S2 < | 14119d 65 67 68 59 51 50 99 99 95 <th< td=""><td>65 66 64 55 53 56 59 51 56 98 51 56 98 51 56 98 51 56 98 51 56 98 51 56 98 51 56 98 51 56 98 51 98 90 96 93 93</td><td>65 65 64 56 53 56 60 61 57 59 53 56 60 60 51 57 99 96 100 95 96 100 95</td><td>thus thus thus</td><td>Status Status 60 62 60 60 58 56 56 55 50 61 58 59 51 58 83 81 83</td><td>%
sequence
identity
scale
100
90
80
70
60
50
50
40</td></th<> | 65 66 64 55 53 56 59 51 56 98 51 56 98 51 56 98 51 56 98 51 56 98 51 56 98 51 56 98 51 56 98 51 98 90 96 93 93 | 65 65 64 56 53 56 60 61 57 59 53 56 60 60 51 57 99 96 100 95 96 100 95 | thus thus thus | Status Status 60 62 60 60 58 56 56 55 50 61 58 59 51 58 83 81 83 | %
sequence
identity
scale
100
90
80
70
60
50
50
40 |
| HEAVY CHAIN B | * Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402
PGDM1403
PGDM1404
PGDM1405
PGDM1405
PGDM1407
PGDM1407
PGDM1410
PGDM1411
PGDM1411
PGT141
PGT142
PGT143
PGT144 | 0041W05d 100
82
93
51
48
48
49
93
51
48
49
93
51
48
49
93
50
44
50
65
65
65
65
66
60 | 1001W09d 82
1000 84
500 51
52 50
84
51
52
51
52
47
52
67
66
55
65
65
65 | COPLWOD 33 84 100 51 50 51 50 49 52 50 81 50 44 65 64 64 66 60 60 60
 | E001/000 51 50 51 100 64 64 72 74 50 66 66 45 77 55 55 56 54 55 56 58 58 58 | *0*FUND50d 48 51 50 64 100 92 58 60 51 94 88 44 62 57 57 55 56 56 | 48 48 49 49 49 49 40 40 40 40 40 40 40 40 40 40 40 40 40 | 49
50
52
58
59
59
58
47
80
53
53
53
53
55
 | L071W09d 49
48
50
74
60
63
74
63
61
47
63
61
49
80
56
56
56
56
56
56
60 | 8041MG9d 79
96
81
50
51
52
49
47
100
51
52
47
51
66
5
65
65
64
61 | 60+LWQ9d 49
51
50
66
94
95
59
63
51
100
88
44
63
59
60
57
58 | 0141W09d 50
50 66
888 87
58 61
52
88
100
44
61
59
860
59 | 1171000 44 47 44 45 44 44 47 49 47 44 100 47 51 51 51 51 51 51 51 51 51 51 51 51 51
 | 21+1WQ9d 52 52 54 77 62 62 80 63 61 47 100 56 56 57 55 58 | 14119d 65 67 65 55 57 58 53 56 66 59 51 56 100 98 99 95 83 | CPL19d 65 66 64 55 57 58 53 56 59 58 51 56 98 90 96 93 81
 | 65
65
64
56
57
59
53
56
65
60
60
51
57
99
96
100
95
83 | ##L19d 64 65 55 51 54 64 57 56 99 39 55 93 95 93 91 00 81 | Spectral 60 62 60 62 60 58 55 60 61 58 59 51 58 83 81 83 81 100
 | %
sequence
identity
scale
100
90
80
70
60
60
50
40 |
HEAVY CHAIN B	* Sequence identity (amino acid) PGDM1400 PGDM1401 PGDM1402 PGDM1405 PGDM1404 PGDM1405 PGDM1407 PGDM1407 PGDM1407 PGDM1401 PGDM1411 PGDM1411 PGDM1411 PGTM411 PGTM42 PGT143 PGT144 PGT145	00FIWQ9d 100 82 93 51 48 49 49 49 50 65 65 65 65 65 64 60	1001W09d 82 100 84 50 51 52 50 84 96 51 52 47 52 67 66 5 65 65 62	Solution	C01 C01 <thc01< th=""> <thc01< th=""> <thc01< th=""></thc01<></thc01<></thc01<>	*0*LWG5d 48 51 50 64 100 92 58 60 51 94 88 44 62 57 57 55 56	48 48 49 64 92 49 64 92 63 52 87 44 62 85 87 44 62 85 87 44 62 55 55 55 56	49 50 52 58 59 59 58 47 80 53 53 53 51 55	L071W09d 49 48 50 74 60 63 74 60 63 74 60 63 61 47 63 61 49 80 56 56 56 56 56 60 87 60 87 60 80 87 60 80 80 80 80 80 80 80 80 80 80 80 80 80	8071WG9d 79 96 81 50 51 52 49 47 51 52 47 51 66 65 64 61	60+LWQ9d 49 51 50 66 94 95 59 63 51 100 88 44 63 59 60 57 58	0141W09d 50 52 50 66 88 75 80 61 52 88 100 44 61 59 58 60 59 58 59	1141000d 44 47 44 45 44 47 49 47 44 100 47 51 51 51 51 51 51	52 52 54 77 62 62 80 61 63 61 47 100 56 57 55 58	14119d 65 67 65 55 57 58 53 56 66 59 51 56 100 98 99 95 83	CPL19d 65 66 64 55 57 58 53 56 65 57 58 51 56 98 90 96 93 81	65 65 64 56 57 59 53 56 65 60 60 51 57 99 96 100 95 83	#FLDd 64 65 65 54 55 51 54 64 57 56 99 95 93 51 100 81	SP1L9d 60 22 60 23 26 <th< td=""><td>% sequence identity scale 100 90 80 70 60 50 40</td></th<>	% sequence identity scale 100 90 80 70 60 50 40
HEAVY CHAIN B	* Sequence identity (amino acid) PGDM1400 PGDM1401 PGDM1402 PGDM1403 PGDM1405 PGDM1405 PGDM1405 PGDM1407 PGDM1407 PGDM1410 PGDM1411 PGT142 PGT143 PGT144 PGT145 PGDM1400	00FIWQ9d 100 82 93 51 48 8 49 49 50 54 49 50 56 5 65 65 65 65 65 65 65 65 100	L0PLWCD9d 82 100 84 50 84 50 48 96 51 52 50 48 96 51 52 67 66 65 52 67 66 88	Solution	S000 S1 S1 S0 S1 S1 S0 S1 S	*000000000000000000000000000000000000	9041W09d 48 52 49 64 92 63 59 63 59 63 59 63 59 63 59 63 55 55 69 69	9041WG9d 49 50 52 72 58 59 100 87 49 59 87 49 59 80 53 53 53 53 53 55 65	L0+LWG9d 49 48 50 40 63 87 100 47 63 80 56 56 56 56 56 56 56 56 56 56 56 56 56	80+LWQ9d 79 96 81 50 51 52 49 47 51 52 47 51 52 47 51 66 65 64 61 88	60+1WQ9d 49 51 50 66 94 95 59 63 51 100 88 84 44 63 59 60 75 8 72	0141W09d 50 52 50 66 88 87 58 60 44 61 59 58 60 44 61 59 58 60 59 72	1141W09d 44 47 44 45 44 447 499 477 444 447 51 51 51 51 51 51 51 65	21+1WQ9d 52 52 54 77 62 80 80 51 63 63 61 56 57 55 58 70 70	17119d 65 67 65 55 57 58 53 56 66 59 51 56 100 98 99 95 83 70	C+LL9d 65 66 64 55 57 58 53 56 65 59 8 100 96 93 81 70	65 65 64 56 57 53 56 65 60 60 51 57 99 96 100 95 83 70	#FLDd 64 65 65 54 55 51 54 64 57 56 99 95 93 91 00 81 70	60 60 62 60 58 56 55 60 61 58 83 81 83 81 100 74	% sequence identity scale 100 90 80 70 60 50 50 40
HEAVY CHAIN B	* Sequence identity (amino acid) PGDM1400 PGDM1401 PGDM1402 PGDM1403 PGDM1405 PGDM1405 PGDM1406 PGDM1407 PGDM1401 PGDM1411 PGT141 PGT142 PGT143 PGT144 PGT144 PGT145 PGDM1400	0071WC9d 100 82 93 51 48 48 49 93 50 44 49 50 44 52 65 65 65 64 60 100 88	L0PLWQ9d 82 100 84 50 52 50 48 96 51 52 50 48 96 51 52 67 66 65 65 65 88 100	Solution	S001 S1 S0 S1 S0 S1 S0 S1 S0 S1 S0 S1 S0 S1 S1 S0 S1 S	400 48 51 50 64 100 92 58 60 51 94 88 44 62 57 57 55 56 69 72 69 72	9000000000000000000000000000000000000	9041WG9d 49 50 52 72 58 59 100 87 49 59 59 59 59 59 53 53 53 53 53 53 53 53 53 53 53 53 53	L09LW09d 49 48 50 63 87 100 47 63 61 49 80 56 56 56 56 56 56 56 56 56 56 56 56 56	80+LWCD9d 79 96 81 50 51 52 49 47 100 51 52 47 51 66 65 65 64 61 88 100	60+1WQ5d 49 51 50 66 94 95 59 63 51 100 88 44 63 59 60 57 58 72 76	0141WG9d 50 52 50 66 88 87 58 61 52 88 61 52 88 61 52 88 60 55 59 58 60 56 59 57 72 76	L111 L121 L121 <thl121< th=""> L121 <thl< td=""><td>21+1WQ9d 52 52 54 77 62 62 80 80 63 61 47 100 56 57 55 58 70 73</td><td>17119d 65 67 65 55 57 58 56 66 59 51 56 100 98 99 95 83 70 72</td><td>C+LL9d 65 66 64 55 57 58 53 56 65 59 58 51 56 98 100 96 93 81 70 72 70 72</td><td>65 65 64 56 57 59 53 56 65 60 60 51 57 99 96 100 95 83 70 72</td><td>FFLL9d 64 65 55 51 54 64 55 51 54 64 57 56 93 95 93 95 100 81 70 72 70 72</td><td>60 62 60 66 56 56 56 56 58 59 51 58 83 81 100 74 72</td><td>% sequence identity scale 100 90 80 70 60 60 50 40</td></thl<></thl121<>	21+1WQ9d 52 52 54 77 62 62 80 80 63 61 47 100 56 57 55 58 70 73	17119d 65 67 65 55 57 58 56 66 59 51 56 100 98 99 95 83 70 72	C+LL9d 65 66 64 55 57 58 53 56 65 59 58 51 56 98 100 96 93 81 70 72 70 72	65 65 64 56 57 59 53 56 65 60 60 51 57 99 96 100 95 83 70 72	FFLL9d 64 65 55 51 54 64 55 51 54 64 57 56 93 95 93 95 100 81 70 72 70 72	60 62 60 66 56 56 56 56 58 59 51 58 83 81 100 74 72	% sequence identity scale 100 90 80 70 60 60 50 40
HEAVY CHAIN B	* Sequence identity (amino acid) PGDM1400 PGDM1401 PGDM1402 PGDM1402 PGDM1404 PGDM1405 PGDM1404 PGDM1407 PGDM1407 PGDM1401 PGDM1411 PGT142 PGT143 PGT144 PGT145 PGDM1400 PGDM1401 PGDM1402	00+LWQSd 00 82 51 48 48 49 93 51 48 49 97 9 50 49 50 55 65 565 65 65 65 64 60 100 88 89 7	L0PLWQ9d 82 100 84 50 51 52 50 48 96 51 52 47 52 47 52 67 66 65 65 62 88 80 90	View View <th< td=""><td>S000 S1 S0 S1 S1 S0 S1 S1 S0 S1 S</td><td>*000000000000000000000000000000000000</td><td>S0PLWG9d 48 48 52 49 64 92 100 59 63 52 95 87 44 62 58 55 56 69 73 71 1</td><td>9071WG9d 49 50 52 58 59 100 87 49 53 53 53 53 53 51 55 65 66 64</td><td>L0PLIWODD 49 488 50 63 87 100 47 63 61 49 80 566 566 564 60 62 64 61</td><td>80+LWG9d 79 96 81 50 51 52 47 100 51 52 47 51 66 65 65 64 61 88 100 90</td><td>60+tW09d 49 51 50 66 94 95 59 63 51 100 88 44 63 59 960 57 58 72 76 74</td><td>0141WG9d 50 52 50 66 88 87 52 88 61 52 88 61 52 88 61 52 88 61 52 88 61 52 88 60 59 59 72 76 74</td><td>1111 11111 1111 1111 <t< td=""><td>21+1W09d 52 52 54 77 62 62 80 80 51 63 61 47 100 56 55 58 70 73 71</td><td>LPLL9d 65 65 55 57 58 53 56 66 59 51 56 66 59 51 56 60 98 99 95 83 70 72 71</td><td>CPLL9d 65 66 64 55 53 56 65 59 58 51 56 58 51 56 59 81 100 93 81 70 72 71</td><td>65 65 64 56 57 59 53 56 65 65 65 60 60 51 57 99 60 51 99 96 100 95 83 70 72 71</td><td>#FLL9d 64 65 55 55 51 54 55 51 54 64 57 56 99 95 100 81 70 72 71 71 71 71</td><td>60 62 60 58 56 55 60 61 58 53 51 58 81 100 74 72 75</td><td>% sequence identity scale 100 90 80 70 60 50 40</td></t<></td></th<>	S000 S1 S0 S1 S1 S0 S1 S1 S0 S1 S	*000000000000000000000000000000000000	S0PLWG9d 48 48 52 49 64 92 100 59 63 52 95 87 44 62 58 55 56 69 73 71 1	9071WG9d 49 50 52 58 59 100 87 49 53 53 53 53 53 51 55 65 66 64	L0PLIWODD 49 488 50 63 87 100 47 63 61 49 80 566 566 564 60 62 64 61	80+LWG9d 79 96 81 50 51 52 47 100 51 52 47 51 66 65 65 64 61 88 100 90	60+tW09d 49 51 50 66 94 95 59 63 51 100 88 44 63 59 960 57 58 72 76 74	0141WG9d 50 52 50 66 88 87 52 88 61 52 88 61 52 88 61 52 88 61 52 88 61 52 88 60 59 59 72 76 74	1111 11111 1111 1111 <t< td=""><td>21+1W09d 52 52 54 77 62 62 80 80 51 63 61 47 100 56 55 58 70 73 71</td><td>LPLL9d 65 65 55 57 58 53 56 66 59 51 56 66 59 51 56 60 98 99 95 83 70 72 71</td><td>CPLL9d 65 66 64 55 53 56 65 59 58 51 56 58 51 56 59 81 100 93 81 70 72 71</td><td>65 65 64 56 57 59 53 56 65 65 65 60 60 51 57 99 60 51 99 96 100 95 83 70 72 71</td><td>#FLL9d 64 65 55 55 51 54 55 51 54 64 57 56 99 95 100 81 70 72 71 71 71 71</td><td>60 62 60 58 56 55 60 61 58 53 51 58 81 100 74 72 75</td><td>% sequence identity scale 100 90 80 70 60 50 40</td></t<>	21+1W09d 52 52 54 77 62 62 80 80 51 63 61 47 100 56 55 58 70 73 71	LPLL9d 65 65 55 57 58 53 56 66 59 51 56 66 59 51 56 60 98 99 95 83 70 72 71	CPLL9d 65 66 64 55 53 56 65 59 58 51 56 58 51 56 59 81 100 93 81 70 72 71	65 65 64 56 57 59 53 56 65 65 65 60 60 51 57 99 60 51 99 96 100 95 83 70 72 71	#FLL9d 64 65 55 55 51 54 55 51 54 64 57 56 99 95 100 81 70 72 71 71 71 71	60 62 60 58 56 55 60 61 58 53 51 58 81 100 74 72 75	% sequence identity scale 100 90 80 70 60 50 40
