

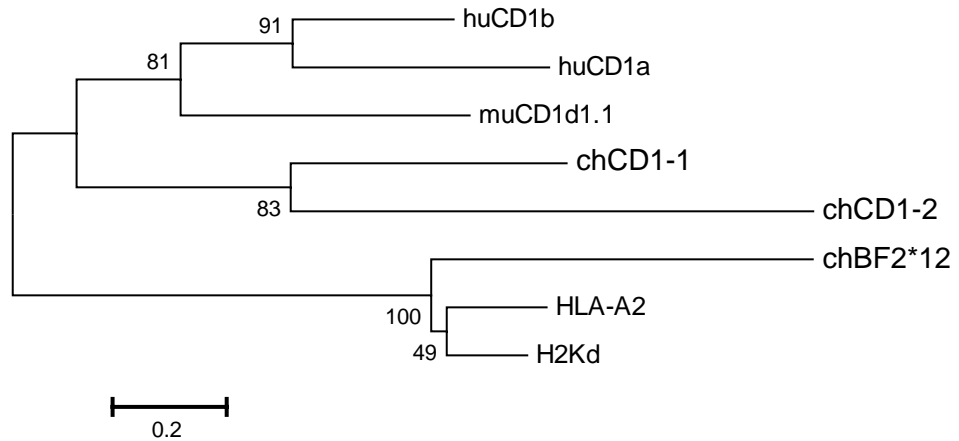
# A. Alpha 1 Domain

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ChCD1-2 : -ETSCPPPEESQFFQLFVTELLGN-VSSTELTGVALLAQVPIMVLDPHTWNLNLCR--PWVQEITAETEVEKKLISFSMVGIRNTIRFHEMTAKAGLD-- : 94
chCD1-1 : -----PEGSHMLKLLHFATFQN-STSVLVGGLCLLGGVVKMGSLDSRTGNIRYYR--PWLRPPLPKGDVDVIESSIKS----YVRDFSRLVQMYTTVP- : 85
huCD1a : -GN-ADGLKEPLSFHVITIASFYN-HSWKQLVSGWLSLQIHTWDSNSSTIVFLW--PWSRGNFSNEBQKLETLFRIRTIKRSFEGIRRYAHELQFE-- : 93
huCD1b : -GNSEHAFQGPSTSFHVITQSSFTN-STWAQTOGSGWLDLQIHWDSDSGTALFLK--PWSKGNFSDKVEAELEELFRVYIFGFAREVQDFAGDFQMK-- : 94
muCD1d1.1 : WGQ-SEAQQKNYIFRCLQMSFFAN-RSWSRTDSVWVWGLQIHTWDSNSATISFTK--PWSQGLKLSNQQWELQOHMFQVYRVSFTRDQLQELVKMMSPKED : 96
chBF2*12 : -AAVCGAAELHLLRYIQAMTDPGPGQPWFVTGVVYDGEVLFVHYNSTAR--RYVPRTEVIAAKADQOYVDGQTIQGGNEQIDRENGLIQRRYINQTG- : 96
HLA-A2 : -LALTQTWAGSHSMRYFFTSVSRPGRGEPFRFIAVGVYVDLQFVRFDSDAASQRMPEPRAFWIEQEG-PEYVDGETRKYKAHSQTHRVDLGTLRGYYNQSEA : 98
H2Kd : -LAPTQTRAGPHSLRYFVTAVSRPGLGEPFRFIAVGVYVDLQFVRFDSADNPRFEPRAFWMBQEG-PEYVDEEQTQRAKSDEQWFRVSLRRTAQRYYNQSKG : 98
  
```

	chCD1-2	chCD1-1	huCD1a	huCD1b	muCD1d1.1	chBF2*12	HLA-A2	H2Kd
chCD1-2	100% 0%							
chCD1-1	22% 40%	100% 0%						
huCD1a	11% 36%	15% 35%	100% 0%					
huCD1b	17% 36%	16% 41%	45% 63%	100% 0%				
muCD1d1.1	12% 34%	16% 41%	30% 57%	37% 56%	100% 0%			
chBF2*12	4% 19%	12% 24%	8% 22%	9% 25%	11% 31%	100% 0%		
HLA-A2	7% 24%	16% 31%	10% 24%	14% 30%	16% 38%	38% 57%	100% 0%	
H2Kd	7% 25%	16% 29%	15% 26%	16% 31%	13% 38%	40% 56%	69% 80%	100% 0%

