

Similarity Results for Diabetes TCR

A1: CASRDRGGGGEKLFF

polyprotein, partial [Coxsackievirus B1] [UEU84431.1](#)

```
Query 1      CASRDR  6
          CASRDR
Sbjct  913   CASRDR  918
```

polyprotein [Coxsackievirus B4] [QQL13732.1](#)

```
Query 1      CASRDR  6
          CASR+R
Sbjct  914   CASRNR  919
```

polyprotein, partial [Coxsackievirus A9] [AAF27783.1](#)

```
Query 1      CASRDR  6
          CASR+R
Sbjct  103   CASRNR  108
```

thioesterase family protein [Clostridium tetani] [WP_130004577.1](#)

```
Query 9      GEKLFF  14
          GEKLFF
Sbjct  91     GEKLFF  96
```

```
>>sp|P06213|INSR_HUMAN Insulin receptor OS=Homo sapiens
      10
EMBOSS GEKLFF
      :...::
sp|P06 GSRLFF
```

Waterman-Eggert score: 21; 14.1 bits; E(1) < 0.68
55.6% identity (66.7% similar) in 9 aa overlap (6-14:1343-1351)

```
      10
EMBOSS RGGGEKLFF
      :...::
sp|P06 RDGGSSLGF
      1350
```

Waterman-Eggert score: 17; 11.8 bits; E(1) < 0.99
45.5% identity (63.6% similar) in 11 aa overlap (2-12:886-896)

```
      10
EMBOSS ASRDRGGGEKL
      .:\ : : ::
sp|P06 VSYRRYGDEEL
      890
```

```
>>sp|P47871|GLR_HUMAN Glucagon receptor OS=Homo sapiens
      10
EMBOSS RGGGEK
      :...:
sp|P47 RGGGSQ
```

A2: CASSAETQYF

capsid protein, partial [Coxsackievirus B4] [APZ85768.1](#)

```
Query   3   SSAET   7
          SSAET
Sbjct   38   SSAET   42
```

polyprotein, partial [Coxsackievirus B2] [CCW33458.1](#)

```
Query   2   ASSAETQY   9
          AS+A T+Y
Sbjct   986   ASTAKTEY   993
```

polyprotein, partial [Coxsackievirus B5] [CCW33415.1](#)

```
Query   2   ASSAETQY   9
          AS+A T+Y
Sbjct   987   ASTAKTEY   994
```

polyprotein [Coxsackievirus B3] [AUF49642.1](#)

```
Query   2   ASSAETQY   9
          AS+A T+Y
Sbjct   1555   ASTAKTEY   1562
```

type VII secretion protein EssB [Clostridium perfringens] : [NWJ12916.1](#)

```
Query   3   SSAETQY   9
          SSAETQY
Sbjct   248   SSAETQY   254
```

hypothetical protein [Clostridioides difficile] [WP_077707125.1](#)

23.5 bits(48) 816 6/6(100%) 6/6(100%) 0/6(0%)

```
Query   5   AETQYF   10
          AETQYF
Sbjct   27   AETQYF   32
```

```
>>sp|P06213|INSR_HUMAN Insulin receptor OS=Homo
      10
EMBOSS ASSAETQYF
      .: .: \::
sp|P06 GSWTEPTYF
      940
```

```
>>sp|P47871|GLR_HUMAN Glucagon receptor OS=Homo

EMBOSS SSAET
      :::::
sp|P47 SSAET
      460
```

A3: CASSFRQGEQETQYFpolyprotein, partial [Coxsackievirus B5] [UEU84385.1](#)

```

Query   7      QGEQE-----TQYF  15
          QG+QE      +QYF
Sbjct  1170  QGDQEQLFNSNVQYF  1183

```

```

Query   2      ASSFRQG   8
          AS F+QG
Sbjct  183  ASKFHQG   189

```

```

Query   10     QETQYF   15
          QE++Y+
Sbjct  936  QESEYY   941

```

polyprotein, partial [Coxsackievirus B2] : [UEU84434.1](#)

```

Query   7      QGEQE-----TQYF  15
          QG+QE      +QYF
Sbjct  1171  QGDQEQLFNSNVQYF  1184

```

```

Query   2      ASSFRQG   8
          AS F+QG
Sbjct  183  ASKFHQG   189

```

polyprotein, partial [Coxsackievirus B4] [QRG33154.1](#)

```

Query   7      QGEQE-----TQYF  15
          QG+QE      +QYF
Sbjct  1168  QGDQEQLFNSNVQYF  1181

```

```

Query   2      ASSFRQG   8
          AS F+QG
Sbjct  183  ASKFHQG   189

```

>>sp|P01308|INS_HUMAN Insulin OS=Homo sapiens OX=9606 GN (110 aa)

>>sp|P01308|INS_HUMAN Insulin OS=Homo sapiens OX=9606 GN (110 aa)

```

10
EMBOSS ASSFRQGEQE
:.... :. :

```

```

sp|P01 AEDLQVGQVE
60

```

>>sp|P06213|INSR_HUMAN Insulin receptor OS=Homo sapiens (1382 aa)

```

EMBOSS CASSFRQG
: .: :::

```

```

sp|P06 CKNSRRQG
300

```

Waterman-Eggert score: 24; 15.6 bits; E(1) < 0.33
 57.1% identity (85.7% similar) in 7 aa overlap (7-13:1047-1053)

```

10
EMBOSS QGEQETQ
.: :.