HEAVY CHAIN B	* Sequence identity (amino acid) PGDM1400 PGDM1401 PGDM1402 PGDM1403 PGDM1405 PGDM1405 PGDM1405 PGDM1407 PGDM1407 PGDM1411 PGDM1412 PGT143 PGT143 PGT144 PGT145 PGDM1400 PGDM1400 PGDM1403	00FLWG9d 100 82 93 51 48 48 49 97 9 50 44 49 79 49 50 44 49 50 44 52 65 65 65 65 65 65 60 100 88 897 71	L0PLWQDd 22 820 84 50 51 52 50 67 66 55 67 66 55 67 66 56 52 88 80 090 73	View View <th< td=""><td>5000 51 500 51 1000 64 64 64 500 66 666 666 555 555 556 558 711 733 7100 71</td><td>*0*LWG9d 48 51 50 64 100 92 58 60 51 94 88 44 62 57 57 55 56 69 72 71 71</td><td>S0PLIWODDd 48 42 49 92 100 59 53 52 95 87 44 62 58 58 55 56 69 73 71</td><td>90+LWQDJd 49 502 72 588 599 588 47 49 598 533 533 533 533 53 55 66 66 64 76</td><td>L0PLIWODD 49 48 50 63 87 100 63 87 47 63 61 49 80 56 56 56 54 60 62 64 61 76</td><td>80+LWQ9d 79 96 81 50 51 52 49 47 100 51 51 52 47 51 66 56 64 61 88 8100 90 73</td><td>60+1WG9d 9 51 50 66 94 95 59 63 51 100 88 44 63 59 60 88 44 59 57 57 57 57 57 72 74 74</td><td>0141W09d 50 50 52 50 66 88 87 58 61 52 88 100 44 61 59 88 60 56 59 72 76 74 73</td><td>L14LMD9d 44 47 44 45 44 47 44 47 47 44 47 47 44 47 51 51 51 51 51 51 51 51 51 51 51 51 51</td><td>2141MG9d 52 52 54 77 62 62 80 51 63 61 63 61 56 55 58 70 73 71 88</td><td>1+1L5d 65 55 57 58 53 56 66 59 51 56 100 98 99 58 70 72 71 69</td><td>656 664 55 57 58 53 56 65 59 51 56 98 100 96 93 81 70 72 71 69</td><td>65 65 64 56 57 59 53 56 65 65 60 60 51 57 99 60 51 57 99 63 70 72 71 68</td><td>*** *** 64 65 55 55 51 54 64 55 55 51 54 64 57 56 99 395 100 81 70 72 71 70</td><td>602 602 58 56 56 55 601 58 591 58 833 81 100 74 75 71</td><td>% sequence identity scale 100 90 80 70 60 50 50 40</td></th<>	5000 51 500 51 1000 64 64 64 500 66 666 666 555 555 556 558 711 733 7100 71	*0*LWG9d 48 51 50 64 100 92 58 60 51 94 88 44 62 57 57 55 56 69 72 71 71	S0PLIWODDd 48 42 49 92 100 59 53 52 95 87 44 62 58 58 55 56 69 73 71	90+LWQDJd 49 502 72 588 599 588 47 49 598 533 533 533 533 53 55 66 66 64 76	L0PLIWODD 49 48 50 63 87 100 63 87 47 63 61 49 80 56 56 56 54 60 62 64 61 76	80+LWQ9d 79 96 81 50 51 52 49 47 100 51 51 52 47 51 66 56 64 61 88 8100 90 73	60+1WG9d 9 51 50 66 94 95 59 63 51 100 88 44 63 59 60 88 44 59 57 57 57 57 57 72 74 74	0141W09d 50 50 52 50 66 88 87 58 61 52 88 100 44 61 59 88 60 56 59 72 76 74 73	L14LMD9d 44 47 44 45 44 47 44 47 47 44 47 47 44 47 51 51 51 51 51 51 51 51 51 51 51 51 51	2141MG9d 52 52 54 77 62 62 80 51 63 61 63 61 56 55 58 70 73 71 88	1+1L5d 65 55 57 58 53 56 66 59 51 56 100 98 99 58 70 72 71 69	656 664 55 57 58 53 56 65 59 51 56 98 100 96 93 81 70 72 71 69	65 65 64 56 57 59 53 56 65 65 60 60 51 57 99 60 51 57 99 63 70 72 71 68	*** *** 64 65 55 55 51 54 64 55 55 51 54 64 57 56 99 395 100 81 70 72 71 70	602 602 58 56 56 55 601 58 591 58 833 81 100 74 75 71	% sequence identity scale 100 90 80 70 60 50 50 40
HEAVY CHAIN B	* Sequence identity (amino acid) PGDM1400 PGDM1401 PGDM1402 PGDM1403 PGDM1405 PGDM1405 PGDM1405 PGDM1407 PGDM1401 PGDM1410 PGDM1411 PGT142 PGT143 PGT144 PGT145 PGDM1400 PGDM1401 PGDM1402 PGDM1404	00+tWC9d 100 82 93 51 48 49 49 49 49 50 44 52 65 65 65 65 64 60 100 88 97 71 69	L0FLWQ9d 82 1000 84 50 51 52 500 51 52 50 66 51 52 7 72 88 80 90 73 72	C000000000000000000000000000000000000																
 | S000 51 501 51 501 51 1000 64 64 72 66 66 65 55 55 55 56 54 711 73 1000 71 | *0*LWG9d 48 48 51 50 64 100 92 58 60 51 94 88 44 62 57 57 55 69 72 71 100 | S0PLWQDDd 48 42 49 92 100 59 63 52 95 87 44 62 58 58 55 56 69 731 71 85 | 90+LWQ9d 49
502
72
58
59
59
58
59
59
58
70
87
49
59
58
70
87
87
87
87
80
53
53
53
53
55
55
66
64
76
67 | L0PHWQ5d 99
498
500
477
633
61
47
633
61
47
633
61
90
56
56
56
56
56
56
60
62
64
61
76
65 | 80+1WG5d 99
96
50
51
52
49
51
52
47
100
51
52
47
100
51
52
47
66
65
65
64
61
88
00
90
73
72 | 60+1WG9d 9
51
50
66
94
95
59
60
88
44
63
59
59
60
72
76
67
74
88 | 0141M09d 0052 0066 888 875 0066 888 007 007 007 007 007 007 007 007 007 | LLPLWQDD 4 447 445 444 457 449 477 444 444 1000 477 511 511 511 655 657 668 67
 | C141W009d 52 552 54 777 62 620 800 511 633 613 61 626 56 556 58 700 73 71 88 72 72 | 1+115d 65 55 57 58 53 56 59 51 100 98 99 53 70 72 71 69 67 | CPLL5d 656 664 557 583 566 599 581 500 993 81 702 711 669 667
</td <td>65 65 65 56 57 59 53 56 60 61 57 99 96 100 95 83 70 71 68 66</td> <td>11 12 13 14 15 16 <th< td=""><td>60 60 60 58 56 55 60 61 58 56 59 51 58 83 81 83 81 74 75 71 69 51</td><td>%
sequence
identity
scale
100
90
80
70
60
60
50
40</td></th<></td> | 65 65 65 56 57 59 53 56 60 61 57 99 96 100 95 83 70 71 68 66 | 11 12 13 14 15 16 <th< td=""><td>60 60 60 58 56 55 60 61 58 56 59 51 58 83 81 83 81 74 75 71 69 51</td><td>%
sequence
identity
scale
100
90
80
70
60
60
50
40</td></th<> | 60 60 60 58 56 55 60 61 58 56 59 51 58 83 81 83 81 74 75 71 69 51
 | %
sequence
identity
scale
100
90
80
70
60
60
50
40 |
| HEAVY CHAIN B | * Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402
PGDM1402
PGDM1404
PGDM1405
PGDM1405
PGDM1405
PGDM1407
PGDM1407
PGDM1410
PGDM1411
PGT142
PGT143
PGT144
PGT145
PGDM1400
PGDM1401
PGDM1401
PGDM1402
PGDM1402
PGDM1403 | 00+LWG5d 00
82
93
51
48
49
49
79
49
50
54
44
52
65
65
65
64
60
100
88
97
71
69
69
69 | L0PLWQ9d 22
1000 84
500 51
52 50
48
96
51
52
47
52
67
66
65
65
65
65
88
1000
90
73
73
73
73 | 201 WOD 3 93 84 1 50 51 50 81 50 81 50 81 50 44 55 64 65 64 65 97 90 100 71 71 71 71 71 71
 | S000 S1 500 51 1000 64 64 50 66 66 45 77 555 56 54 58 71 73 7100 71 71 71 | *0*LW000d 48 50 64 1000 92 58 60 51 94 62 57 55 56 69 72 71 100 85 57 | S0FLWQDSd 8 48 52 64 92 63 52 95 63 52 95 58 59 55 56 69 73 71 85 100 52 | 90+1WQ9d 49 502 72 58 59 100
 87 49 59 58 47 80 53 53 51 55 66 64 76 67 67 67 67 | L0PLINICIDA 49
48
50
47
60
63
74
60
63
74
63
61
49
80
56
56
56
56
60
62
64
61
76
65
64
61
76
65
64 | 80+1WG5d 99
96
81
50
51
52
49
66
65
65
47
100
51
52
47
100
51
52
47
100
51
52
73
73
73
73 | 604FMQ9d
49
51
50
66
49
55
63
51
00
88
44
63
559
60
57
58
72
76
74
86
96 | 0141M09d 50
52
50
66
88
87
52
88
60
52
58
60
59
59
72
76
44
60
59
59
72
76
73
85
82 | L14LMG9d 447 44 45 44 447 499 477 444 445 100 477 511 511 65 657 668 667 62 100 657 668 667 62 100 657 668 667 62 100 657 668 667 62 100 657 668 667 62 100 657 668 667 62 100 657 658 657 657 658 657 657 657 657 657 657 657 657 657 657
 | CL1FLWQDDd 52 54 77 62 80 51 63 61 47 1000 56 57 55 70 73 71 88 70 73 71 88 72 72 | 14119d 65 55 57 8 53 56 66 59 51 56 00 99 95 83 70 72 71 9 66 66 66 66 66 66 99 95 83 70 72 71 9 66 | 65 66 64 55 57 85 56 59 8 51 56 98 51 56 59 8 11 69 93 81 70 72 71 69 66 <td>65 65 66 65 56 64 57 59 53 56
 60 60 51 57 99 96 100 95 70 72 71 66 66 66</td> <td>11 12 13 14 15 16 <th< td=""><td>60 60 56 56 57 60 61 58 58 83 81 83 100 74 72 75 69 69</td><td>%
sequence
identity
scale
100
90
80
70
60
60
50
40</td></th<></td> | 65 65 66 65 56 64 57 59 53 56 60 60 51 57 99 96 100 95 70 72 71 66 66 66 | 11 12 13 14 15 16 <th< td=""><td>60 60 56 56 57 60 61 58 58 83 81 83 100 74 72 75 69 69</td><td>%
sequence
identity
scale
100
90
80
70
60
60
50
40</td></th<> | 60 60 56 56 57 60 61 58 58 83 81 83 100 74 72 75 69 69
 | %
sequence
identity
scale
100
90
80
70
60
60
50
40 |
| IN HEAVY CHAIN B | * Sequence
identity
(amino acid)
PGDM1400
PGDM1402
PGDM1402
PGDM1402
PGDM1405
PGDM1406
PGDM1406
PGDM1406
PGDM1407
PGDM1407
PGDM1409
PGDM1409
PGDM1411
PGT141
PGT141
PGT142
PGT143
PGT144
PGT144
PGT144