<u>% Identity</u>
<u>% Similarity</u>



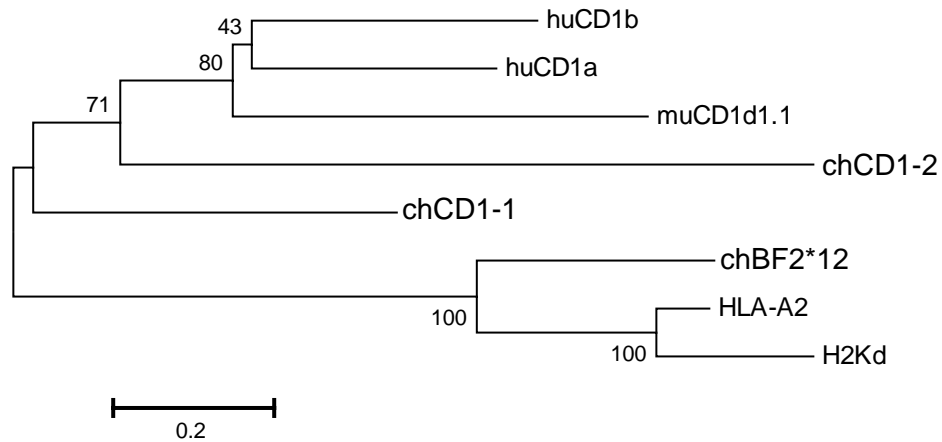
## B. Alpha 2 Domain

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ChCD1-2 : YPRVFCIHTGCKL-YTNGTRWSFVNIIGEGCRLLVYVELSRERVPQRST-LLAKVMSNTLTDLRAVSGFLEHIFSSFPNMTLMLHEGRTDLERR : 94
chCD1-1 : YPFVFCSSIGCCL-QSNGTIRTFFDIAYEGONFIRENLDAQTIDQMQRN-QLSAKAHLMANASTLNEVLIQVLLNDTCVDILRLFTQAGKADLER- : 93
huCD1a : YPFETQVTGGCEL-HSGKVSQSFLQLAYCGSDFVSFQNN--LPLYPVAGNMAKHFCKVLNQNHENDITHNLSDFCPRETLGLLDAGKAHLORQ : 93
huCD1b : YPFETQGIACCEL-HSGGATVSLRGLGCLDFLSVKNAS--CVPSPEGGSRAOKFCALIIQYQGIMETVRILLYEFCPRVLLGVLNAGKADLORQ : 93
muCD1d1.1 : YPIETQLSAGCEM-YPGNASESFLHVAFCCKYVIRFWGTS--QTVPGAPSWLDDLPKVLNADQGTSAIVQMLNDTCPLFVVRGLLEAGKSDLKQ : 93
chBF2*12 : GSHTVQWMYGCDI-LEGGPIRGYQMAVDCRDFTAIDKGTMTTAAVPEAVPTKRKWE---EESPERWKNYLEETCVEWLRRLRYLYGKAELEGR : 91
HLA-A2 : GSHTVQRMYGCDVGSDFRFLRGLYHQYAVDGKDYIALKEDLRSTAAADMAAQTTKHKWE---AAHVAEQLRAYLEGTCEVWLRRLRYLYGKAELEGR : 92
H2Kd : GSHTFRMFGCDVGSDFRLLRGLYHQYAVDGRDYIALNEDLKTAAADTAALITRRKWE---QAGDAEYRYAYLEGECEVWLRRLRYLYGKAELEGR : 92
  
```

	chCD1-2	chCD1-1	huCD1a	huCD1b	muCD1d1.1	chBF2*12	HLA-A2	H2Kd
chCD1-2	100% 0%							
chCD1-1	23% 53%	100% 0%						
huCD1a	25% 50%	29% 52%	100% 0%					
huCD1b	23% 46%	32% 47%	51% 66%	100% 0%				
muCD1d1.1	21% 46%	28% 50%	45% 63%	38% 54%	100% 0%			
chBF2*12	13% 31%	25% 46%	23% 41%	22% 40%	15% 38%	100% 0%		
HLA-A2	13% 26%	22% 44%	22% 40%	19% 36%	17% 34%	52% 66%	100% 0%	
H2Kd	13% 26%	21% 41%	16% 36%	16% 31%	15% 30%	50% 68%	76% 83%	100% 0%