```

```

sp|P06 KGEAETR

```

1050

Waterman-Eggert score: 23; 15.1 bits; E(1) < 0.45
 80.0% identity (100.0% similar) in 5 aa overlap (3-7:726-730)

EMBOSS SSFRQ
 ::::.
 sp|P06 SSFRK
 730

>>sp|P01275|GLUC_HUMAN Pro-glucagon OS=Homo sapiens OX=9 (180 aa)
 10

EMBOSS ASSFRQGEQETQY

 sp|P01 VSSYLEGQAAKEF
 110

>>sp|Q99259|DCE1_HUMAN Glutamate decarboxylase 1 OS=Homo (594 aa)
 10

EMBOSS RQGEQETQYF
 \:
 Sp|Q99 KNGEEQTVQF
 110

A4: CASSISNTGELFF

VP1, partial [Coxsackievirus B1] [AEI98579.1](#)

Query 1 CASSISNT 8
 CA+ ++NT
 Sbjct 48 CATYTNNT 55

>>sp|Q16849|PTPRN_HUMAN Receptor-type tyrosine-protein p (979 aa)
 10

EMBOSS SSISNTGELF
 ... : ::
 sp|Q16 SAVSAHGCLF
 40

T-cell receptor beta V20-3J2.2, TCRBV20-3J2.2 {complementarity determining region 3}
 [human, peripheral T-lymphocytes, insulin-dependent diabetes mellitus patient GAD65.05,

Query 1 CASSIS--NTGELFF 13
 CA SI \ NTGELFF
 Sbjct 1 CAWSIGSRNTGELFF 15

T-cell receptor beta V21-2J2.7, TCRBV21-2J2.7 {complementarity determining region 3}
 [human, peripheral T-lymphocytes, insulin-dependent diabetes mellitus patient GAD65.05,

Query 1 CASSISNTGE 10

Sbjct 1 CASS S++GE
CASSQSHSGE 10

A5: CASSLLAGDNEQFF

polyprotein, partial [Coxsackievirus B5] [UEU84385.1](#)

Query 8 GDNEQFF 14
GD+EQ F
Sbjct 1171 GDQEQLF 1177

polyprotein, partial [Coxsackievirus B4] [QRG33154.1](#)

Sequence ID: Length: 1210Number of Matches: 1

Query 8 GDNEQFF 14
GD+EQ F
Sbjct 1169 GDQEQLF 1175

polyprotein, partial [Coxsackievirus B2] [UEU84434.1](#)

Sequence ID: Length: 1221Number of Matches: 1

Query 8 GDNEQFF 14
GD+EQ F
Sbjct 1172 GDQEQLF 1178

polyprotein [Coxsackievirus B1] [AKF40402.1](#)

Sequence ID: Length: 2182Number of Matches: 1

Query 8 GDNEQFF 14
GD+EQ F
Sbjct 1168 GDQEQLF 1174

efflux RND transporter periplasmic adaptor subunit [Clostridium perfringens] [WP_221372394.1](#)

Query 6 LAGDNEQF 13
L GDNE+F
Sbjct 310 LSGDNEEF 317

tetanus toxoid-specific T-cell receptor beta chain [human, peripheral blood mononuclear cells, clone AKG6, Peptide Partial, 115 aa] [Homo sapiens] [AAB25559.1](#)

Query 1 CASSL-LAGDNEQFF 14
CASSL LAG NEQFF
Sbjct 91 CASSLKLGGNEQFF 105

>>sp|P47871|GLR_HUMAN Glucagon receptor OS=Homo sapiens

EMBOSS ASSLLAGD

: : : : : :

sp|P47 ASSVLVID

190

```
EMBOSS ASSLLAG
      ... :::
sp|P47 AETPLAG
```

myosin IA [Homo sapiens] [KAI2566481.1](#)

```
Query 5 LLAGDNEQ 12
      LLAG +EQ
Sbjct 42 LLAGADEQ 49
```

A6: CASSLPGGAGNEQFF

capsid protein VP1, partial [Coxsackievirus B6] [AEX14714.1](#)

```
Query 2 ASSLPGGAGN 11
      A++LPGG N
Sbjct 15 ADTLPGGPSN 24
```

hemolysin A [Clostridioides difficile] [VTQ90367.1](#)

```
Query 2 ASSLPGGAGNEQFF 15
      AS LPG GN +FF
Sbjct 230 ASPLPGPSGNVEFF 243
```

helix-turn-helix transcriptional regulator [Clostridioides difficile] [HBF9370847.1](#)

```
Query 4 SLPGGAGNEQ 13
      S+ GGAGNE+
Sbjct 63 SIAGGAGNEE 72
```

Lysozyme family protein [Clostridioides difficile] [HBH3061466.1](#)

```
Query 1 CASSLPGGAGN 11
      CA SL GG+GN
Sbjct 270 CAVSLFGGGGN 280
```

```
>>sp|Q99259|DCE1_HUMAN Glutamate decarboxylase 1 OS=Homo
      10
EMBOSS LPGGAGNEQ
      ... :::
sp|Q99 LPAKNGEEQ
      110
```

```
>>sp|P01275|GLUC_HUMAN Pro-glucagon OS=Homo sapiens
      10
EMBOSS ASSLPGGAGNE
      .: : : :...:
sp|P01 SSYLEGQAAKE
      110
```

```
>>sp|P06213|INSR_HUMAN Insulin receptor OS=Homo sapiens (
      10
EMBOSS ASSLPGGAG
      .. : :...
sp|P06 AALLLGAAG
      20
```

T-cell receptor beta V21-1J2.5, TCRBV21-1J2.5 {complementarity determining region 3}
[human, peripheral T-lymphocytes, insulin-dependent diabetes mellitus patient GAD65.05,

```
Query 1 CASSLPGGAGNE-QFF 15
      CASS PG G+E Q+F
Sbjct 1 CASSWPG--GHETQYF 14
```