PGT144
PGT144
PGT144
PGT144
PGT144
PGT144
PGDM1400
PGDM1400
PGDM1403
PGDM1403
PGDM1403
PGDM1403 | 00+tWG9d
1000
82
93
51
48
49
93
51
48
49
93
50
44
97
950
44
97
50
44
265
655
65
65
664
60
1000
88
97
71
69
65
65
65 | L0PLWQDDd 22
8200
84
500
511
522
67
665
655
652
888
1000
900
732
73
665
655
655
655
655
655
655
655
655
65 | C0+LWQDD 3 93 84 100 51 50 81 50 81 50 64 64 64 64 64 64 64 71 71 64 64
 | S00FLWQ9d 51 500 64 64 64 64 66 45 77 555 556 54 58 71 71 70 71 71 76 | *0*LW000d 48 510 64 1000 92 58 60 511 94 82 57 55 56 69 72 71 100 85 67 | S0PLWQDSd 48 48 249 64 92 100 59 63 52 95 63 587 44 62 58 595 56 69 73 71 71 71 71 100 67 | 90+LWQ5d 49 502 72 58 59 87
 49 59 58 57 80 53 53 51 55 66 64 76 71 100 72 | L0PLWQ9d 9 48 50 74 60 63 87 100 47 63 61 49 80 566 566 54 60 62 64 61 76 56 64 93 93 | 80+LWQ9d 9
96 81
50 51
52 49
47
1000
51
52 47
51
66 65
64
61
88
100
90
73
2
73
66 | 604FIMG9d
49
50
66
95
55
63
51
1000
57
58
60
57
58
72
76
74
74
86
96
67
72 | 0141MG9d 50 52 50 666 88 87 55 666 887 558 61 52 88 61 52 88 61 52 88 61 52 88 61 559 72 76 74 73 85 88 269 72 76 74 73 85 88 269 72 76 74 73 85 88 269 72 76 74 73 85 88 75 75 75 75 75 75 75 75 75 75 75 75 75 | LLFLWQDDd 44 447 444 447 449 477 444 447 499 51 655 677 68 667 668 667 662 666 1
 | C14FIMQ9d 52 554 77 62 62 80 80 511 63 63 61 47 100 56 57 55 58 70 73 71 88 872 72 78 72 | 1+1129d 65 7 8 5< | 656 64 55 57 58 56 59 81 100 93 81 70 72 71 69 66 65 66 65 66
 | 65 64 56 57 59 56 60 51 57 99 90 95 83 70 71 66 64 66 | ##L19d 645 55 51 54 57 59 33 95 100 81 70 72 71 70 86 66 70 71 70 86 66 66 66 66 66 66 66 < | 571103 60 602 60 58 56 55 60 58 59 51 83 81 100 74 72 75 71 69 64
 | %
sequence
identity
scale
100
90
80
70
60
50
50
40 |
| HAIN HEAVY CHAIN B | * Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402
PGDM1403
PGDM1405
PGDM1405
PGDM1405
PGDM1407
PGDM1407
PGDM1401
PGDM1410
PGDM1411
PGT141
PGT141
PGT142
PGT143
PGT144
PGT145
PGDM1400
PGDM1400
PGDM1401
PGDM1402
PGDM1400
PGDM1402
PGDM1400
PGDM1402
PGDM1400
PGDM1402
PGDM1402
PGDM1404
PGDM1405
PGDM1407
PGDM1406
PGDM1407
PGDM1406
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407 | 0071W0001
1000
82
93
51
48
48
49
979
49
500
44
452
655
655
655
654
60
1000
88
977
71
69
965
652
652
652
652
652
652
652
652
652
6 | L0PLWQ9d 82
84
50
51
52
50
48
96
51
52
47
52
47
52
47
66
65
565
65
65
88
800
90
73
72
366
66
64 | C0+LWQDSd 93 93 84 100 51 50 81 50 81 50 84 54 65 64 66 97 90 71 71 71 64 61 64
 | 501 50 51 50 51 50 51 50 64 72 74 50 66 66 45 55 56 55 56 58 71 71 71 76 76 76 | *0*LWQ9d 48 48 50 64 100 92 58 60 51 94 88 444 62 57 57 556 69 71 100 85 67 657 57 | S0FLWQDS 48 48 52 49 64 92 63 59 63 52 87 44 62 68 58 55 69 73 71 85 100 67 64 67 64 | 90+LWQ9d 49 49 52 72 58 59
 100 87 49 58 47 80 53 53 53 55 66 64 76 67 100 93 53 | L0PLWQ9d 9 48 50 74 603 877 1000 477 663 611 49 800 566 566 564 60 62 641 766 564 93 1000 676 654 93 1000 676 655 656 655 655 655 655 655 655 655 | 80+LWG9d 9
96 81
50 51
52 49
47
1000
51
52 47
51
66
65
64
61
88
100
90
73
72
66
64
61 | 6041MG9d 49
51
50
66
94
95
59
63
51
100
88
84
44
63
59
60
57
58
72
67
74
74
86
66
7
67
67
64
96 | 0141MG9d 50 52 50 666 88 7 58 61 52 88 100 56 59 72 76 74 73 85 269 67 74 73 58 269 67 74 74 74 74 74 74 75 75 75 75 75 75 75 75 75 75 75 75 75 | LLFLWDDD 44 47 44 45 44 47 49 47 44 44 47 49 47 44 44 47 51 51 51 51 51 51 51 51 51 51 51 51 51
 | 21+1/2009d 32 522 54 777 62 800 80 511 63 614 47 1000 56 575 558 701 88 722 78 76 78 76 78 | 141L9d 55 557 58 53 56 65 59 51 66 59 99 51 66 65 65 99 51 66 65 65 99 51 66 65 65 99 51 66 65 65 65 65 65 65 65 65 65 65 65 65 | 74L19d 566 64 557 58 53 566 59 58 100 96 93 81 702 71 69 66 63 56 53 56 53 56 59 58 100 96 93 81 702 71 69 66 63 55 56 53 56 57 58 51 69 93 81 702 71 69 66 63 55 56 57 58 51 66 53 58 51 66 53 58 51 66 53 51 66 63 51 66 63 51 66 63 51 66 63 51 66 63 51 66 63 51 66 63 51 66 63 51 63 51 63 51 66 63 51 64 51 64 65 65
 | 65 64 56 65 64 56 57 53 56 60 51 57 99 96 100 95 83 702 71 68 66 66 64 62 | 171 100 100 </td <td>581100 60 62 60 58 56 55 60 61 58 59 51 58 59 51 83 81 100 74 75 71 69 64 62</td> <td>%
sequence
identity
scale
100
90
80
70
60
60
50
40</td> | 581100 60 62 60 58 56 55 60 61 58 59 51 58 59 51 83 81 100 74 75 71 69 64 62
 | %
sequence
identity
scale
100
90
80
70
60
60
50
40 |
| F CHAIN HEAVY CHAIN B | * Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402
PGDM1402
PGDM1404
PGDM1405
PGDM1404
PGDM1405
PGDM1407
PGDM1401
PGDM1411
PGT141
PGT142
PGT143
PGT144
PGT144
PGT145
PGDM1400
PGDM1401
PGDM1402
PGDM1402
PGDM1403
PGDM1403
PGDM1403
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405 | 00+tWG9d
100
82
93
51
84
84
84
99
93
51
82
93
51
84
84
99
95
04
45
265
65
65
65
64
60
100
88
97
1
69
69
65
62
88
87 | L0PLWQ9d 82
500 84
501 52
500 84
51 52
500 48
51 52
50 65
65
65
65
65
65
65
65
65
65
65
65
65
6 | C0+FIMOD 33 84 1000 51 50 50 50 50 50 50 54 54 65 64 65 64 65 900 100 71 71 64 61 90 2 2 | S000 S11 500 511 1000 64 64 72 744 76 555 56 544 58 711 71 76 73 71 76 73 71 | *0*LWG9d #8 48 51 500 64 92 58 60 51 94 88 444 62 577 555 560 722 711 1000 857 725 711 1000 857 722 72 713 1000 857 672 72 | S0FLWQDD 48 48 52 49 64 59 63 52 95 87 44 62 58 59 55 56 69 73 71 85 100 67 64 73 71 | 9011000 49 50 52 72 58 59 100 87 59 59 58 74 49 59 53 53 53 51 55 66 64 67 67 67 67 67 67 67 67 67 67 67 67 67 | L0PLWQDD 49
48
50
74
60
387
100
47
63
87
100
47
63
56
56
56
64
176
65
49
3
100
64
64
176
65
64
176
65
64
176
65
64
176
65
64
176
65
65
176
176
176
176
176
176
176
176
176
176 | 804FMG29d 79
96
81
50
51
52
49
47
51
52
47
51
52
47
51
52
47
51
52
47
51
52
47
51
52
47
51
52
47
51
52
47
51
52
49
66
56
56
56
57
52
49
60
51
52
52
52
52
52
52
52
52
52
52
52
52
52 | 60+LWQ9d 49 51 50 66 94 95 51 100 88 63 59 60 57 58 72 76 74 86 667 64 76 764 76 | 0141MG9d 50 52 50 66 88 87 58 61 52 88 100 44 61 55 86 65 59 72 76 74 73 85 86 96 76 76 76 76 76 76 76 76 76 76 76 76 76 | LLFLWQDD 44 47 44 44 44 44 44 44 44 44 44 44 44 | ZL12 Subscription Subscription <thsubscription< th=""> Subscription</thsubscription<> | 1+1120d 65 55 57 58 53 56 59 55 56 1000 98 99 95 83 70 72 71 69 66 66 72 70 66 66 72 71 66 66 72 71 66 66 72 71 71 76 66 66 72 71 71 71 76 66 53 72 71 71 72 76 72 76 72 71 74 | 7+L19d 65 666 64 55 75 85 53 56 59 58 51 56 98 100 93 81 70 72 76 66 63 72 76 66 63 72 71 67 66 63 72 71 96 72 71 96 72 71 96 72 71 96 72 71 96 72 71 96 65 72 71 96 72 71 96 72 71 96 72 71 96 72 71 96 72 71 96 72 71 96 72 71 96 72 71 96 72 71 96 72 71 96 72 71 96 72 71 96 72 71 96 72 71 96 71 71 71 71 71 71 < | 65 64 56 65 64 56 57 53 56 60 51 57 99 96 100 95 83 70 71 68 66 64 62 72 | ##LL9d 4 65 55 51 54 55 51 54 64 70 70 88 86 63 72 70 68 66 63 72 70 68 66 63 72 70 68 66 63 72 70 68 63 72 70 | 541153d 60 62 60 58 56 56 56 58 83 81 100 74 72 75 69 69 64 62 72 | %
sequence
identity
scale
100
90
80
70
60
50
40 |
| SHT CHAIN HEAVY CHAIN B | * Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402
PGDM1402
PGDM1403
PGDM1406
PGDM1406
PGDM1406
PGDM1407
PGDM1400
PGDM1410
PGDM1411
PGT141
PGT141
PGT144
PGT144
PGT144
PGT144
PGT144
PGT144
PGT144
PGDM1400
PGDM1400
PGDM1403
PGDM1403
PGDM1404
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM14 | 00+tWQ0Jd 000 82 93 511 48 48 49 979 49 50 444 52 655 655 655 655 656 64 60 1000 88 977 711 69 96 55 28 88 72 20 55 52 50 55 50 50 50 50 50 50 50 50 50 50 50 | L0PLWQ9d 82
100
84
50
51
52
50
67
66
51
52
67
66
51
52
67
66
51
52
73
66
4
100
90
73
72
73
66
4
100
90
77
72
73 | C04FIMICODI 93 84 1000 511 50 81 500 811 500 81 500 81 500 444 645 660 900 1000 711 711 644 641 610 900 711 711 641 900 741 741 611 900 741 741 641 900 741 741 641
 | S000 51 500 51 1000 64 64 72 74 66 66 66 65 55 54 58 71 71 76 73 74 73 74 73 74 73 74 73 74 73 | *0*LWG9d 48 48 51 50 64 100 92 58 60 94 88 44 62 57 55 56 69 72 71 100 85 675 65 72 86 | S0PLWQDS 48 48 52 49 64 92 100 59 63 95 87 44 62 58 55 56 69 73 71 71 85 100 67 64 73 96 92 |
9011000
49
50
52
72
58
59
1000
87
59
59
59
59
59
59
59
59
59
59
59
59
59 | L041MGDd 49
488
507
60
63
87
100
63
61
49
63
61
49
63
61
49
63
61
49
63
61
63
66
66
66
66
66
66
66
66
66
66
66
66 | 804FMG9d 79
96
81
50
51
52
49
47
51
52
47
51
52
47
51
52
47
51
52
47
51
52
47
51
52
47
51
52
47
51
52
47
51
52
51
52
73
66
65
65
65
65
65
73
72
73
66
64
100
73
72
73
66
72
73
72
73
73
66
72
73
72
73
72
73
72
73
72
73
72
73
72
73
72
73
72
73
72
73
72
73
72
73
72
73
72
73
72
73
72
73
72
73
73
72
73
73
72
73
73
73
73
73
73
73
73
74
73
74
75
74
75
74
75
75
75
75
75
75
75
75
75
75
75
75
75 | 6041M0Dd 49
51
50
66
59
59
63
51
100
88
44
63
59
57
58
72
76
74
86
96
67
74
74
86
96
67
74
74
86
96
67
74
74
86
96
75
75
72
76
74
76
76
76
76
76
76
76
76
76