<u>% Identity</u>
<u>% Similarity</u>



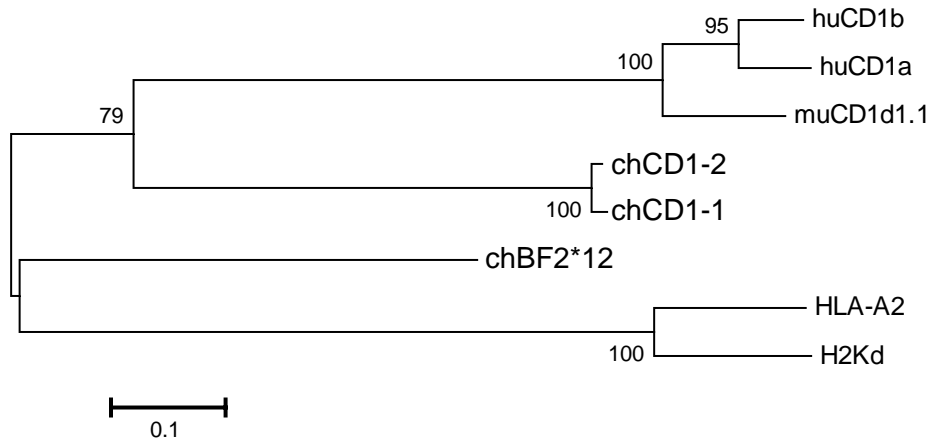
### C. Alpha 3 Domain

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ChCD1-2 : -VPPMAVVFARTAGVQVLLVCRVTSFYPRPIAVVWLRDGREVPPSPALSTCVLPNADLTYQLRSLLWSPQDGHGYACRVCHCSLGDRSLLVLPW : 95
chCD1-1 : -QPPMAVVFARTAGQAQLLVCRVTSFYPRPIAVVWLRDGREVPPSPALSTCVLPNADLTYQLRSLLWSPQDGHGYACRVCHCSLGDRSLLVLPW : 95
huCD1a : VKPEAWLSHGPPSPGPGHQLVCHVSGFYPKPVWVWMMRGEOEQQGT---QRDILPSADCTWYLRATLEWAAEAAADLSCRVRHSSLEGQDITVLYW : 93
huCD1b : VKPEAWLSSGPPSPGPGHQLVCHVSGFYPKPVWVWMMRGEOEQQGT---QLDILPNAWNTWYLRATLDVADAEAAAGLSCRVRHSSLEGQDITVLYW : 93
muCD1d1.1 : EKPVAVLSSVPSAHGHRQLVCHVSGFYPKPVWVWMMRGDQEQQGT---HRDFLPNADCTWYLRATLDVVEAEAEAGLSCRVRHSSLEGQDITVLYW : 93
chBF2*12 : ERPEVRVW-GKEA-DGIITLSCRAHGFYPRPIVVSWLKDGAVRGQD--AHSGLVINGDGTVHTWVITDAQPCDGDKYQCRVBEASTP-QPGYYSW : 91
HLA-A2 : DAPKTHMTHHAVS-DHEATLRQWALSFYPAEITLWQRDGEDQTQD--TELVETRPAGDGTQKWAAVVWPSQEQRYTCHVQHEGLP-KPTITRW : 92
H2Kd : DSEKAHVITYHPRS-QVDVTLRQWALGFYBADITLWQLNGEDLTQD--MELVETRPAGDGTQKWAAVVWPLQEQNYTCHVQHEGLP-EPTITRW : 92
  
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	chCD1-2	chCD1-1	huCD1a	huCD1b	muCD1d1.1	chBF2*12	HLA-A2	H2Kd
chCD1-2	100% 0%							
chCD1-1	97% 97%	100% 0%						
huCD1a	34% 56%	34% 57%	100% 0%					
huCD1b	35% 57%	35% 58%	89% 93%	100% 0%				
muCD1d1.1	35% 56%	35% 57%	77% 84%	78% 83%	100% 0%			
chBF2*12	38% 51%	38% 52%	31% 51%	31% 50%	30% 48%	100% 0%		
HLA-A2	27% 39%	27% 39%	24% 43%	22% 40%	24% 40%	32% 47%	100% 0%	
H2Kd	26% 41%	25% 40%	24% 44%	23% 41%	25% 40%	32% 45%	76% 86%	100% 0%