T-cell receptor beta V6-2J1.4, TCRBV6-2J1.4 {complementarity determining region 3} [human,
peripheral T-lymphocytes, insulin-dependent diabetes mellitus patient GAD65.05, Peptide Query

```
1 CASSLPGGA-GNEQFF 15
      CASS PG A G+E FF
Sbjct 1 CASSPPGRADGDELFF 16
```

A7: CASSPPGLGEQYF

polyprotein, partial [Coxsackievirus B5] [CCW33443.1](#)

```
Query 1 CASSP 5
      CASSP
Sbjct 508 CASSP 512
```

polyprotein [Coxsackievirus B4] [WHA31326.1](#)

```
Query 1 CASSP 5
      CASSP
Sbjct 1074 CASSP 1078
```

```
Query 3 SSPPGL 8
      SSP GL
Sbjct 795 SSPGGL 800
```

polyprotein [Coxsackievirus B3] [SPS68031.1](#)

```
Query 1 CASSP 5
      CASSP
Sbjct 1076 CASSP 1080
```

polyprotein [Coxsackievirus B2] [BBA80352.1](#)

```
Query 1 CASSP 5
      CASSP
Sbjct 1078 CASSP 1082
```

polyprotein [Coxsackievirus A9] [AUF49631.1](#)

Query 1 CASSP 5
 CASSP
 Sbjct 1092 CASSP 1096

polyprotein [Coxsackievirus A6] [WAW78347.1](#)

Query 2 ASSPP 6
 ASSPP
 Sbjct 203 ASSPP 207

Query 3 SSPPG--LGEQY 12
 S PG L QY
 Sbjct 704 STTPGMLL--QY 713

VP1 polyprotein, partial [Coxsackievirus B2] [UWV17742.1](#)

Query 2 ASSPPG 7
 ASS PG
 Sbjct 78 ASSTPG 83

hypothetical protein [Clostridioides difficile] [HBN6128498.1](#)

Query 2 ASSPPGLG 9
 AS+PPGLG
 Sbjct 54 ASTPPGLG 61

macro domain-containing protein [Clostridium perfringens] [WP_143860178.1](#)

Query 8 LGEQYF 13
 LGEQYF
 Sbjct 193 LGEQYF 198

collagenase [Clostridium botulinum C str. Stockholm] [EGO88204.1](#)

Query 8 LGEQYF 13
 LGEQYF
 Sbjct 297 LGEQYF 302

>>sp|P47871|GLR_HUMAN Glucagon receptor OS=Homo sapiens (

EMBOSS ASSPPGLG
 ::: :: :
 sp|P47 ASSSPGHG
 440

tropomyosin 1 (alpha), isoform CRA_1 [Homo sapiens] [EAW77632.1](#)

Query 2 ASSPP-GLGE 10
 A SPP GLGE
 Sbjct 60 AGSPPRGLGE 69

T-cell receptor beta V6-2J1.4, TCRBV6-2J1.4 {complementarity determining region 3} [human, peripheral T-lymphocytes, insulin-dependent diabetes mellitus patient GAD65.05, [AAB46915.1](#)

Query 1 CASSPPG 7
 CASSPPG
 Sbjct 1 CASSPPG 7

A8: CASSPRDGSSYNEQFFpolyprotein, partial [Coxsackievirus A9] [BAE44079.1](#)

Query 1 CASSP 5
 CASSP
 Sbjct 65 CASSP 69

VP1, partial [Coxsackievirus A10] [UYR00073.1](#)

Query 2 ASSPRDGSS 10
 A S RD SS
 Sbjct 284 ANSARDSSS 292

polyprotein, partial [Coxsackievirus B5] [CCW33443.1](#)

Query 1 CASSP 5
 CASSP
 Sbjct 508 CASSP 512

polyprotein [Coxsackievirus B4] [ANY27029.1](#)

Query 1 CASSP 5
 CASSP
 Sbjct 1074 CASSP 1078

polyprotein [Coxsackievirus B3] [SPS68031.1](#)

Query 1 CASSP 5
 CASSP
 Sbjct 1076 CASSP 1080

polyprotein [Coxsackievirus B2] [BBA80352.1](#)

Query 1 CASSP 5
 CASSP
 Sbjct 1078 CASSP 1082

DUF4145 domain-containing protein [Clostridium perfringens] [MDM0977544.1](#)

Query 6 RDGSSYNE 13
 RDGS YNE
 Sbjct 422 RDGSKYNE 429

Query 6 RDGSSYNE 13
 R+GS YNE
 Sbjct 338 RNGSKYNE 345

Query 6 RDGSSYNE 13
 R+GS YNE
 Sbjct 380 RNGSKYNE 387

reverse transcriptase domain-containing protein [Clostridium perfringens] [WP_158524188.1](#)

Query 9 SSYNEQF 15
 S YNEQF
 Sbjct 203 SNYNEQF 209

DNA topoisomerase III [Clostridioides difficile] [HAU5417622.1](#)

Query 7 DGSSYNEQF 15
 D YNEQF
 Sbjct 48 DAATYNEQF 56

```

Query   9      SSYNEQF   15
          S YNEQF
Sbjct  218    SNYNEQF   224

```

type I restriction modification DNA specificity domain protein [Clostridioides difficile P28]
[EQJ55303.1](#)

```

Query   4      SPRDGSSYNEQ-----FF   16
          SP  GSSYNE+      FF
Sbjct  26      SPS-GSSYNEESIGTIFF   42

```

coenzyme F420-0:L-glutamate ligase [Clostridioides difficile] [WP_271641823.1](#)

```

Query   2      ASSPRDGSSYNEQF   15
          ASS  DGS YN+Q+
Sbjct  225    ASSV-DGSGYNDQY   237