76
76
76
76 | 0141M0Dod 50
50
50
66
88
87
58
60
52
50
66
88
87
58
80
44
459
58
60
44
459
58
50
72
76
74
38
58
85
85
85
85
72
76
85
85
85
85
85
85
85
85
85
85
80
85
80
80
80
80
80
80
80
80
80
80
80
80
80 | L1FLWQDd 44 47
44 47
44 44
44 44
44
44
44
47
44
44
44
47
44
44
47
44
44
 | CL14LWQDod S2 S2 S4 77 S2 S2 S4 77 S2 S2 S4 77 S2 S2 S4 S3 S6 S5 S5 S6 70 73 71 88 72 72 78 73 71 88 72 72 73 75 55 58 70 73 75 73 75 73 75 75 76 73 75 75 76 73 75 76 73 75 76 73 75 76 73 75 76 73 75 76 73 75 76 73 75 76 73 75 76 73 75 76 73 75 76 75 76 73 75 76 73 75 76 75 76 75 76 76 75 76 76 76 76 76 | 17110d 65 55 58 53 56 59 51 56 59 51 56 100 98 99 83 70 72 71 66 66 63 72 71 66 66 63 72 66 63 72 66 63 72 66 63 72 66 63 72 66 63 72 66 63 72 66 63 72 66 63 72 66 63 72 66 63 72 66 63 72 66 63 72 66 63 72 66 63 72 66 63 72 66 63 72 66 63 72 66 65 63 72 66 65 72 66 65 72 66 65 72 66 72 73 74 74 74 74 74 74 <t< td=""><td>74119d 65 666 64 55 58 53 56 59 58 51 56 98 100 96 93 81 70 72 71 666 653 72 666 653 72 666 663 72 666<!--</td--><td>EPIL50 65 64 56 64 57 59 53 56 60 60 51 57 99 96 65 63 70 71 86 66 64 22 71 866 66 64 72 71 866 66 64 72 71 866 66 64 72 83 70 72 71 866 66 64 72 83 70 72 71 866 66 64 72 83 70 72 71 866 66 64 72 83 70 72 71 866 66 64 72 83 70 72 71 866 66 64 72 83 70 72 71 86 83 70 72 83 70 72 83 70 72 83 70 72 71 83 70 72 83 72</td><td>171LDd 64 65 55 51 54 55 51 54 55 51 54 55 95 95 95 95 9100 81 70 72 71 70 86 86 63 72 70</td><td>60 62 60 62 60 56 56 56 57 58 81 83 81 74 72 75 71 69 64 272 73 22</td><td>%
sequence
identity
scale
100
90
80
70
60
50
50
40</td></td></t<> | 74119d 65 666 64 55 58 53 56 59 58 51 56 98 100 96 93 81 70 72 71 666 653 72 666 653 72 666 663 72 666
</td <td>EPIL50 65 64 56 64 57 59 53 56 60 60 51 57 99 96 65 63 70 71 86 66 64 22 71 866 66 64 72 71 866 66 64 72 71 866 66 64 72 83 70 72 71 866 66 64 72 83 70 72 71 866 66 64 72 83 70 72 71 866 66 64 72 83 70 72 71 866 66 64 72 83 70 72 71 866 66 64 72 83 70 72 71 86 83 70 72 83 70 72 83 70 72 83 70 72 71 83 70 72 83 72</td> <td>171LDd 64 65 55 51 54 55 51 54 55 51 54 55 95 95 95 95 9100 81 70 72 71 70 86 86 63 72 70</td> <td>60 62 60 62 60 56 56 56 57 58 81 83 81 74 72 75 71 69 64 272 73 22</td> <td>%
sequence
identity
scale
100
90
80
70
60
50
50
40</td> | EPIL50 65 64 56 64 57 59 53 56 60 60 51 57 99 96 65 63 70 71 86 66 64 22 71 866 66 64 72 71 866 66 64 72 71 866 66 64 72 83 70 72 71 866 66 64 72 83 70 72 71 866 66 64 72 83 70 72 71 866 66 64 72 83 70 72 71 866 66 64 72 83 70 72 71 866 66 64 72 83 70 72 71 86 83 70 72 83 70 72 83 70 72 83 70 72 71 83 70 72 83 72 | 171LDd 64 65 55 51 54 55 51 54 55 51 54 55 95 95 95 95 9100 81 70 72 71 70 86 86 63 72 70 | 60 62 60 62 60 56 56 56 57 58 81 83 81 74 72 75 71 69 64 272 73 22
 | %
sequence
identity
scale
100
90
80
70
60
50
50
40 |
| LIGHT CHAIN HEAVY CHAIN B | * Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402
PGDM1402
PGDM1403
PGDM1405
PGDM1406
PGDM1406
PGDM1407
PGDM1410
PGDM1411
PGT141
PGT142
PGT143
PGT144
PGT144
PGT145
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1406
PGDM1407
PGDM1406
PGDM1407
PGDM1406
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407 | 00+tWQ0Jd
100
82
93
51
48
48
49
97
95
00
49
50
65
65
65
65
64
60
88
897
71
69
965
65
88
872
72
25 | L0PLWQDd 82
100 84
50 51
52 50
67
66
65
65
65
65
65
88
00
73
72
73
66
64
100
73
76
66
64
100
73
76
76
76
76 | C04FIMICPOd 93 84 1000 51 50 50 51 50 81 50 50 81 50 64 65 60 97 900 711 71 64 61 90 74 74 74 74 74 74
 | 8000000000000000000000000000000000000 | *0*LWQ9d 48 51 50 64 51 50 64 50 51 94 88 60 51 94 88 57 55 69 72 71 100 85 67 65 72 86 85 | S0PLWQDD 48 52 49 64 59 63 52 95 63 52 95 56 69 73 71 71 85 55 69 73 71 71 85 55 66 73 71 71 85 73 71 71 85 73 71 71 85 73 71 71 86 73 71 71 85 73 71 71 85 73 71 71 86 82 23 74 74 74 < | 901 902 902 902 902 902 902
 902 902 902 902 902 902 902 903 902 903 903 904 903 905 903 903 903 903 903 904 903 905 903 903 903 903 903 904 903 905 903 904 903 905 903 904 903 905 903 905 903 904 903 905 903 904 903 905 903 904 903 905 903 904 903 905 903 904 904 905 | L0PLWQDJ 49 48 50 63 74 66 63 74 63 66 74 66 66 74 66 66 74 67 66 66 74 67 66 66 74 66 66 74 66 66 74 66 66 74 74 74 74 74 74 74 74 74 74 74 74 74 | 804FMG9d 79
96
81
50
51
52
49
47
51
52
49
47
51
52
49
51
52
49
51
52
49
51
52
49
51
52
65
65
65
65
64
61
88
100
90
73
27
3
66
66
67
67
90
67
87
90
87
87
87
87
87
87
87
87
87
87
87
87
87 | 60+LWQOJd 49 51 50 66 94 95 51 100 66 59 63 51 100 88 44 63 59 60 57 58 72 76 74 86 67 64 66 100 85 | 0141M000
500
520
500
668
887
588
61
52
888
601
59
58
601
72
76
74
73
58
609
72
76
74
73
58
609
67
60
76
83
100
66
83
83
82
609
67
83
83
83
83
83
83
83
83
83
83
83
83
83 | LLFLWQDd 44 47 44 44 44 44 44 44 44 44 44 44 44
 | CLFFLWQODd 52 52 54 77 62 62 63 61 63 63 61 63 63 64 64 65 65 55 58 70 73 71 88 72 78 76 75 76 75 76 76 76 | 1+1129d 65 67 65 55 57 58 53 66 59 51 56 66 59 51 56 66 59 95 51 56 66 59 95 51 56 66 59 95 51 56 66 59 95 51 56 66 59 95 51 56 66 57 71 69 67 66 65 37 26 68 68 50 72 71 69 67 66 65 37 26 88 50 72 71 69 67 68 68 50 72 71 69 76 66 65 37 26 88 85 70 72 71 69 76 66 63 72 71 69 76 66 65 72 73 88 70 72 71 69 76 <t< td=""><td>CPLLDd 65 66 64 55 75 83 56 65 98 100 96 93 81 702 71 69 66 65 63 72 71 69 67 66 65 63 72 71 69 67 68 68 64 65 63 72 71 69 67 68 68 65 72 71 69 76 66 63 72 71 69 76 66 63 72 71 69 76 66 63 68 66 64 65 63 72 71 69 76 66 63 72 71 69 76 66 63 68 66 68 66 68 66 68 66 68 66 68 68 68 68 70 70 71 69 70 70 71 69 70 <</td><td>65 64 57 593 56 65 64 57 593 56 65 60 61 57 99 61 00 95 83 702 71 68 66 64 62 76 68 66 64 62 76 68 67 68</td><td>171L0d 64 65 65 55 51 54 57 56 95 935 100 81 70 72 71 70 68 66 63 72 70</td><td>60 62 60 62 60 56 56 56 55 55 51 58 381 83 81 100 742 75 71 69 64 62 72 73 73 73 73 73 74 73 73 74 73 74 73 74 73 73 74 73 74 73 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 74 74 75 74 74 74 75 74 74 75 74 74 75</td><td>%
sequence
identity
scale
100
90
80
70
60
60
50
40</td></t<> | CPLLDd 65 66 64 55 75 83 56 65 98 100 96 93 81 702 71 69 66 65 63 72 71 69 67 66 65 63 72 71 69 67 68 68 64 65 63 72 71 69 67 68 68 65 72 71 69 76 66 63 72 71 69 76 66 63 72 71 69 76 66 63 68 66 64 65 63 72 71 69 76 66 63 72 71 69 76 66 63 68 66 68 66 68 66 68 66 68 66 68 68 68 68 70 70 71 69 70 70 71 69 70 <
 | 65 64 57 593 56 65 64 57 593 56 65 60 61 57 99 61 00 95 83 702 71 68 66 64 62 76 68 66 64 62 76 68 67 68 | 171L0d 64 65 65 55 51 54 57 56 95 935 100 81 70 72 71 70 68 66 63 72 70 | 60 62 60 62 60 56 56 56 55 55 51 58 381 83 81 100 742 75 71 69 64 62 72 73 73 73 73 73 74 73 73 74 73 74 73 74 73 73 74 73 74 73 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 73 74 74 74 74 75 74 74 74 75 74 74 75 74 74 75
 | %
sequence
identity
scale
100
90
80
70
60
60
50
40 |
| LIGHT CHAIN HEAVY CHAIN B | * Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402
PGDM1402
PGDM1405
PGDM1404
PGDM1405
PGDM1407
PGDM1407
PGDM1409
PGDM1410
PGDM1411
PGT142
PGT143
PGT144
PGT144
PGT1445
PGDM1400
PGDM1400
PGDM1400
PGDM1407
PGDM1408
PGDM1408
PGDM1409
PGDM1409
PGDM1409
PGDM1409
PGDM1409
PGDM1409
PGDM1409
PGDM1409
PGDM1409
PGDM1409
PGDM1409
PGDM1401
PGDM1401 | 00+1/MODd 00
82
93
51
48
48
48
93
50
44
49
97
9
50
44
49
50
44
50
65
65
65
65
65
66
60
100
88
89
97
11
69
69
69
69
69
69
62
88
27
27
26
57
27
26
57
27
27
27
27
27
27
27
27
27
27
27
27
27 | L0PLWQ9d 82
1000 84
50 51
52 50
48
96
51
52
47
52
47
52
67
66
56
52
73
72
73
66
64
100
90
90
73
72
73
66
64
100
76
65
73 | C04FIMODOL 93 84 100 50 81 500 81 500 81 500 84 64 64 64 64 64 65 600 97 900 100 711 71 61 90 74 61 97 74 67 71 | S001 S01 51 50 51 50 53 51 64 64 64 72 55 55 56 54 56 54 71 71 71 76 76 73 68 88 | *0*LWQ9d 48 48 51 50 64 92 58 60 51 94 88 602 57 575 55 69 72 711 100 805 67 655 72 66 85 67 65 72 86 | S0PLWQ9d 48 48 52 49 64 52 95 52 95 57 44 62 58 59 55 50 71 71 85 100 67 64 73 796 82 62 72 | 90+LWQ9d 49
50
52
72
8
59
100
53
53
53
51
55
66
64
76
67
67
69
66
67
8
66
67
8 | L001/W000 49 48 50 48 50 63 87 60 63 87 63 61 63 61 65 56 55 56 64 76 65 64 76 64 67 65 64 67 65 64 76 | 8041MG9d 79
96
81
50
51
52
49
47
100
51
52
49
47
100
51
52
47
51
52
47
100
51
52
47
100
51
52
47
100
51
52
47
100
51
52
47
73
73
73
73
76
66
56
67
73
77
73
76
66
77
73
77
76
76
77
77
77
77
77
77
77
77
77
77 | 607LW0004 49
51
50
66
94
95
95
63
51
66
94
95
96
35
100
88
84
44
63
59
60
57
57
58
72
76
4
74
86
66
75
67
64
75
75
83
75
75
83
75
75
83
75
75
80
80
80
80
80
80
80
80
80
80
80
80