<b>% Identity</b>
<b>% Similarity</b>



## D. Alpha 1 and 2 Domains (Antigen Binding Pocket)

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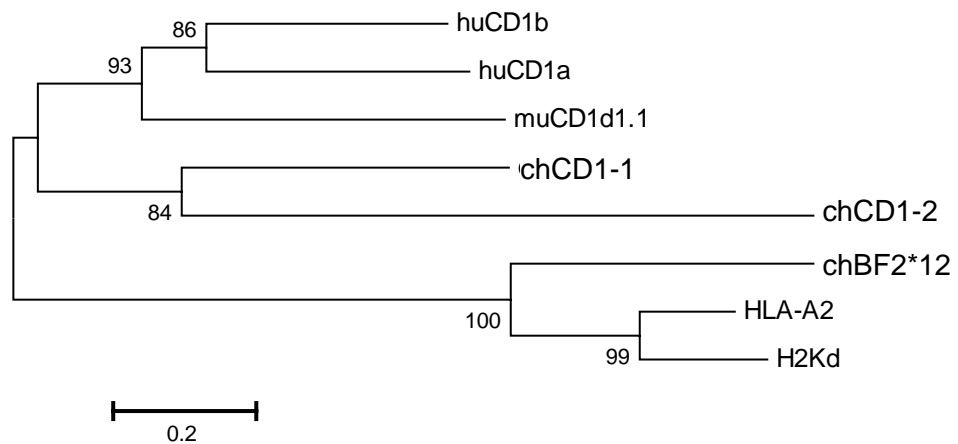
ChCD1-2 : -ETSCPPPEESQFFOLFYLLELGN-VSSTELTGVALLAVPIMVLDPHTW--NLNICRPPWQEITAETEVKKL LSFMSVGRINTIRFMHEMTAKAGLD--
chCD1-1 : -----PEGSHMLKLLHFATFQN-STSVLVGGLCLLGVKMGSLDSRTG--NIRYYRPPWRPSPKGDVDVLESSIKSYVRDFSRIVQMYT-----TVP
huCD1a : -GN-ADGLKEPLSFHVITWIASFYN-HSWKQNLVSGWLSLDTHTWDSNNS--TIVFLWPWSRGNFSNEBQKLETLFRIRTI RSFEGIRRYAHELQFE--
huCD1b : -GNSEHAFQGPSTSFHVITWIASFYN-STWAQTOGSGWLDLQIHLGWDSDSG--TAIFLKPWSKGNFSDKVEAELEEIFRVYIFGFAREVQDFAGDFQMK--
muCD1d1.1 : WGQ-SEAQQKNYIFRCLQSSSFAN-RSWSRTDSVWVWGLDQTHRWSDNSA--TISFTKPPWSQGLSNQVQEKLOHMFQVYRVSFTRDIQELVKMMSPKED
chBF2*12 : -AAVCGAAAELHLRLRYIQTAMTDPGPGQPWFVTVGVVDGELFVHYNSTAR--RYVPRTEWLAAKADQOYDGGQTOICGQNEQIDRENGLILQRRYNTQ-G
HLA-A2 : -LALTQTWAGSHSMRYFFTSVSRPGRGEPRFIAVGVVDLDTQFVRFDSDAASQRMPEPRAPIWIEQEG-PEYDGETRKRKVAHSQTHRVDLGLTRGYYNQSEA
H2Kd : -LAPTQTRAGPHSLRYFVITAVSRPGLGEPRFIAVGVVDLDTQFVRFDSADNPRFEPRAPIWMBQEG-PEYDDEQTQRAKSDEQWFRVSLRRTAQRYYNQSKG
  
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ChCD1-2 : YPRVFCIHTCCKLYING-TRWSFVNI GEGCRDLVTVELSRERWVQORSTLLAKVMSNTLTDLRAVSGFLEHIFSSFPNMI LMLHEBCFTDLERR
chCD1-1 : YPFVFCSSIGCBLQING-TTRTFDIAVEGONFLRFENLDAGTWDQMOHNLQSAKAHLMANASTLNVEIQVLENDTCVDLRLFTQAGKADLER-
huCD1a : YPFETQVTGGCBLHSGK-VSGSFLOLAWQCSDFVSNNSWLPYPVAGNMAKHFCVVLNQNQHEN-DITHNLSDTCPRFSLGLDAGRAHLORQ
huCD1b : YPFETQGIACBLHSGG-AIVSFLRGALGGLDFLSVKNASCVSPSEGGSSRAQKFCALIIQYQGIM-ETVRIILLYETCPRLVLLGVNAGKADLORQ
muCD1d1.1 : YPIETQLSAGCBMYPGN-ASESFLHVAFCCKYVRFVWGTSWQTVPGAPSWLDDLPIKVLNADQGTS-ATVQMLNDTCPLFVRGLLEACKSDLKQ
chBF2*12 : GSHTVQWMMYCDILEGG-PIRGYYQMYDGRDFTAFDKG--TMTFTAAVPEAVPTKRKWEESSEP-ERWKNYLEETQVEVLRRYVLENGKAELEERR
HLA-A2 : GSHTVQRMVYCDILEGG-PIRGYYQMYDGRDFTAFDKG--LRSWTAADMAAQTTRKHWEEAHHVA-EQLRAYLEGTQVEVLRRYVLENGKAELEERR
H2Kd : GSHTVQRMVYCDILEGG-PIRGYYQMYDGRDFTAFDKG--LKTWTAADTAALITRKRKWEQAGDA-EYFRAYLEGTQVEVLRRYVLENGKAELEERR
  