```

>>sp|P06213|INSR_HUMAN Insulin receptor OS=Homo sapiens

```

EMBOSS  CASSPRDGS
          : :... \:
sp|P06  CCSCPKTDS
          710

```

```

          10
EMBOSS  ASSPRDGSSYNEQ
          ...: .: : :::
sp|P06  AEQPYQGLS-NEQ
          1240

```

```

>>sp|P01275|GLUC_HUMAN Pro-glucagon OS=Homo sapiens OX=9  (
          10
EMBOSS  DGSSYNE
          : ::: :
sp|P01  DVSSYLE
          110

```

```

          10
EMBOSS  DGSSYNE
          :::/\.:
sp|P01  DGSFSDE
          150

```

```

          10
EMBOSS  ASSPRDGSSYNE
          .:: .:... .:
sp|P01  VSSYLEGQAAKE
          110

```

```

>>sp|P47871|GLR_HUMAN Glucagon receptor OS=Homo sapiens  (
          10
EMBOSS  ASSPRDGSSYNE
          .::: : \.:
sp|P47  SSSPGHGPPSKE
          440

```

```
>>sp|Q16849|PTPRN_HUMAN Receptor-type tyrosine-protein p
      10
EMBOSS  RDGSSYNE
      ::::  .:
sp|Q16  RDGSRVSE
      220
```

A9: CASSYGTVNSPLHF

3D protein, partial [Coxsackievirus A6] [QHJ89586.1](#)

```
Query  5      YGTVN  9
      YGTVN
Sbjct  102    YGTVN  106
```

polyprotein [Coxsackievirus A7] [ADZ11086.1](#)

```
Query  5      YGTVN  9
      YGTVN
Sbjct  1832   YGTVN  1836
```

polyprotein [Coxsackievirus A10] [USC32123.1](#)

Sequence ID: Length: 2193Number of Matches: 1

```
Query  5      YGTVN  9
      YGTVN
Sbjct  1833   YGTVN  1837
```

polyprotein, partial [Coxsackievirus A1] [WBR19144.1](#)

```
Query  6      GTVNS  10
      GTVNS
Sbjct  399    GTVNS  403
```

polyprotein, partial [Coxsackievirus B2] [BAD11195.1](#)

```
Query  5      YGTVNSPLHF  14
      YG  NS LH+
Sbjct  20    YG--NSLLHY  27
```

hypothetical protein [Clostridium perfringens] [MDK0841415.1](#)

```
Query  5      YGTVNSPL  12
      YGT+N+PL
Sbjct  54    YGTINTPL  61
```

diguanylate kinase [Clostridioides difficile] [KPI54855.1](#)

```
Query  3      SSYGTVNSPLH  13
      SSYGTVN+ L+
Sbjct  120   SSYGTVNTVLQ  130
```

transporter substrate-binding domain-containing protein [Clostridioides difficile] [MDI0267395.1](#)

```
Query 3      SSYGTVNSPLH 13
          SSYGTVN+ L+
Sbjct 120    SSYGTVNTVLQ 130
```

hemolysin III-like protein [Clostridioides difficile] [VTR07327.1](#)

```
Query 2      ASSYGTVNS 10
          ASSYGTV S
Sbjct 12      ASSYGTVGS 20
```

replication endonuclease, partial [Clostridioides difficile] [WP_032509971.1](#)

```
Query 1      CASSYGTVNSPLHF 14
          C+ +YGT+N LHF
Sbjct 120    CVPEYGTANGRLHF 133
```

```
>>sp|P06213|INSR_HUMAN Insulin receptor OS=Homo sapiens
          10
```

```
EMBOSS CASSYGTVNS
      : : : : :
sp|P06 CPSGY-TMNS
          320
```

```
          10
EMBOSS GTVNSPLHF
      :. .: :.
sp|P06 GSWTEPTYF
          940
```

```
>>sp|P47871|GLR_HUMAN Glucagon receptor OS=Homo sapiens
          10
```

```
EMBOSS ASSYGTVNSPLH
      .: .: .: :
sp|P47 TSNHRASSSPGH
          430          440
```

A10: CATGLAANTGELFF

polyprotein [Coxsackievirus B5] [AVJ35742.1](#)

```
Query 3      TGLAAN 8
          TGL+AN
Sbjct 15      TGLSAN 20
```

```
Query 6      AANTG 10
          AA+TG
Sbjct 601     AAETG 605
```

```

Query   5      LAANT   9
          LA+NT
Sbjct  1642  LAINT   1646

```

VP1, partial [Coxsackievirus A22] [AFN66229.1](#)

```

Query   6      AANTGELF  13
          A NT++LF
Sbjct  38      ADNTADLF  45

```

VP1, partial [Coxsackievirus A10] [QNN25656.1](#)

```

Query   5      LAANT   9
          LAANT
Sbjct  28      LAANT   32

```

```

Query   6      AANTG   10
          AA+TG
Sbjct  49      AAETG   53

```

DUF4956 domain-containing protein, partial [Clostridium perfringens] [WP_265881915.1](#)

```

Query   3      TGLAANTGELF  13
          TGL A+TGE+F
Sbjct  114      TGLSASTGEIF  124

```

collagen-like protein [Clostridioides difficile] [NJI82831.1](#)

```

Query   2      ATGLAANTGE  11
          ATGL++NTGE
Sbjct  49      ATGLTGNTGE  58