80 | 0171W09d 50 52 50 66 88 87 58 100 56 59 72 76 44 61 59 88 60 56 97 74 73 85 26 69 67 78 3100 68 76 | L1FLWQDDd 44 47 44 47 44 47 49 47 44 44 47 51 51 51 51 51 51 65 65 67 62 64 65 64 65 68 100 62 65 | Cltruwood S2 | 14119d 65 67 55 57 58 56 66 59 51 66 59 51 66 69 95 83 70 72 71 69 66 63 72 66 63 72 68 <th< td=""><td>CP1LDd 65 66 64 55 55 56 55 58 51 56 59 81 70 72 71 69 66 63 72 68 65 68 65 68 65 66 63 72 68 68 65 68 <th< td=""><td>E+115d 65 64 57 59 53 66 60 61 57 99 60 60 91 90 95 83 70 72 71 68 66 64 62 72 68 66 64 62 72 68 66 64 62 72 68 66 64 62 72 68 66 64 62 72 68 67 65 67 66 67 <th< td=""><td>7+1L9d 64 65 55 55 51 64 57 549 55 993 995 100 81 702 71 70 68 66 63 72 70 68 66 63 72 70 64 69 70 70 64 69 70 70 68 66 63 72 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 70 70 70 70 70 70 70 70 70 70 70 70</td><td>SPILIO 60 62 60 62 60 58 55 60 61 58 59 51 58 83 81 100 74 72 75 71 69 64 62 72 73 64 62 72 73 64 62 73 73 64 70</td><td>%
sequence
identity
scale
100
90
80
70
60
50
40</td></th<></td></th<></td></th<> | CP1LDd 65 66 64 55 55 56 55 58 51 56 59 81 70 72 71 69 66 63 72 68 65 68 65 68 65 66 63 72 68 68 65 68 <th< td=""><td>E+115d 65 64 57 59 53 66 60 61 57 99 60 60 91 90 95 83 70 72 71 68 66 64 62 72 68 66 64 62 72 68 66 64 62 72 68 66 64 62 72 68 66 64 62 72 68 67 65 67 66 67 <th< td=""><td>7+1L9d 64 65 55 55 51 64 57 549 55 993 995 100 81 702 71 70 68 66 63 72 70 68 66 63 72 70 64 69 70 70 64 69 70 70 68 66 63 72 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 70 70 70 70 70 70 70 70 70 70 70 70</td><td>SPILIO 60 62 60 62 60 58 55 60 61 58 59 51 58 83 81 100 74 72 75 71 69 64 62 72 73 64 62 72 73 64 62 73 73 64 70</td><td>%
sequence
identity
scale
100
90
80
70
60
50
40</td></th<></td></th<> | E+115d 65 64 57 59 53 66 60 61 57 99 60 60 91 90 95 83 70 72 71 68 66 64 62 72 68 66 64 62 72 68 66 64 62 72 68 66 64 62 72 68 66 64 62 72 68 67 65 67 66 67 <th< td=""><td>7+1L9d 64 65 55 55 51 64 57 549 55 993 995 100 81 702 71 70 68 66 63 72 70 68 66 63 72 70 64 69 70 70 64 69 70 70 68 66 63 72 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 70 70 70 70 70 70 70 70 70 70 70 70</td><td>SPILIO 60 62 60 62 60 58 55 60 61 58 59 51 58 83 81 100 74 72 75 71 69 64 62 72 73 64 62 72 73 64 62 73 73 64 70</td><td>%
sequence
identity
scale
100
90
80
70
60
50
40</td></th<> | 7+1L9d 64 65 55 55 51 64 57 549 55 993 995 100 81 702 71 70 68 66 63 72 70 68 66 63 72 70 64 69 70 70 64 69 70 70 68 66 63 72 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 69 70 70 64 70 70 70 70 70 70 70 70 70 70 70 70 | SPILIO 60 62 60 62 60 58 55 60 61 58 59 51 58 83 81 100 74 72 75 71 69 64 62 72 73 64 62 72 73 64 62 73 73 64 70 | %
sequence
identity
scale
100
90
80
70
60
50
40 |
| LIGHT CHAIN HEAVY CHAIN B | * Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402
PGDM1402
PGDM1404
PGDM1405
PGDM1406
PGDM1406
PGDM1407
PGDM1406
PGDM1400
PGDM1411
PGT141
PGT141
PGT144
PGT144
PGT144
PGT144
PGT144
PGT144
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1401
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM | 00+1W000d
82
93
51
48
49
49
50
44
49
50
65
65
65
65
65
65
65
65
65
65
65
65
65 | L0PLWQ9d 82
100 84
50 51
52 47
52 47
52 47
52 47
52 67
66
65
65
62
8100
90
90
73
72
73
66
44
100
65
72
73
66
44
100
65
72
73 | C0+LWIC90d 93 84 1000 501 50 841 500 811 500 812 500 813 500 814 544 645 664 665 660 900 1000 711 711 641 900 744 677 71 71
 | S0PFIMOD 51 50 51 50 51 64 64 72 74 50 66 45 55 56 45 575 56 58 71 71 71 76 73 68 88 | *0+LWQ9d 48 48 51 50 64 100 92 58 60 51 94 60 51 94 62 57 55 69 72 71 100 85 67 72 86 67 72 | S0PLWQODd 48 522 49 64 92 1000 59 87 44 62 58 55 55 69 73 711 71 71 71 71 71 73 96 62 72 66 72 | 9011W090 49 500 522 58 59 1000 87 49 508 53 55 65 66 64 67 67 67 100 93 66 66 78 66 67
85 65 66 66 78 65 65 66 66 78 65 65 66 66 78 65 65 66 66 78 65 65 66 66 78 65 65 66 66 78 65 65 66 66 78 65 65 66 66 78 65 65 65 65 65 65 65 65 65 65 65 65 65 | L001LWG00d 49 48 50 60 63 74 60 63 74 63 61 49 80 65 64 61 65 64 61 76 64 64 64 64 64 64 64 76 64 76 64 76 64 76 64 76 64 76 64 76 64 76 64 76 64 76 64 76 64 76 64 76 76 76 | 8041MG9d 79
96
81
50
51
52
49
47
100
51
52
47
100
51
52
47
100
51
52
47
100
51
52
47
100
51
52
47
100
51
52
47
100
51
52
65
65
65
65
65
65
65
65
65
65
65
73
73
73
66
65
65
73
73
73
73
73
73
73
73
73
73
73
73
73 | 60+LWQOd 49 51 50 66 94 95 63 51 100 88 44 63 51 100 88 44 63 59 60 57 58 72 76 74 76 66 76 64 76 65 75 65 75 | 0171M09d 50 52 50 66 88 87 58 100 66 87 72 76 73 85 26 97 76 83 100 68 76 83 76 83 76 85 86 76 83 76 85 86 76 83 76 85 86 76 85 86 76 85 86 76 85 86 76 85 86 76 85 85 85 85 85 85 85 85 85 85 85 85 85 | L11 WCD 44 44 47 44 44 44 47 44 44 47 47 51 51 51 51 51 51 51 51 51 51 51 51 51 51 51 51 51 55 6
 | CliffWQOd 52 52 54 52 52 54 77 62 62 63 61 47 100 56 55 58 70 73 71 88 72 72 78 76 73 75 76 69 100 68 100 68 100 68 100 68 100 68 100 68 100 68 100 68 100 68 100 68 100 68 100 68 100 68 100 68 100 10 | 14119d 65 67 55 57 58 53 56 66 59 51 56 56 59 51 56 66 59 51 56 66 59 51 56 66 59 51 56 66 59 51 56 66 59 51 56 66 59 51 56 66 59 51 56 66 59 51 56 66 59 51 56 66 59 51 56 66 52 72 71 69 66 56 72 68 65 68 65 68 65 68 65 68 65 68 65 68 65 68 65 68 65 68 65 68 65 68 65 68 65 68 65 68 65 68 65 68 65 65 65 66 <td< td=""><td>CPLLDd 65 66 4 55 7 8 53 56 65 59 8 100 96 8 11 69 8 11 69 8 11 69 8 11 69 8 11 69 8 11 69 8 11 69 8 11 69 66 65 72 68 65 68</td><td>85 65 64 57 59 53 56 65 60 51 59 96 100 95 33 70 71 66 66 64 62 72 68 66 64 62 72 68 66 64 62 72 68 66 64 65 67 65</td><td>7+1L9d 64 65 55 55 51 54 55 55 51 64 57 56 93 30 81 70 72 71 68 68 66 72 70 64 63 72 70 64 69 70 64 69 70 64 69 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 <th< td=""><td>String String 60 62 60 62 60 58 56 55 60 61 58 58 83 81 100 74 75 71 69 64 72 73 64 70 74 74</td><td>%
sequence
identity
scale
100
90
80
70
60
50
40</td></th<></td></td<> | CPLLDd 65 66 4 55 7 8 53 56 65 59 8 100 96 8 11 69 8 11 69 8 11 69 8 11 69 8 11 69 8 11 69 8 11 69 8 11 69 66 65 72 68 65 68
 | 85 65 64 57 59 53 56 65 60 51 59 96 100 95 33 70 71 66 66 64 62 72 68 66 64 62 72 68 66 64 62 72 68 66 64 65 67 65 | 7+1L9d 64 65 55 55 51 54 55 55 51 64 57 56 93 30 81 70 72 71 68 68 66 72 70 64 63 72 70 64 69 70 64 69 70 64 69 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 64 63 72 70 <th< td=""><td>String String 60 62 60 62 60 58 56 55 60 61 58 58 83 81 100 74 75 71 69 64 72 73 64 70 74 74</td><td>%
sequence
identity
scale
100
90
80
70
60
50
40</td></th<> | String String 60 62 60 62 60 58 56 55 60 61 58 58 83 81 100 74 75 71 69 64 72 73 64 70 74 74
 | %
sequence
identity
scale
100
90
80
70
60
50
40 |
| LIGHT CHAIN HEAVY CHAIN B | * Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402
PGDM1403
PGDM1405
PGDM1405
PGDM1406
PGDM1406
PGDM1407
PGDM1410
PGDM1411
PGT142
PGT141
PGT142
PGT143
PGT144
PGT145
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1400
PGDM1401
PGDM1400
PGDM1400
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1401
PGDM1411
PGDM1411 | 00+1W000d 100
82
93
51
48
48
49
49
50
44
49
50
44
49
50
44
49
50
65
65
65
66
64
60
100
88
77
71
69
96
95
28
872
72
57
70
70 | L0PLWGOd 82
1000 84
50 51
52 47
52 67
66 55
655
655
655
65
65
65
65
65
65
65
65
6 | COPFINICIPAL 93 84 1000 51 50 51 50 81 500 81 50 501 50 44 655 64 65 64 65 60 97 90 100 71 71 64 6100 74 74 71 71 71 71 71 71
 | 80+LWQ9d 51 50 51 50 64 64 64 74 50 55 55 54 58 71 71 76 76 73 74 73 74 76 73 74 73 88 69 | *0*LWG9d 48 51 50 50 51 56 64 100 92 88 60 51 100 92 88 64 69 71 71 100 85 56 67 65 56 67 65 72 65 67 28 86 85 67 72 65 72 67 | SOPLWG9d 48 52 49 92 63 52 50 63 52 87 44 92 95 87 44 52 87 44 58 55 69 73 11 85 67 64 73 96 82 62 66 66 | 9011W09d 49
502
72
58
59
508
72
58
59
508
72
58
50
53
53
51
55
66
64
76
67
69
66
67
69
66
67
85
55 | L001/W000d 49 48 50 63 71 63 63 71 63 61 49 80 56 56 56 62 64 61 76 65 56 61 76 55 56 62 64 61 93 100 64 64 63 100 64 67 63 33 100 64 67 63 63 64 63 63 64 67 63 63 64 63 63 64 64 63 63 64 64 64 63 63 64 | 80+LWG9d 79 96 81 50 51 52 47 100 51 52 47 100 51 52 47 100 51 52 47 100 51 52 65 65 66 61 88 80 90 73 27 73 66 61 000 76 65 73 72 72 | 60+LWQ9d 49 49 51 50 66 94 51 50 66 94 53 51 100 88 44 59 53 100 88 444 59 50 57 58 72 76 4 86 67 64 76 100 83 65 75 68 68 | 0171MG9d 50 52 50 66 88 87 58 61 52 88 61 52 88 61 52 88 61 52 88 61 52 88 60 56 59 72 76 74 73 58 52 69 67 74 73 58 50 66 65 72 76 83 100 68 76 68 76 68 76 68 76 68 76 68 76 68 76 68 76 68 76 68 76 68 76 68 76 76 76 76 76 76 76 76 76 76 76 76 76 | L1FLWQDDL 44 47 44 44 47 44 44 47 44 44 47 51 51 51 51 51 51 51 51 51 65 66 64 65 68 67 68 67 68 67 68 65 68 00 65 65 68 00 65 55
 | CLFLWQDDd 52 52 54 52 54 62 52 54 62 603 63 61 63 63 61 47 55 58 70 71 88 72 78 76 73 75 76 100 68 68 68 | 14119d 65 67 5 55 57 5 53 56 6 59 5 5 5 5 5 6 6 59 5 5 6 6 5 9 5 5 6 6 5 9 9 5 8 3 70 7 7 1 69 6 | 74119d 65 66 64 55 57 53 56 55 53 56 55 58 51 56 59 58 51 56 98 903 81 70 77 1 69 67 68 68 68 68 68 68 68 100
