(A)

Beta 1 subunit

```
1               17
2F16_N|PDBID|CHAIN|SEQUENCE      ------------------------------TSIMAVTFKDGVILGADSRT
1IRU_H|PDBID|CHAIN|SEQUENCE      ------------------------------TTIMAVQFDGGVVLGADSRT
Q8I0U7                           MDVVNESQIKCHEEKSWDDEYDIKTPISDGTTIIGIIYDNGVMLACDSRT
*:*:.: :..**:*..****

21        31  35          47    53
2F16_N|PDBID|CHAIN|SEQUENCE      TTGAYIANRVTDKLTRVHDKIWCCRSGSAADTQAIADIVQYHLELYTSQY
1IRU_H|PDBID|CHAIN|SEQUENCE      TTGSYIANRVTDKLTPIHDRIFCCRSGSAADTQAVADAVTYQLGFHSIEL
Q8I0U7                           SSGTFISNKCSRKINRINENLYVCRSGASAHSQKIIEIIKHYCVSMKNEN
::*::*:*: : *:. :::.:: ****::*.:* : : : :     . :

2F16_N|PDBID|CHAIN|SEQUENCE      G-------------------------------------------------
1IRU_H|PDBID|CHAIN|SEQUENCE      NE------------------------------------------------
Q8I0U7                           RKKGRFHEGETIYDETTYDEEIDIDSINYLDYNNNNDNNLVTKNKYFYED
|<----------------------  54  residues insert ----

2F16_N|PDBID|CHAIN|SEQUENCE      -----TPSTETAASVFKELCYENKDNLTAGIIVAGYDDKNKGEVYTIPLG
1IRU_H|PDBID|CHAIN|SEQUENCE      -----PPLVHTAASLFKEMCYRYREDLMAGIIIAGWDPQEGGQVYSVPMG
Q8I0U7                           KFNDYNPLVENVAHITKKIIYTNNNFLSCALIFGGYDKIKKQQLYAVNLN
---->|* ....* : *:: *  .: * ..:*..*:*  :  ::*:: :.

129
2F16_N|PDBID|CHAIN|SEQUENCE      G-SVHKLPYAIAGSGSTFIYGYCDKNFRENMSKEETVDFIKHSLSQAIKW
1IRU_H|PDBID|CHAIN|SEQUENCE      G-MMVRQSFAIGGSGSSYIYGYVDATYREGMTKEECLQFTANALALAMER
Q8I0U7                           GSIIEKHDFAVSGSGSIYIQSYLQDKYKKFMTKKECFNLILNCVKYAMHN
*  : :  :*:.**** :* .* : .::: *:*:* .::  :.:  *:.

166
2F16_N|PDBID|CHAIN|SEQUENCE      DGSSGGVIRMVVLTAAGVERLIFYPDEYEQL--------
1IRU_H|PDBID|CHAIN|SEQUENCE      DGSSGGVIRLAAIAESGVERQVLLGDQIPKFAVATLPPA
Q8I0U7                           DNSSGGLIRIVNITKSFVEEFTVVNTQMNFQY-------
*.****:**:. :: : **.  .   :
```

B)