```

```

>sp|P06213|INSR_HUMAN Insulin receptor OS=Homo sapiens
10

```

```

EMBOSS LAANTGELFF
      . . . . .
sp|P06 LTITQGKLFF
      450

```

```

EMBOSS ATGLAAN
      :: :.:.
sp|P06 ATSLAGN
      930

```

```

10
EMBOSS CATGLAANTGEL
      : .: . :. :
sp|P06 CPSGYTMNSSL
      320

```

```

10
EMBOSS ATGLAANTG
      :. : :. :
sp|P06 AAEELEANLG
      380

```

A11: CSVNRGGTDTQYF

polyprotein [Coxsackievirus A10] [AXF74005.1](#)

Query 6 GGTD-TQY 12
GGTD T+Y
Sbjct 662 GGTDTTTEY 669

VP1, partial [Coxsackievirus A4] [AEP43815.1](#)

Query 1 CSVNRGGT-DT--QYF 13
C VN GT +T +YF
Sbjct 1 CVVNSNGTRETHVEYF 16

peptide-methionine (S)-S-oxide reductase [Clostridioides difficile P28] [EQJ59459.1](#)

Query 2 SVNRRGGTDT--QY 12
SVNR G+DT QY
Sbjct 120 SVNRRQGNDSGSQY 132

glycoside hydrolase family 31 protein, partial [Clostridium perfringens] [WP_274541760.1](#)

Query 7 GTDTQY 12
GTDTQY
Sbjct 60 GTDTQY 65

```
>>sp|Q16849|PTPRN_HUMAN Receptor-type tyrosine-protein p
      10
EMBOSS CSVNRGGTDT
      :: : : :
sp|Q16 CSDGAGRTGT
      910
```

TCR DIA 1 CSVEATRADTQYFG

polyprotein [Coxsackievirus B5] [QQL13737.1](#)

Sequence ID: Length: 2185Number of Matches: 4

Query 7 RADTQY 12
RAD QY
Sbjct 2103 RADDQY 2108

polyprotein, partial [Coxsackievirus B3] [UPI41528.1](#)

Query 7 RADTQY 12
RAD QY
Sbjct 2103 RADDQY 2108

30S ribosomal protein S2 [Clostridium perfringens] [NWJ13795.1](#)

Query 4 EATRADTQYF 13
 EATRA QYF
 Sbjct 83 EATRAG-QYF 91

M4 family metallopeptidase [Clostridium perfringens] [WP_003463430.1](#)

Query 7 RADTQYF 13
 RA TQYF
 Sbjct 506 RATTQYF 512

lambda toxin [Clostridium perfringens] [BAA08311.1](#)

Query 7 RADTQYF 13
 RA+TQYF
 Sbjct 506 RATTQYF 512

alpha-galactosidase [Clostridium perfringens] [WP_279857802.1](#)

Query 2 SVEATRADTQYFG 14
 S+E TRA++ YFG
 Sbjct 589 SLE-TRANVAYFG 600

>>sp|P01275|GLUC_HUMAN Pro-glucagon OS=Homo sapiens OX=9

EMBOSS SVEATRAD
 ::
 sp|P01 SFSASQAD

>>sp|Q99259|DCE1_HUMAN Glutamate decarboxylase 1 OS=Homo (
 10
 EMBOSS VEATRADTQY
 : :: . : :
 sp|Q99 VNATAGTTVY
 350

>>sp|Q16849|PTPRN_HUMAN Receptor-type tyrosine-protein p
 10

EMBOSS SVEATRADTQY
 ... :.. :..
 sp|Q16 QTQETRTLTF
 860 870
 10

EMBOSS VEATRADTQ
 : :.
 sp|Q16 AEGTPASTR
 880

10
 EMBOSS EATRADTQY
 :.....:
 sp|Q16 EGAHGDTTF
 620

10
 EMBOSS CSVEATRADT
 :: : .. :
 sp|Q16 CSDGAGRTGT

910

T-cell receptor beta V21-1J2.5, TCRBV21-1J2.5 {complementarity determining region 3}
 [human, peripheral T-lymphocytes, insulin-dependent diabetes mellitus patient GAD65.05,
 Peptide Partial, 23 aa] [Homo sapiens] [AAB46917.1](#)

```
Query   9   DTQYFG   14
          +TQYFG
Sbjct  10   ETQYFG   15
```

TCR DIA 2 CASSLAVIRTDQTQYFG

VP1, partial [Coxsackievirus A24] [ADA84739.1](#)

```
Query  12   TQYFG   16
          TQYFG
Sbjct  49   TQYFG   53
```

RNA-dependent RNA polymerase, partial [Coxsackievirus B4] [AAR16059.1](#)

```
Query   9   RTDTQY   14
          RTD+QY
Sbjct  141   RTDEQY   146
```

polyprotein, partial [Coxsackievirus A13] [UBM82664.1](#)

```
Query   3   SSLAVI    8
          SSLA+I
Sbjct  461   SSLAII   466
```

polyprotein, partial [Coxsackievirus B3] [UPI41540.1](#)

```
Query   9   RTDTQY   14
          RTD+QY
Sbjct  1533   RTDEQY   1538
```

```
Query   2   ASSL     5
          ASSL
Sbjct  1331   ASSL   1334
```

polyprotein [Coxsackievirus B5] [QQL13741.1](#)

```
Query   9   RTDTQY   14
          RTD+QY
Sbjct  2103   RTDEQY   2108
```

```
Query   2   ASSL     5
          ASSL
Sbjct  1901   ASSL   1904
```


polyprotein [Coxsackievirus B2] : [BBA80346.2](#)

Query 9 RTDTQY 14
RTD QY
Sbjct 2105 RTDEQY 2110

site-2 protease family protein [Clostridium perfringens] [WP_208364430.1](#)

Query 2 ASSLAVI---RTDTQYFG 16
A SL+VI /\+T+YFG
Sbjct 112 AASLGVIGVLVSKNTEYFG 130

hypothetical protein [Clostridium perfringens] [WP_075823906.1](#)