 | 85 65 64 57 59 53 56 65 66 64 57 59 53 56 65 60 51 57 99 61 50 95 35 56 65 60 51 57 99 96 100 95 83 70 71 68 66 64 62 72 68 67 65 67 98 98 65 67 98 98 65 67 98 98 66 64 62 72 68 65 67 98 98 65 67 98 98 66 64 62 72 68 65 67 98 98 65 67 98 98 66 64 67 98 66 64 62 67 98 66 64 66 64 67 98 66 64 66 64 67 66 64 | ##L15d 64 65 55 55 51 64 57 69 93 95 100 81 70 71 70 68 66 63 72 71 70 68 66 63 72 70 64 69 97 <t< td=""><td>SPELED 60 62 65 66 65 56 55 60 61 58 58 83 81 100 74 75 71 69 64 62 73 76 46 72 73 74 73 74 73 74 73 74 73 73 64 70 74 <t< td=""><td>%
sequence
identity
scale
100
90
80
70
60
60
50
40</td></t<></td></t<> | SPELED 60 62 65 66 65 56 55 60 61 58 58 83 81 100 74 75 71 69 64 62 73 76 46 72 73 74 73 74 73 74 73 74 73 73 64 70 74 <t<
td=""><td>%
sequence
identity
scale
100
90
80
70
60
60
50
40</td></t<> | %
sequence
identity
scale
100
90
80
70
60
60
50
40 |
| LIGHT CHAIN HEAVY CHAIN B | * Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402
PGDM1403
PGDM1404
PGDM1405
PGDM1404
PGDM1405
PGDM1407
PGDM1407
PGDM1411
PGT141
PGT142
PGT143
PGT144
PGT144
PGT145
PGDM1400
PGDM1401
PGDM1401
PGDM1402
PGDM1403
PGDM1403
PGDM1403
PGDM1403
PGDM1404
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1405
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407 | 00+IW00d
100
82
93
51
48
49
99
99
50
44
52
65
65
65
64
00
100
88
97
71
69
69
662
88
97
72
65
70
70
70
70 | L0PLWQOd 82
1000 84
50 51
52 47
52 67
66 55
62
88
1000 90
90
90
73
72
73
66
64
100
90
73
72
72
72
72 | COPFINGOO 93 84 1000 93 84 1000 51 50 500 500 50 500 500 50 500 500 50 500 500 1000 711 71 61 900 74 67 711 71 71 711 71 71
 | 80+LWQ9d 51 50 51 50 51 50 66 44 50 66 66 45 55 55 55 54 58 71 71 76 74 73 68 69 68 69 68 | *0*LMG9d 48 51 50 64 100 92 860 51 94 88 44 62 57 55 56 69 72 71 100 85 67 65 72 67 66 85 67 67 66 | SOPLWG9d 48 52 49 92 100 63 52 49 63 52 63 52 87 44 58 55 55 55 609 73 71 85 711 85 56 69 73 71 85 26 64 73 64 73 72 66 66 66 | 9011W09d
49
502
58
59
58
57
58
53
53
53
53
53
53
53
53
55
66
64
67
67
69
66
67
67
69
66
64
65
65
66
4 | L0FLWQODd 49 48 500 63 63 61 49 48 50 63 61 47 63 61 49 62 64 61 65 56 65 64 61 65 64 61 64 67 63 62 64 64 67 64 67 63 62 64 63 62 | 80FLWQGd 79
96
81
50
51
52
47
100
51
52
47
100
51
52
47
100
51
52
47
66
65
65
64
61
88
109
90
73
72
73
66
64
61
77
27
27
27 | 60+LWQ9d 49 49 51 50 66 94 51 50 63 51 60 88 44 63 59 53 60 57 58 72 76 74 86 667 64 700 83 657 55 68 68 | 0141M000d 50
52 50
52 50
52 50
52 50
52 50
53 50
53 50
53 50
54 60
55 50
56 50
56 50
56 50
56 50
56 50
56 50
56 50
57 76
4 73
85 26 60
88 20
56 60
88 70
57 70
77 70
85 20
66 88 70
72 76
74 77
85 20
66 88 70
72 76
74 77
76 80
76 60
88 70
80
80
80
80
80
80
80
80
80
80
80
80
80 | L11 WG9d 44 47 44 45 44 47 49 47 44 400 47 51 51 51 51 51 51 51 51 51 51 51 51 51 65 67 68 60 65 68 000 65 <t< td=""><td>CLFLWQOOd 52 52 54 77 62 60 80 51 63 61 47 55 58 70 55 58 70 73 71 72 72 78 76 70 68 68 68 67 69</td><td>14119d 65 67 58 53 56 66 59 51 56 66 59 51 56 66 59 51 56 66 59 51 56 66 63 70 71 66 63 72 76 66 63 72 68 68 68 68 1000 98 98 99 83 70 72 71 69 67 66 63 72 88 88 1000 98 98 99 95 83 70 72 71 69 67 66 63 72 88 88 1000 98 99 98 98 99 98 98 99 99 93 83 70 72 76 66 63 26 68 68 68 68 68 68 68 68 68 68 68 68 68 68 68</td><td>741L9d 65 66 64 55 53 56 65 59 58 51 56 59 58 51 56 98 100 96 93 81 70 72 76 66 63 72 68 68 68 68 68 68 68 1000 98 98 1000 98 98 1000 98 1000 98 1000 98 1000 98 1000 98 1000 100</td><td>KPLL9d 65 65 64 57 59 56 66 60 61 57 99 96 60 61 57 99 96 60 61 57 99 96 60 61 57 99 96 60 61 57 70 71 68 66 64 62 72 76 68 67 98 9100 99 96 67 98 9100 91 93 93 96 66 66 64 62 72 71 68 66 66 67 98 9100 93 93 96 96 97 98 9100 91 92 92 91 91 91 91</td><td>#+L9d 64 65 55 54 55 55 54 64 55 55 54 93 95 935 9100 81 70 72 70 666 63 72 70 64 69 97 97 97 97 97</td><td>SPFLEDd 600 600 580 560 550 601 580 581 583 811 833 811 833 811
 833 811 833 811 833 811 833 811 833 811 833 811 833 811 833 811 837 744 745 753 649 642 723 733 6470 744 74</td><td>%
sequence
identity
scale
100
90
80
70
60
50
40</td></t<> | CLFLWQOOd 52 52 54 77 62 60 80 51 63 61 47 55 58 70 55 58 70 73 71 72 72 78 76 70 68 68 68 67 69 | 14119d 65 67 58 53 56 66 59 51 56 66 59 51 56 66 59 51 56 66 59 51 56 66 63 70 71 66 63 72 76 66 63 72 68 68 68 68 1000 98 98 99 83 70 72 71 69 67 66 63 72 88 88 1000 98 98 99 95 83 70 72 71 69 67 66 63 72 88 88 1000 98 99 98 98 99 98 98 99 99 93 83 70 72 76 66 63 26 68 68 68 68 68 68 68 68 68 68 68 68 68 68 68 | 741L9d 65 66 64 55 53 56 65 59 58 51 56 59 58 51 56 98 100 96 93 81 70 72 76 66 63 72 68 68 68 68 68 68 68 1000 98 98 1000 98 98 1000 98 1000 98 1000 98 1000 98 1000 98 1000 100
 | KPLL9d 65 65 64 57 59 56 66 60 61 57 99 96 60 61 57 99 96 60 61 57 99 96 60 61 57 99 96 60 61 57 70 71 68 66 64 62 72 76 68 67 98 9100 99 96 67 98 9100 91 93 93 96 66 66 64 62 72 71 68 66 66 67 98 9100 93 93 96 96 97 98 9100 91 92 92 91 91 91 91 | #+L9d 64 65 55 54 55 55 54 64 55 55 54 93 95 935 9100 81 70 72 70 666 63 72 70 64 69 97 97 97 97 97 | SPFLEDd 600 600 580 560 550 601 580 581 583 811 833 811 833 811 833 811 833 811 833 811 833 811 833 811 833 811 833 811 833 811 837 744 745 753 649 642 723 733 6470 744 74
 | %
sequence
identity
scale
100
90
80
70
60
50
40 |
| LIGHT CHAIN HEAVY CHAIN B | * Sequence
identity
(amino acid)
PGDM1400
PGDM1401
PGDM1402
PGDM1402
PGDM1403
PGDM1404
PGDM1406
PGDM1406
PGDM1407
PGDM1406
PGDM1400
PGDM1410
PGDM1411
PGT141
PGT144
PGT144
PGT144
PGT144
PGDM1400
PGDM1400
PGDM1400
PGDM1401
PGDM1402
PGDM1400
PGDM1404
PGDM1406
PGDM1407
PGDM1406
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1408
PGDM1407
PGDM1407
PGDM1408
PGDM1407
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1408
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM1407
PGDM140 | 00+IWC004
100
82
93
51
48
49
979
49
49
49
49
49
49
49
49
50
56
56
56
56
56
56
56
56
56
56 | LOPLWC004
82
1000
51
55
50
48
45
50
51
52
67
65
65
52
67
65
65
65
65
88
800
90
73
72
73
66
44
100
76
65
73
27
72
72 | COPFINGOOd 93 84 1000 51 50 52 50 1 50 50 54 65 64 65 64 65 60 97 100 71 71 64 90 74 67 71 71 71 71 71 71 71 | S0PLWQ9d 51 50 51 50 51 50 66 66 66 55 55 54 58 71 71 76 73 74 68 88 69 69 67 | tot: tot: <thto:< th=""> tot: tot: t</thto:<> | SOPLWGOd 48 52 49 64 92 700 63 59 63 58 59 55 66 69 73 71 71 71 71 700 67 73 96 62 72 66 66 66 66 | 90P1/WCOd 49
502
558
59
508
57
59
58
59
59
58
57
55
55
55
55
55
55
55
55
55
55
55
55 | LOPLWQ9d 49
48
50
74
60
387
100
47
63
61
49
80
56
55
6
40
62
46
17
65
64
93
06
4
67
63
63
26
63
64
63
65
66
56
65
66
63
66
63
66
63
66
63
66
63
66
63
66
66 | 80FLWGOd 79
96
81
50
51
52
47
100
51
52
47
51
52
47
51
52
47
51
52
47
51
52
47
51
52
47
51
52
47
51
52
47
51
52
47
51
52
49
47
51
52
52
52
52
52
52
52
52
52
52
52
52
52 | 60+LWQ9d 49 49 51 66 94 95 59 63 51 100 88 44 63 59 60 57 58 72 76 74 74 76 64 76 758 68 68 68 68 67 76 | 0171W000d 50
52
50
66
88
87
58
61
52
50
66
88
87
61
52
50
66
88
87
61
52
50
52
50
66
88
87
72
76
47
73
85
86
66
59
72
76
47
73
85
86
66
88
87
70
66
88
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
70
87
88
87
88
87
70
87
88
87
88
87
87
87
87
87
87
87
87
87 | L1PEWG9d 44 47 44 47 44 47 44 47 47 51 51 51 51 51 51 51 65 665 668 600 69 65 65 65 65 64 | CLEFLWQDDd 52 52 52 54 77 62 80 80 80 63 61 63 61 63 61 63 71 80 56 57 55 70 73 71 88 72 78 73 75 69 68 68 67 69 68 69 68 | 1+115d 65 67 55 57 8 53 56 59 59 59 56 100 99 95 58 70 71 69 66 65 72 68 65 68 65 68 65 68 65 68 65 80 99 97 71 69 66 65 72 68 65 68 65 80 99 97 97 | 741L9d 65 66 64 55 55 53 56 59 58 56 59 58 56 59 58 56 59 58 56 59 58 56 59 58 56 59 58 56 59 58 56 59 58 56 59 58 56 59 58 56 59 58 56 59 58 56 57 71 69 66 65 72 68 65 65 68 <th< td=""><td>CP1LDD 65 65 64 65 65 66 60 60 61 57 93 56 66 60 60 57 99 61 100 95 83 70 71 68 66 64 62 72 68 66 64 62 72 68 67 65 67 98 98 100 97 97 97 97 97 97 97 98 98 100 97 97</td><td>#+L9d 64 65 65 64 65 55 55 51 54 64 57 56 93 95 93 95 93 100 81 70 72 71 70 68 66 63 72 70 64 99 97 97 100</td><td>SPLLDd 60 26 60 26 58 56 55 60 1 58 58 55 55 60 74 75 71 69 64 72 73 64 74 74 74 74 74 74</td><td>%
sequence
identity
scale
100
90
80
70
60
50
40</td></th<> | CP1LDD 65 65 64 65 65 66 60 60 61 57 93 56 66 60 60 57 99 61 100 95 83 70 71 68 66 64 62 72 68 66 64 62 72 68 67 65 67 98 98 100 97 97 97 97 97 97 97 98 98 100 97 97 | #+L9d 64 65 65 64 65 55 55 51 54 64 57 56 93 95 93 95 93 100 81 70 72 71 70 68 66 63 72 70 64 99 97 97 100 | SPLLDd 60 26 60 26 58 56 55 60 1 58 58 55 55 60 74 75 71 69 64 72 73 64 74 74 74 74 74 74 | %
sequence
identity
scale
100
90
80
70
60
50
40 |