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	chCD1-2	chCD1-1	huCD1a	huCD1b	muCD1d1.1	chBF2*12	HLA-A2	H2Kd
chCD1-2	100% 0%							
chCD1-1	23% 48%	100% 0%						
huCD1a	16% 40%	23% 43%	100% 0%					
huCD1b	19% 41%	25% 45%	48% 65%	100% 0%				
muCD1d1.1	17% 41%	23% 46%	37% 60%	37% 55%	100% 0%			
chBF2*12	8% 25%	17% 33%	16% 31%	15% 31%	15% 35%	100% 0%		
HLA-A2	9% 26%	17% 37%	17% 33%	18% 35%	17% 36%	45% 61%	100% 0%	
H2Kd	9% 24%	18% 34%	16% 31%	17% 32%	13% 34%	45% 62%	72% 82%	100% 0%

% Identity
% Similarity



## E. Alpha 1, 2, and 3 Domains

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GagaCD1.1 : --ETSCPPPEESQFFOLFVYTLNLLGN-VSSTELTGVALLADVPIMVLPHTWNLNICR--EIVQEIETAETEVEKLLSFSMVGIRNTRFMMHMTAKAGLD-- : 94
chCD1-1 : -----PEGSHMLKLLHFATFQN-STSVLVGGLGLLGVKMGSLDSRTGNIRVYR--EPLRPSLPKGDVDVLESSIKSYVRDFSRIVQMYTTVP----- : 85
huCD1a : --GN-ADGLKEPLSFHVIVIASFYFN-HSWKQNLVSGWLSLQHTHTWDSNSSTIVELW--EWSRGNFNSNEEIKLETLEFRIRTIRESFECIRRYAHELQFEE-- : 93
huCD1b : --GNSEHAFQGGPFSFHVIVQESSFTN-STWAQTQGSGLDLDLQIHGWSDSDSGTATFLK--EWSKGNFSDKEVAELLEEIRVYVIFGFAREVQDFAGDFQMK-- : 94
muCD1d1.1 : WGQ-SEAQKKNYIFRCLQMSFFAN-RSWRSTDSVVLGLDLOTHRWSNDSATISFTK--EWSQGLKLSNQQEKLQHMVFQVYRVSFTRDIQELVKMMSPKED : 96
chBF2*12 : --AAVCGAAAELHILRYIQTAMTDPGPGQWVFTVGVVDGELFVHYNSTAR--RYVPRTEWIAAKADQOYVDGQTQIQGGNEQIDREMLGILQRRYNTQ-TG : 96
HLA-A2 : --LALTQTWAGSHSMRYFFTSVSRPGRGEPFRFIAVGVVDLQFVRFSDAASQRMEPRAPWIEQEG-PEYVDGETRQVKAHQSQTHRVDTGLTRGYNQSEA : 98
H2Kd : --LAPTQTRAGPHSLRYFVAVSRPGLGEPFRFIAVGVVDLQFVRFSDADNPRPEPRAPWIEQEG-PEYVDGETQRAKSDEQWFRVSLRTAQRYYNQSKG : 98