Query 4 SLAVIRTDQY 14
SLAV+ T+T Y
Sbjct 258 SLAVVITETKY 268

NUDIX domain-containing protein [Clostridium perfringens] [EGT3616113.1](#)

Sequence ID: Length: 147Number of Matches: 1

Query 6 AVIRTDQYF 15
AV+RT+T YF
Sbjct 33 AVVRTSTGYF 42

minor capsid protein [Clostridium perfringens] [WP_110082846.1](#)

Query 4 SLAVIRTD 12
SL VIRT+T
Sbjct 180 SLRVIRTET 188

prolipoprotein diacylglycerol transferase [Clostridium perfringens] [ELC8365287.1](#)

Query 8 IRTDTQYF 15
IRTD+ YF
Sbjct 217 IRTDSLIF 224

hypothetical protein LZD60_16220 [Clostridium perfringens] [WCM70067.1](#)

Query 7 VIRTD 12
VIRTD
Sbjct 217 VIRTD 222

DNA mismatch repair protein [Clostridium botulinum] [MBN1069351.1](#)

Query 3 SSLAVIRTDQY 14
SSLA+IR D Y
Sbjct 392 SSLAIIRYDNKY 403

phage N-6-adenine-methyltransferase [Clostridium botulinum] [WP_012047611.1](#)

Sequence ID: Length: 140Number of Matches: 1

Query 9 RTDTQYF 15
RTDT YF
Sbjct 98 RTDTRYF 104

```
>>sp|P06213|INSR_HUMAN Insulin receptor OS=Homo sapiens (
10
EMBOSS SLAVIRTDQYF
..... . .:
sp|P06 NLTVIRGSRFF
110
10
```

```
EMBOSS SLAVIRTDQTQYFG
      .: .:. .: .:
sp|P06 KLRLIRGETLEIG
      420
```

>>sp|P47871|GLR_HUMAN Glucagon receptor OS=Homo sapiens

```
EMBOSS ASSLAVI
      :.:.:.:
sp|P47 ASSVLVI
      190
      10
EMBOSS SSLAVIRTDQTQY
      .... :.:.:
sp|P47 TELVCNRTFDKY
      60
```

T-cell receptor beta V21-1J2.5, TCRBV21-1J2.5 {complementarity determining region 3}
[human, peripheral T-lymphocytes, insulin-dependent diabetes mellitus patient GAD65.05,
Peptide Partial, 23 aa] [Homo sapiens] [AAB46917.1](#)

```
Query 11 DTQYFG 16
      +TQYFG
Sbjct 10 ETQYFG 15
```

TCR DIA 3 CAVGALAGTASKLTG

polyprotein [Coxsackievirus A6] [QKZ25788.1](#)
Sequence ID: Length: 2201Number of Matches: 2

```
Query 2 AVGALAGT 9
      AV ALAGT
Sbjct 576 AVSALAGT 583

Query 7 AGTASKL 13
      AG A KL
Sbjct 1382 AGRAAKL 1388
```

pyruvate oxidase [Clostridium perfringens] : [NWJ14174.1](#)

```
Query 3 VGALAGTA-SKLTG 15
      VGALA A KLTG
Sbjct 54 VGALAAAADAKLTG 67
```

MFS transporter [Clostridium perfringens] [WP_283694243.1](#)

```
Query 3 VGALAGTASK 12
      VGAL GT SK
Sbjct 312 VGALSGTVSK 321
```

dihydroorotate dehydrogenase [Clostridium perfringens] [MDO4534443.1](#)

Query 3 VGALAGTASK-LT 14
 VGAL+G+ SK LT
 Sbjct 34 VGALGGISSKGLT 46

DNA polymerase III subunit alpha [Clostridium perfringens] [EJT5937192.1](#)

Query 3 VGALAGTASKLT 14
 +G +AGT +KLT
 Sbjct 1075 IGSIAGTNTKLT 1086

Blp family class II bacteriocin [Clostridium perfringens] [WP_139934343.1](#)

Query 2 AVGALAGT 9
 AVGAL+GT
 Sbjct 50 AVGALVGT 57

SH3 domain-containing protein, partial [Clostridium perfringens] [WP_270204657.1](#)

Query 7 AGTASKLTG 15
 AGT SK+TG
 Sbjct 316 AGTSSKVTG 324

tape measure protein [Clostridium perfringens] [EJT5929836.1](#)

Query 3 VGALAG----TASKL 13
 VGALAG +A KL
 Sbjct 879 VGALAGGILLVAAKL 893

DUF421 domain-containing protein [Clostridium botulinum] [WP_012344633.1](#)

Query 3 VGALAGTAS 11
 +GA+AGTAS
 Sbjct 44 IGAIAGTAS 52

hydroxyethylthiazole kinase [Clostridium botulinum] [WP_043989494.1](#)

Query 1 CAVGAL-AGTAS 11
 C VGAL A+TAS
 Sbjct 175 CMVGALTAATAS 186

>>sp|P06213|INSR_HUMAN Insulin receptor OS=Homo sapiens
 10

EMBOSS ALAGTAS

 sp|P06 SLAGNGS
 930

EMBOSS CAVGA

 sp|P06 CSVAA

10
 EMBOSS AVGALA-GTASKL
 :.....
 sp|P06 AVAALLLGAAGHL
 20

10
 EMBOSS LAGTASK
 :
 sp|P06 LLGVVSK
 1090

```

      10
EMBOSS  AVGALAGTAS
      :... :...
sp|P06  ATGGRRGAAA
      10
      10
EMBOSS  AVGALAGTASKLTG
      :. .... : :
sp|P06  AAPLLVAVAALLLG
      20
      10
EMBOSS  AVGALAGTAS
      ..... :...
sp|P06  TVAAFPNTSS
      780