Beta 2 subunit

```
1
2F16_H|PDBID|CHAIN|SEQUENCE      ----------------------------------------TTIVGVKFN
1IRU_I|PDBID|CHAIN|SEQUENCE      ----------------------------------------TTIAGVVYK
Q8I6T3                           MKLEYINILKEENGGYNFDNLKRNEILKEKGVKFPQFRKTGTTICGLVCQ
*** *:  :

17 20         31  35        45  49  53
2F16_H|PDBID|CHAIN|SEQUENCE      NGVVIAADTRSTQGPIVADKNCAKLHRISPKIWCAGAGTAADTEAVTQLI
1IRU_I|PDBID|CHAIN|SEQUENCE      DGIVLGADTRATEGMVVADKNCSKIHFISPNIYCCGAGTAADTDMTTQLI
Q8I6T3                           NAVILGADTRATEGPIVADKNCSKLHYISKNIWCAGAGVAGDLEHTTLWL
:.:::.****:*:* :******:*:* ** :*:*.***.*.* : .*  :

2F16_H|PDBID|CHAIN|SEQUENCE      GSNIELHSLYTSREPRVVSALQMLKQHLFKYQGHIGAYLIVAGVDPTGSH
1IRU_I|PDBID|CHAIN|SEQUENCE      SSNLELHSLSTGRLPRVVTANRMLKQMLFRYRGYIGAALVLGGVDVTGPH
Q8I6T3                           QHNVELHRLNTNTQPRVSMCVSRLTQELFKYQGYKVCAIVLGGVDVNGPQ
*:*** * *.  ***  .   *.* **:*:*:  . :::.*** .*.:

129
2F16_H|PDBID|CHAIN|SEQUENCE      LFSIHAHGSTDVGYYLSLGSGSLAAMAVLESHWKQDLTKEEAIKLASDAI
1IRU_I|PDBID|CHAIN|SEQUENCE      LYSIYPHGSTDKLPYVTMGSGSLAAMAVFEDKFRPDMEEEEAKNLVSEAI
Q8I6T3                           LYGIHPHGSSCLLPFTALGSGSLNAMAVLEAKYRDNMTIEEGKNLVCEAI
*:.*:.***:    : ::***** ****:* ::: ::  **. :*..:**

166
2F16_H|PDBID|CHAIN|SEQUENCE      QAGIWNDLGSGSNVDVCVMEIGKDAEYLRNYLTPNVREEKQ-KSYKFPRG
1IRU_I|PDBID|CHAIN|SEQUENCE      AAGIFNDLGSGSNIDLCVISKNK-LDFLRPYTVPNKKGTRL-GRYRCEKG
Q8I6T3                           CAGIFNDLGSGGNVDICVITKDS-YQHIRPYKEPNMRLYHLPHPTIYPKG
***:******.*:*:**:  ..  :.:* *  ** :  :        :*

2F16_H|PDBID|CHAIN|SEQUENCE      TTAVLKESI-----------VNICD--
1IRU_I|PDBID|CHAIN|SEQUENCE      TTAVLTEKITPLEIEVLEETVQTMDTS
Q8I6T3                           TTPILSEKIEYIK-----KFISVEDA-
**.:*.*.*           :.  *
```

(C)

Beta 5 subunit

```
2F16_K|PDBID|CHAIN|SEQUENCE      --------------------------------------------------
1IRU_L|PDBID|CHAIN|SEQUENCE      --------------------------------------------------
Q8IJT1                           MVIASDESFMNEIDNLINDVEDERIDNDELEFCVAPVNVPRNFIKYAQTQ

1               17  21        31  35
2F16_K|PDBID|CHAIN|SEQUENCE      ----------TTTLAFRFQGGIIVAVDSRATAGNWVASQTVKKVIEINPF
1IRU_L|PDBID|CHAIN|SEQUENCE      ----------TTTLAFKFRHGVIVAADSRATAGAYIASQTVKKVIEINPY
Q8IJT1                           NKKLFDFHKGTTTLAFKFKDGIIVAVDSRASMGSFISSQNVEKIIEINKN
******:*: *:***.****: * :::**.*:*:****

45      53
2F16_K|PDBID|CHAIN|SEQUENCE      LLGTMAGGAADCQFWETWLGSQCRLHELREKERISVAAASKILSNLVYQY
1IRU_L|PDBID|CHAIN|SEQUENCE      LLGTMAGGAADCSFWERLLARQCRIYELRNKERISVAAASKLLANMVYQY
Q8IJT1                           ILGTMAGGAADCLYWEKYLGKIIKIYELRNNEKISVRAASTILSNILYQY
:********** :**  *.   :::***::*:*** ***.:*:*::***

129
2F16_K|PDBID|CHAIN|SEQUENCE      KGAGLSMGTMICGYTRKEGPTIYYVDSDGTRLKGDIFCVGSGQTFAYGVL
1IRU_L|PDBID|CHAIN|SEQUENCE      KGMGLSMGTMICGWDKR-GPGLYYVDSEGNRISGATFSVGSGSVYAYGVM
Q8IJT1                           KGYGLCCGIILSGYDHT-GFNMFYVDDSGKKVEGNLFSCGSGSTYAYSIL
** **. * ::.*: :  *  ::***..*.::.*  *. ***..:**.::

166
2F16_K|PDBID|CHAIN|SEQUENCE      DSNYKWDLSVEDALYLGKRSILAAAHRDAYSGGSVNLYHVTEDGWIYHGN
1IRU_L|PDBID|CHAIN|SEQUENCE      DRGYSYDLEVEQAYDLARRAIYQATYRDAYSGGAVNLYHVREDGWIRVSS
Q8IJT1                           DSAYDYNLNLDQAVELARNAIYHATFRDGGSGGKVRVFHIHKNGYDKIIE
*  *.::*.:::*  *.:.:*  *:.**. *** *.::*: ::*:    .

2F16_K|PDBID|CHAIN|SEQUENCE      -HDVGELFWKVKEEEGSFNNVIG
1IRU_L|PDBID|CHAIN|SEQUENCE      -DNVADLHEKYS---GSTP----
Q8IJT1                           GEDVFDLHYHYTNPEQKDQYVM-
.:* :*. : .    .
```