Fig. S3. Newly isolated somatic variants are highly divergent from the PGT141–145 sequences. A sequence identity matrix was created using the somatic variants PGDM1400–1412 and PGT141–145. Values listed are (A) nucleotide percent identity and (B) amino acid percent identity colored according to the key. Sequence identities were calculated using Clustal Omega (1).

1. Sievers F, et al. (2011) Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. Mol Syst Biol 7:539.

SANG SAL

Heavy chain



Fig. S4. Sequences of the newly isolated somatic variants can be found in a next-generation sequencing (NGS) dataset. Heavy-chain and light-chain sequences of the newly isolated somatic variants were queried in a previously published NGS dataset (1). The frequency of sequences is plotted in terms of percent identity to the listed antibody sequence and percent divergence from the germline gene. The number of sequences is colored according to the key.

1. Zhu J, et al.; NISC Comparative Sequencing Program (2013) Mining the antibodyome for HIV-1-neutralizing antibodies with next-generation sequencing and phylogenetic pairing of heavy/light chains. Proc Natl Acad Sci USA 110(16):6470–6475.

Virus	Clade	GT121 + PGDM1400	PGDM1400	PG9	PGT145	PGV04	PGT121	PGT151	PGDM1401	PGT128	PGT1403	CAP256-VRC26.08	CAP256-VRC26.09	PGDM1402	PGDM1403	PGDM1404	PGDM1405	PGDM1406
6535.3	в	0.004	0.857	0.288	> 50	1.49	0.002	0.001	> 10	0.004	> 50	> 10	> 10	> 10	> 5	2	> 10	> 5
QH0692.42	в	0.110	> 10	> 50	> 50	0.425	0.302	0.029	> 10	0.029	> 50	> 10	> 10	1.19	> 5	> 2	> 10	> 5
SC422661.8	В	0.034	0.550	2.97	0.024	0.060	0.038	0.005	0.017	1.08	3.80	> 10	> 10	> 10	> 5	> 2	> 10	> 5
TRO.11	в	0.189	0.940	> 50	0.192	0.291	0.005	>50	0.156	0.011	0.111	> 10	> 10	> 10	> 5	>2	> 10	>5
AC10.0.29	в	0.026	0.081	0.097	0.010	> 10	0.024	0.007	0.007	0.008	0.042	> 10	> 10	> 10	> 5	> 2	> 10	> 5
RHPA4259.7	в	0.013	0.730	49.0	0.029	0.033	0.015	0.006	0.051	0.026	0.054	> 10	> 10	> 10	> 5	> 2	> 10	> 5
REJ04541.67	В	0.005	0.001	0.010	0.001	0.047	4.77	0.018	0.001	>50	9.16	> 10	> 10	> 10	>5	>2	> 10	>5
WT04160 33	B	0.256	> 10	0.005	> 50	0.110	0.334	0.496	> 10	>50	> 50	> 10	> 10	> 10	> 5	>2	> 10	> 5
CAAN5342.A2	в	0.007	> 10	13.0	6.68	1.05	0.007	0.005	> 10	0.514	> 50	> 10	> 10	> 10	> 5	> 2	> 10	> 5
WEAU_d15_410_5017	B (T/F)	0.007	0.008	3.70	1.95	0.042	0.026	0.010	0.086	0.032	> 50	> 10	> 10	> 10	> 5	ND	0.033	ND
1006_11_C3_1601	B (T/F)	0.003	1.65	0.212	> 50	0.082	0.002	2.89	> 10	0.011	> 50	> 10	> 10	> 10	> 5	> 2	> 10	> 5
1054_07_1C4_1499 1056 10 TA11 1826	B (T/F)	0.053	> 10	> 50	> 50	0.354	0.064	0.008	> 10	0.035	> 50	> 10	> 10	> 10	>5	ND	> 10	ND
1012_11_TC21_3257	B (T/F)	0.006	0.051	0.185	0.009	0.034	0.003	>50	0.009	0.011	0.008	> 10	> 10	1.12	> 5	> 2	> 10	> 5
6240_08_TA5_4622	B (T/F)	0.042	> 10	1.65	> 50	2.64	0.033	0.046	> 10	0.019	> 50	> 10	> 10	> 10	> 5	> 2	> 10	> 5
6244_13_B5_4576	B (T/F)	0.051	> 10	> 50	7.27	0.314	0.061	>50	> 10	0.020	> 50	> 10	> 10	> 10	>5	>2	> 10	> 5
SC05 8C11 2344	B (T/F)	0.008	2.06	1.23	0.093	0.222	0.019	0.060	0.195	0.017	0.540	> 10	> 10	> 10	>5	>2	> 10	>5
Du156.12	с	0.003	0.002	0.056	0.001	0.018	0.004	0.005	0.003	0.017	0.023	0.006	0.010	0.503	> 5	> 2	> 10	> 5
Du172.17	С	0.025	4.08	0.314	> 50	0.118	0.033	0.003	> 10	0.028	> 50	> 10	> 10	> 10	0.621	2	> 10	2.6
Du422.1	c	0.024	0.001	0.228	22.6	> 10	0.039	4.60	0.001	0.039	> 50	0.005	0.009	> 10	>5	>2	> 10	> 5
ZM19/M.PB/ ZM214M.PL15	c	0.055	> 10	> 50	> 50	0.604	>50	0.003	> 10	>50	> 50	0.019	0.012	> 10	>5	>2	> 10	>5
ZM233M.PB6	с	0.005	0.001	0.003	0.025	0.020	3.69	0.027	0.001	>50	0.139	0.001	0.003	0.097	LT	LT	LT	LT
ZM249M.PL1	С	0.001	0.001	0.040	1.44	ND	>50	0.004	0.001	39.7	0.411	ND	ND	ND	> 5	> 2	> 10	> 5
ZM53M.PB12	c	0.001	0.002	0.064	0.367	1.28	0.001	>50	0.007	>50	0.011	0.001	0.002	0.228	> 5	>2	0.012	> 5
ZM109F.PB4 ZM135M.PL10a	c	0.606	0.005	> 50	> 50	> 10	0.716	>50	> 10	>50	> 50	> 10	> 10	> 10	> 5	>2	> 10	>5
CAP45.2.00.G3	c	0.008	0.006	0.004	0.001	0.002	1.63	0.007	0.005	>50	1.34	0.004	0.033	0.412	0.118	0.007	0.009	> 5
CAP210.2.00.E8	С	0.011	0.001	0.167	37.8	> 10	26.3	0.010	0.006	>50	0.570	0.001	0.002	> 10	> 5	2	0.003	> 5
HIV-001428-2.42	c	0.002	0.001	0.006	0.001	0.007	0.014	0.027	0.007	0.026	> 50	0.059	0.417	> 10	> 5	ND	0.063	ND
HIV-0013095-2.11 HIV-16055-2.3	c	0.003	0.001	0.016	9.27	> 10	>50	>50	0.375	>50	> 50	0.002	0.015	2.09	0.086	> 2	> 10	>5
HIV-16845-2.22	c	> 50	> 10	14.9	> 50	> 10	3.97	>50	> 10	0.181	> 50	> 10	> 10	> 10	LT	LT	LT	LT
Ce0393_C3	C (T/F)	0.003	0.004	0.013	0.112	> 10	>50	>50	> 10	>50	> 50	0.131	0.166	1.24	0.001	>2	>50	> 5
Ce1176_A3	C (T/F)	0.011	0.020	0.007	> 50	1.52	0.013	0.006	> 10	0.009	> 50	0.006	0.008	> 10	> 5	> 2	> 10	> 5
Ce2010_F5	C (T/F)	> 50	> 10	> 50	> 50	0.210	>50	>50	> 10	>50	> 50	> 10	> 10	> 10	> 5	>2	> 10	> 5
Ce2060_G9	C (T/F)	0.002	0.002	0.047	0.016	0.312	>50	0.135	0.003	>50	0.216	0.001	0.002	0.258	0.114	2	0.020	5
Ce703010054_2A2	C (T/F)	0.003	0.002	0.018	> 50	0.120	>50	0.013	> 10	>50	> 50	0.024	0.035	> 10	5	ND	>50	ND
BF1266.431a	C (T/F)	0.003	0.002	0.043	1.35	> 10	>50	>50	0.501	>50	> 50	0.002	0.003	> 10	LT	LT	LT	LT
246F_C1G	C (T/F)	0.033	> 10	> 50	> 50	> 10	0.041	>50	> 10	0.005	> 50	0.026	0.255	0.606	>5	ND	> 10	ND
249M_B10 ZM247v1(Rev-)	C (T/F)	0.013	0.001	0.066	7.19	> 10 ND	>50	0.007	> 10	0.021	8.57	ND	ND	> 10 ND	0.094	ND ≥ 2	> 10	0.173
7030102001E5(Rev-)	C (T/F)	0.004	0.002	> 50	> 50	0.522	0.009	0.001	> 10	0.007	> 50	> 10	> 10	> 10	> 5	ND	> 10	ND
1394C9G1(Rev-)	C (T/F)	0.001	0.001	0.021	0.001	0.178	0.264	0.022	0.002	0.011	0.010	0.001	0.002	0.146	0.013	0.038	0.004	0.041
Ce704809221_1B3	C (T/F)	0.021	0.090	0.060	0.102	0.180	0.025	>50	0.016	0.026	0.124	> 10	> 10	2.12	> 5	>2	> 10	> 5
CNE19 CNE20	BC	0.001	0.001	0.018	0.103	> 10	0.008	>50	0.105	>50	> 50	> 10	> 10	0.146	0.022	2	> 10	>5
CNE21	BC	0.001	0.001	0.067	0.001	0.203	0.007	0.004	0.001	0.010	0.003	0.006	0.008	0.100	0.004	0.001	0.001	0.021
CNE17	BC	0.001	0.001	0.090	0.091	0.353	7.60	0.093	0.001	0.432	0.005	0.005	0.010	0.445	0.060	2	10	> 5
CNE30	BC	0.072	> 10	> 50	4.66	0.575	0.048	>50	> 10	>50	5.40	> 10	> 10	> 10	ND	> 2	ND	> 5
CNE52 CNE53	BC	0.308	0.293	0.036	0.020	0.120	2.05	0.004	> 10	>50	> 50	> 10	> 10	> 10	0.041 ND	>2	> 10	>5
CNE58	BC	0.002	0.001	0.029	0.183	0.023	>50	0.004	0.001	13.8	0.014	0.002	0.003	0.351	0.023	0.002	0.002	>5
MS208.A1	A	0.008	0.002	0.097	0.334	0.031	>50	0.001	0.002	>50	0.183	0.014	0.009	> 10	LT	LT	LT	LT
Q23.17	A	0.001	0.001	0.004	1.32	0.023	0.001	0.007	0.001	0.009	0.308	0.005	0.028	0.012	0.004	0.001	0.001	> 5
Q461.e2	A	0.050	0.039	1.91	7.80	0.340	>50	12.6	0.236	>50	35.2	0.126	0.099	> 10	> 5	>2	> 10	> 5
0330.v4.c3	A	0.005	0.002	0.014	0.200	0.127	0.050	0.004	0.001	1.60	0.021	0.003	0.123	0.138	0.041	0.005	0.006	>5
0260.v5.c36	A	0.008	0.007	2.41	> 50	0.439	0.053	0.427	0.045	0.058	> 50	> 10	> 10	1.43	5	> 2	> 10	> 5
191955_A11	A (T/F)	0.001	0.001	0.032	0.001	> 10	>50	0.004	0.002	14.2	0.002	0.002	0.008	0.072	LT	LT	LT 0.162	LT
T257-31	CRF02_AG	0.003	0.002	0.034	5.18	0.413	>50	0.003	0.010	>50	4.00	0.003	0.004	0.586	0.007	0.044	> 10	0.819
928-28	CRF02_AG	0.046	0.030	0.082	> 50	0.428	44.2	>50	0.307	>50	> 50	0.016	0.022	> 10	0.181	2	> 10	> 5
263-8	CRF02_AG	0.023	0.002	0.243	32.1	0.054	0.648	0.005	0.015	0.342	3.34	0.034	0.020	2.11	0.019	>2	> 10	> 5
T250-4	CRF02_AG	0.001	0.001	0.002	0.002	> 10	0.001	0.327	0.001	0.001	0.022	0.001	0.001	0.042	0.007	0.001	0.006	5
T278-50	CRF02_AG	0.108	0.102	1.61	10.3	LT	>50	0.002	> 10	0.031	> 50	LT	LT	LT	>5	>2	> 10	>5
T255-34	CRF02_AG	0.056	0.002	0.034	> 50	0.057	18.7	0.002	0.003	>50	45.3	> 10	> 10	0.182	5	2.0	10	5
235-47	CRF02_AG	0.003	0.001	0.958	3.21	0.007	0.137	38.1	0.011	>50	> 50	0.003	0.063	0.043	LT	LT	LT	LT
620345.c01 C1080.c03	CRE01_AE	0.002	0.001	23.6	0.241	> 10	>50	>50	> 10	>50	0.038	0.008	0.011	> 10	>5	>2	> 10	>5
R2184.c04	CRF01_AE	0.003	0.001	0.197	0.073	ND	>50	>50	0.004	20,1	0.596	ND	ND	ND	0.233	2	> 10	>5
R1166.c01	CRF01_AE	0.552	0.486	1.10	2.27	0.026	>50	>50	0.073	>50	1.263	0.086	0.122	2.15	5	> 2	> 10	> 5
R3265.c06	CRF01_AE	0.004	0.006	0.103	0.037	> 10	>50	>50	> 10	>50	> 50	> 10	> 10	> 10	0.226	0.098	> 10	> 5
C3347.c11	CRF01_AE	0.004	0.004	0.046	0.005	> 10	>50	>50	> 10	0.001	> 50	> 10	> 10	> 10	0.060	2	> 10	>5
CNE8	CRF01_AE	0.002	0.006	1.09	0.272	0.200	>50	>50	0.026	0.019	4.031	0.036	0.027	0.230	>5	> 2	> 10	>5
CNE5	CRF01_AE	0.001	0.001	0.007	0.001	0.147	>50	>50	0.003	0.018	0.011	0.001	0.003	0.131	0.090	0.002	0.009	> 5
BJOX009000.02.4	CRF01_AE	0.294	0.763	3.12	0.117	0.592	2.86	>50	0.072	0.001	0.070	> 10	> 10	> 10	> 5	> 2	> 10	> 5
BJOX015000.11.5	CRF01_AE (T/F)	0.179	1.86	1.23	> 50	0.251	>50	>50	> 10	0.001	> 50	> 10	> 10	> 10	>5	> 2	> 10	>5
BJOX025000.01.1	CRF01_AE (1/F)	0.302	0.019	0.368	6.63	> 10	>50	>50	> 10	>50	> 50	> 10	> 10	> 10	0.049	>2	> 10	>5
BJOX028000.10.3	CRF01_AE (T/F)	0.610	0.121	1.65	> 50	> 10	>50	>50	> 10	0.024	> 50	> 10	> 10	> 10	0.247	ND	> 10	ND
X1193_c1	G	0.009	0.036	0.212	0.013	0.024	0.016	0.004	0.007	>50	0.053	0.023	0.021	2.91	> 5	> 2	> 10	> 5
X1254_c3	G	0.033	> 10	0.132	5.60	0.040	0.014	0.309	> 10	>50	> 50	> 10	> 10	> 10	0.093	2	> 10	> 5
X2088_c9 X2131_C1_R5	G	0.004 ND	> 10	> 50	> 50	> 10	0.003	>50	> 10	>50	> 50	> 10	> 10	> 10	> 5 ND	>2	> 10 ND	>5
P1981_C5_3	G	0.001	0.003	0.388	5.41	0.129	0.001	0.021	0.004	0.019	24.7	0.004	0.006	> 10	0.119	0.009	0.005	> 5
X1632_S2_B10	G	0.008	0.009	0.282	0.012	0.008	>50	0.061	0.002	>50	17.8	0.005	0.005	> 10	> 5	2	0.013	> 5
A07412M1.vrc12	D	0.010	0.012	0.744	0.002	0.124	0.009	0.246	0.004	>50	7.62	0.004	0.026	> 10	5	> 2	> 10	> 5
231965.c01	0	0.004	0.003	0.679	0.403	0.074	>50	0.001	> 10	>50	> 50	> 10	> 10	> 10	>5	>2	> 10	>5
6480.v4.c25	CD	0.007	> 10	ND	> 50	0.027	0.001	ND	> 10	0.003	> 50	> 10	> 10	> 10	> 5	>2	> 10	>5
6952.v1.c20	CD	0.020	0.089	> 50	3.12	0.017	0.056	49.2	> 10	>50	> 50	> 10	> 10	> 10	> 5	>2	> 10	> 5
6811.v7.c18	CD	0.001	> 10	> 50	> 50	0.060	0.001	ND	> 10	0.003	> 50	> 10	> 10	> 10	> 5	ND	> 10	ND
89-F1_2_25	CD	0.001	0.001	0.402	0.800	> 10	>50	22.9	0.002	>50	0.001	0.001	0.001	0.155	0.001	2	0.001	5
6041.v3.c23	AC	0.189	0.002	0.235	0.964	0.005	>50	0.002	0.010	>50	> 50	> 10	> 10	> 10	>5	ND	0.012	ND
6540.v4.c1	AC	0.002	0.001	0.066	0.080	> 10	>50	0.006	0.001	11.8	0.032	0.007	0.010	0.257	5	0.001	0.009	> 5
6545.v4.c1	AC	0.002	0.001	0.084	0.114	> 10	>50	0.004	0.001	>50	0.032	0.008	0.008	0.260	> 5	0.001	> 10	> 5
0815.v3.c3 3103.v3.c10	ACD	0.007	> 10	> 50	> 50	0.035	0.025	>50	> 10	0.030	> 50	> 10	> 10	> 10	>5	> 2	> 10	> 5 ND
0100.T0.010			WILL W			0.000		0.014		0.014	0.10	10	10	10			10	