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GagaCD1.1 : YPRVFCIHTGCKLYLNG-TRWSFVNIIGEGRDLVTVYELSRERWVPRQSTLLAKVMSNTLTDLRAVSGFLEHIFSSFPFNILMLHEGRTDLEHRRVPEMA : 193
chCD1-1 : YPFVRCSSIGCBLOQNG-TIRTFFDIAVEGQNEIRENLDAQTWDQMHNLQSAKAEHLMANASTLNEVIQVLENDTQVDLRLFIQAGKADLER-QEPMA : 183
huCD1a : YPFETQVTGGCELHSGK-VSGSFLQIAYQGSDFVSEFNNSWLPYYPV-AGNMAKHFCVKVNLQNHENDITHNLSDTQPRFLLGLLDAGKAHLQROVKPEA : 191
huCD1b : YPFETQGIACCELHSGG-ATVSEFLRCALGGLDFLSVKNASCVPSP-EWSSRAQKFCALIIQYQIGIMETVRILLYETQPRVLLGLVFNAGKADLQROVKPEA : 192
muCD1d1.1 : YPIETQLSAGCEBMYPGN-ASESFLHVAFCCKYVIRFWGTSWQTVPG-APSWLDLPIKVLNADQGTSAIVQMLNDTQPLFVRGLLEACKSDLEKQEKPEVA : 194
chBF2*12 : GSHTVQWMYGCDIILEGG-PIRGYQMAVDCRDFTAFDKGTMTFTAA---VPEAVPTKRKWESESEPERWKNYLEETQVBNLRRYVVEYKRAELGRRRREPEV : 192
HLA-A2 : GSHTVQRMVGCDDVGSDFWRFLRCYHQYAVDCKDYIALKEDLRSWTAA---DMAAQTTKHKWEAAHVAEQLRAYLEGTQVBNLRRYVVEYKRAELGRRRREPEV : 195
H2Kd : GSHTVQRMVGCDDVGSDFWRLLRCYHQYAVDGRDYIALNEDLKTWTAA---DTAALITRRKWEQAGDAEYRYRAYLEGEQVBNLRRYVVEYKRAELGRRRREPEV : 195

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GagaCD1.1 : VVVFAR-TAGQVQLLVCRVTSFYPRPIAVTWLDRDGREVPPSPALSTGTVPINADLTYQLRSITLLVSPQDGHGVACRVQHCSSLGDRSLLVLPW : 283
chCD1-1 : VVVFAR-TAGQAQLLVCRVTSFYPRPIAVTWLDRDGREVPPSPALSTGTVPINADLTYQLRSITLLVSPQDGHGVACRVQHCSSLGDRSLLVLPW : 273
huCD1a : WLSHGSPSPGPHLQLVCHVSGFYPKFVWMMWRGEEQEQ---GTQRCDLIPNADGTYWYLRATIDVADGEAAGLSCRVKHSSLEGODLIIYVW : 279
huCD1b : WLSHGSPSPGPHLQLVCHVSGFYPKFVWMMWRGEEQEQ---GTQRCDLIPNANWYWYLRATIDVADGEAAGLSCRVKHSSLEGODLIIYVW : 280
muCD1d1.1 : WLSVSPSSAHGHRQLVCHVSGFYPKFVWMMWRGEEQEQ---GTHRCDFIPNADGTYWYLRATIDVADGEAAGLSCRVKHSSLEGODLIIYVW : 282
chBF2*12 : RW-WGKEADG-IITLSCRAGFYPRPIAVTWLDRDGREVPPSPALSTGTVPINADLTYQLRSITLLVSPQDGHGVACRVQHCSSLGDRSLLVLPW : 278
HLA-A2 : HMTTHAVSDH-EATRCWALSFYPAHITLITWQDGEDQT--QDTBELVETRPAGDGTQKWAAVVVPSCQEQRVYTCVQHEGLP-KPITLIRW : 282
H2Kd : HVTYHPRSQV-DVITRCWALGFYPAHITLITWQDGEDLT--QDMELVETRPAGDGTQKWAAVVVPSCQEQRVYTCVQHEGLP-KPITLIRW : 282

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	chCD1-2	chCD1-1	huCD1a	huCD1b	muCD1d1.1	chBF2*12	HLA-A2	H2Kd
chCD1-2	100%							
	0%							
chCD1-1	48%	100%						
	65%	0%						
huCD1a	24%	26%	100%					
	47%	48%	0%					
huCD1b	25%	30%	62%	100%				
	47%	50%	74%	0%				
muCD1d1.1	23%	26%	50%	51%	100%			
	47%	49%	68%	65%	0%			
chBF2*12	18%	25%	20%	20%	19%	100%		
	33%	38%	37%	37%	39%	0%		
HLA-A2	15%	21%	19%	19%	19%	40%	100%	
	32%	39%	36%	37%	37%	56%	0%	
H2Kd	15%	21%	18%	19%	17%	41%	73%	100%
	31%	37%	35%	35%	35%	56%	83%	0%

<u>% Identity</u>
<u>% Similarity</u>