```

```

>>sp|P47871|GLR_HUMAN Glucagon receptor OS=Homo sapiens
      10
EMBOSS  ALAGTASKL
      :... :...
sp|P47  AILGGLSKL

```

```

>>sp|Q99259|DCE1_HUMAN Glutamate decarboxylase 1 OS=Homo
EMBOSS  VGALAGT
      :. :...
sp|Q99  VNATAGT

```

```

>>sp|Q16849|PTPRN_HUMAN Receptor-type tyrosine-protein p
      10
EMBOSS  ALAGTASKL
      :..... :
sp|Q16  ALAGVAGLL
      590
      10
EMBOSS  AGTASKLT
      :.....
sp|Q16  AGASSSLS
      170

```

zinc transporter SLC39A7 isoform 2 [Homo sapiens] [NP_001275706.1](#)

```

Query  2      AVGALAGTA  10
      AVGALAGTA
Sbjct  263    AVGALAGTA  271

```

KE4 protein [Homo sapiens] [AAD12305.1](#)

```

Query  2      AVGALAGTA  10
      AVGALAGTA
Sbjct  388    AVGALAGTA  396

```

myosin, heavy polypeptide 7B, cardiac muscle, beta, isoform CRA_c [Homo sapiens]

[EAW76238.1](#)

```

Query  2      AVGALA   7
      AVGALA

```

Sbjct 418 AVGALA 423

intermembrane lipid transfer protein VPS13A isoform A [Homo sapiens] [NP_150648.2](#)

Query 2 AVGALAGTASKLTG 15

AVG+LAG+ASK+TG

Sbjct 2913 AVGGLAGAASKITG 2926

vacuolar protein sorting 13 homolog A [Homo sapiens] [KAI2552925.1](#)

Query 2 AVGALAGTASKLTG 15

AVG LAG ASK TG

Sbjct 2913 AVGGLAGAASKITG 2926

chorea-acanthocytosis [Homo sapiens] [AAK61861.1](#)

Query 2 AVGALAGTASKLTG 15

AVG LAG ASK TG

Sbjct 2913 AVGGLAGAASKITG 2926

TCR diabetic 4: CASSLATSGGGSDTQYFG

Chain E, The light chain of fab 9B5 [Coxsackievirus A16] [7YMS_E](#)

Query 8 SGGGSDTQY 16

SG GS TQY

Sbjct 63 SGSGSGTQY 71

Query 7 TSGGGS 12

TSGG+S

Sbjct 126 TSGGAS 131

polyprotein, partial [Coxsackievirus B3] [ADW53828.1](#)

Query 8 SGGGSDTQYFG 18

S GGS TQ FG

Sbjct 406 SNGGSGTQVFG 416

polyprotein, partial [Coxsackievirus B3] [QRG33196.1](#)

Query 14 TQYFG 18

TQY+G

Sbjct 1089 TQYYG 1093

Query 11 GSDTQYFG 18

G+ TQ FG

Sbjct 409 GTGTQVFG 416

polyprotein [Coxsackievirus B5] [AKD28015.1](#)

Query 4 SLATSGGGSDTQYFG 18

S+AT+G TQ FG

Sbjct 404 SIATNG----TQVFG 414

Query 5 LATSGGGS 12
 LA++ +GS
 Sbjct 1319 LASTNAGS 1326

M20/M25/M40 family metallo-hydrolase, partial [Clostridium perfringens] [WP_238001092.1](#)

Query 8 SGGGSDT 14
 SGGGSDT
 Sbjct 92 SGGGSDT 98

peptidase M20 [Clostridium perfringens] [PWX11336.1](#)

Query 8 SGGGSDT 14
 SGGGSDT
 Sbjct 303 SGGGSDT 309

beta-galactosidase [Clostridium perfringens] [CAG9352954.1](#)

Query 11 GSDT-QYF 17
 GSDT QYF
 Sbjct 33 GSDTVQYF 40

phage/plasmid primase, P4 family [Clostridium perfringens] [WP_197926775.1](#)

Query 10 GGS-DTQYF 17
 GGS +TQYF
 Sbjct 244 GGSLNTQYF 252

M20/M25/M40 family metallo-hydrolase [Clostridium tetani] [WP_035111056.1](#)

Query 6 ATSGGGSD 13
 A SGGGSD
 Sbjct 315 AASGGGSD 322

phage tail tape measure protein [Clostridium botulinum] [WP_205427851.1](#)

Query 2 ASSLATSG 9
 ASSLAT G
 Sbjct 563 ASSLATAG 570

Query 2 ASSLATSGGGS 12
 A S+A /GGGS
 Sbjct 1406 APSIASGGGGS 1416

```
>>sp|P06213|INSR_HUMAN Insulin receptor OS=Homo sapiens (
      10
EMBOSS ASSLATSGGGSDTQYF
      :.:.:. .:. .:. .:.
sp|P06 ATSLAGNGSWTEPTYF
      930      940
      10
EMBOSS TSGGGSDTQY
      :.:. .:. :
sp|P06 TYGAKSDIIY
      610
      10
EMBOSS SLATSGGGSDTQ
      . . .:.:. .:.
sp|P06 ATSLAGNGSWTE
      930
```

```

      10
EMBOSS ATSGGGSD
      ...: ...
sp|P06 TSSGTGAE
      750

>>sp|P47871|GLR_HUMAN Glucagon receptor OS=Homo sapiens (
      10
EMBOSS ASSLATSGGGSDTQYFG
      ...: : : . \::
sp|P47 ASSSPGHGPPSKELQFG
      440      450

      10
EMBOSS SLATSGGGSDT
      ... .:.....
sp|P47 QFGRGGGSQDS
      450

      10
EMBOSS SLATSGGGS
      ...: :: :
sp|P47 ALAILGGLS
      160

>>sp|Q99259|DCE1_HUMAN Glutamate decarboxylase 1 OS=Homo
      10
EMBOSS ASSLATSGGGSD
      ...: .....:
sp|Q99 SSSATSSNAGAD
      10

      10
EMBOSS ASSLATSGGGS
      ...: ....:
sp|Q99 ASSTPSSSATS
      10

>>sp|Q16849|PTPRN_HUMAN Receptor-type tyrosine-protein p (
      10
EMBOSS SSLATSGGGSDTQY
      ....: ...: .
sp|Q16 AALGPEGAHGDTTF
      620

      10
EMBOSS SSLATSGG
      .....:
sp|Q16 GGLGGSGG
      10