Fig. S5. Neutralization breadth and potency of somatic variants compared with other HIV-1 broadly neutralizing antibodies. Somatic variants were tested on a cross-clade pseudovirus panel. Neutralization IC₅₀ values are colored from highly potent (red) to less potent (green). LT, viruses for which there were low titers; ND, not determined.



Fig. S6. PGDM1400 neutralizes viruses to completion as much as PGT121. MPNs were determined for PGDM1400 on a 106-virus panel (Fig. S5). For comparison, PGT151, which was reported to exhibit incomplete neutralization activity (1), and PGT121 and 12A12, which have been shown to achieve generally complete neutralization for the majority of viruses, were measured in parallel. Each data point represents a different virus on a cross-clade 106-virus panel (Fig. S5). The median MPN with interquartile range is shown for each antibody.

1. Falkowska E, et al. (2014) Broadly neutralizing HIV antibodies define a glycan-dependent epitope on the prefusion conformation of gp41 on cleaved envelope trimers. *Immunity* 40(5): 657–668.



Fig. S7. Somatic variants bind to cell-surface BG505 Env despite not neutralizing the BG505 pseudovirus. (A) Somatic variants were tested for binding to BG505 Env expressed on the surface of 293T cells. Antibody PGT151, which binds specifically to cleaved Env, and antibody b6, which binds to uncleaved Env, were included for comparison. (B) Antibodies also were tested for neutralization against the BG505 pseudovirus. Values shown are neutralization IC_{50} in micrograms per milliliter.



Fig. S8. Among the newly isolated somatic variants, only PGDM1401 is autoreactive by the HEp2 assay. Somatic variants were tested for autoreactivity using the HEp2 cell assay kit according to the manufacturer's protocol. 4E10 was included as a positive control.



Fig. S9. Binding of mAbs to BG505 SOSIP.664-aviB by Octet. Antibodies PGT145, PGDM1400, PGDM1401, PGDM1403, PGDM1405, and PGDM1407 were analyzed for binding to BG505 SOSIP.664-AviB by Octet. Black curves represent measured data points; red curves represent best-fit lines following analysis.

DNAS

<

Heavy chain (V _H 1-8)	
Nested PCR reaction	5' to 3' sequence
PCR 1 Forward	ATGGACTGGATTTGGAGGAT
PCR 1 Reverse	GGAAGGTGTGCACGCCGCTGGTC
PCR 2 Forward	ATGGACTGGATTTGGAGGATCCTCTTCTTGG
PCR 2 Reverse	GTTCGGGGAAGTAGTCCTTGAC
Light chain (V _k 2-28)	
Nested PCR reaction	5' to 3' sequence
PCR 1 Forward	ATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGC
PCR 1 Reverse	GTTTCTCGTAGTCTGCTTTGCTCA
PCR 2 Forward	GCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGG
PCR 2 Reverse	GTGCTGTCCTTGCTGTCCTGCT

Table S1. Primers used for amplification of variable heavy- and light-chain genes

Table S2. Data collection and refinement statistics for SSRL 11-1

Data collection	
Wavelength, Å	0.97947
Space group	P2 ₁
Unit cell a, b, c, Å	55.7, 149.2, 109.9
α, β, γ, °	90, 100.9, 90
Resolution (Å)*	40–3.1 (3.2–3.1)
Completeness*	96.7 (98.6)
Redundancy*	3.4 (3.5)
No. total reflections	108,438
No. unique reflections	30,950
l/σ*	6.8 (1.7)
R _{merge} *' [†]	16.7 (58.4)
R _{pim} * ^{,‡}	10.4 (35.7)
CC _{1/2} * ^{,§}	97.4 (50.1)
Refinement statistics	
Resolution, Å	40–3.1
No. reflections total/R _{free}	30,926/1,544
R _{cryst} ¶/R _{free}	22.1/25.3
Rmsd bond length, Å	0.003
Rmsd bond angles, °	0.8
Protein atoms	10,427
Wilson B-value, Å ²	57.7
B-value overall, Å ²	61.5
Ramachandran favored, %	95.4
Ramachandran allowed, %	99.9
Molprobity all-atom clashscore	7.8
PDB ID code	4RQQ

*Values in parentheses are for the highest resolution shell.

 ${}^{t}R_{merge} = \Sigma |I-\langle I \rangle | / \Sigma \langle I \rangle$, where I is the observed intensity, and $\langle I \rangle$ is the average intensity of multiple observations of related reflections.

*R_{pim} = Σ hkl (1/(n - 1))1/2 Σ i | lhkl,i - <lb kl > |/ Σ hkl Σ i lhkl,i, where *lhkl*,*i* is the scaled intensity of the *i*th measurement of reflection *h*, *k*, *l*, <*lhkl* > is the average intensity for that reflection, and *n* is the redundancy. $CC_{1/2} = correlation coefficient of half-datasets (1).$

 ${}^{\P}\mathsf{R}_{\mathsf{cryst}} = \Sigma hkl||\mathsf{Fobs}|-|\mathsf{Fcalc}||/\Sigma hkl||\mathsf{Fobs}|.$

 $^{\parallel}R_{free}$ calculated as for R_{cryst} but for 5% of the reflections excluded from refinement.

1. Karplus PA, Diederichs K (2012) Linking crystallographic model and data quality. Science 336(6084):1030–1033.