```

Chain E, T-CELL-RECEPTOR, A3.10-beta chain [Homo sapiens] [6XC9_E \(Tran et al., 2021\)](#)

```

Query 1 CASSLATSGGGSDTQYFG 18
      CASSL SGG DTQYFG
Sbjct 90 CASSLSASGGATDTQYFG 107

```

Tran,M.T., Faridi,P., Lim,J.J., Ting,Y.T., Onwukwe,G.,
 Bhattacharjee,P., Jones,C.M., Tresoldi,E., Cameron,F.J., La

Gruta,N.L., Purcell,A.W., Mannering,S.I., Rossjohn,J. and
 Reid,H.H.
 TITLE T cell receptor recognition of hybrid insulin peptides bound to
 HLA-DQ8
 JOURNAL Nat Commun 12 (1), 5110 (2021)

TCR diabetic 5: CAVVNMDSNYQ

Chain A, 2C protein [Coxsackievirus B3] [6S3A_A](#)

Query 2 AVVNMD 7
 AVV MD
 Sbjct 57 AVVIMD 62

penicillin-binding transpeptidase domain-containing protein [Clostridium perfringens]
[WP_224374358.1](#)

Query 5 NMDSNYQ 11
 N+DSNYQ
 Sbjct 724 NLDSNYQ 730

DNA topoisomerase IV subunit A [Clostridium tetani] [WP_035140929.1](#)

Query 3 VVNMDSNY 10
 VVNM+ NY
 Sbjct 148 VVNMEDNY 155

AAA family ATPase [Clostridium perfringens] [WP_198630792.1](#)

Query 4 VNMDSNY 10
 VNMD NY
 Sbjct 594 VNMDENY 600

flavodoxin-dependent (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase [Clostridium
 perfringens] [MDM0468235.1](#)

Query 1 CAVVNMDSNY 10
 CAV++MD Y
 Sbjct 55 CAVLDMDAAY 64

pyridoxal-dependent decarboxylase [Clostridium perfringens] [WP_164812910.1](#)

Query 2 AVVNMDSN 9
 A+VN+DSN
 Sbjct 101 AIVNLDSN 108

CehA/McbA family metallohydrolase [Clostridium perfringens] [EJT6500362.1](#)

Query 3 VVNM-DSN 9
 VVNM DSN
 Sbjct 1445 VVNMDDSN 1452

carbohydrate kinase family protein [Clostridium botulinum] [EJO5346805.1](#)

```
Query 2      AVVNMDS 8
          AVV+MDS
Sbjct 114    AVVDMDS 120
```

```
>>sp|P47871|GLR_HUMAN Glucagon receptor OS=Homo sapiens
          10
EMBOSS VVNMDSNYQ
      :...: :...:
sp|P47  VAKMYSSFQ
          140
```

TCR diabetic 6: CADAGGTSYKLFG

polyprotein [Coxsackievirus A6] [QKZ25766.1](#)

```
Query 9      YKLFG 13
          YKLFG
Sbjct 1527    YKLFG 1531
```

VP1, partial [Coxsackievirus A20] [AFV68031.1](#)

```
Query 4      AGGTSYKLF 12
          AGGT \KLF
Sbjct 49      AGGTSKLF 57
```

L-ribulose-5-phosphate 3-epimerase [Clostridium perfringens] [NWJ14549.1](#)

```
Query 1      CADAGGT 7
          CADAGGT
Sbjct 65      CADAGGT 71
```

TetR/AcrR family transcriptional regulator [Clostridium perfringens] [EGT3616816.1](#)

Sequence ID: Length: 189Number of Matches: 1

```
Query 7      TSYKLF 12
          TSYKLF
Sbjct 14      TSYKLF 19
```

phage tail family protein [Clostridium botulinum] [NFI38802.1](#)

```
Query 7      TSYKLF 12
          TSYKLF
Sbjct 20      TSYKLF 25
```

FtsW/RodA/SpoVE family cell cycle protein [Clostridium botulinum] [EJP6472118.1](#)

```
Query 4      AGGT-SYKLF 12
          AG T SYKLF
Sbjct 235     AGATISYKLF 244
```

D-alanyl-D-alanine carboxypeptidase [Clostridium perfringens] [MDO4534228.1](#)

Sequence ID: Length: 460 Number of Matches: 1

```
Query 8      SYKLFG 13
          SYKLFG
Sbjct 336    SYKLFG 341
```

glycoside hydrolase family 16 protein [Clostridium perfringens] [MDM0455782.1](#)

```
Query 5      GGTSYK 10
          GGTSYK
Sbjct 368    GGTSYK 373
```

```
>>sp|P47871|GLR_HUMAN Glucagon receptor OS=Homo sapiens  (
          10
EMBOSS AGGT--SYKLF
      : :: : :::
sp|P47 AQGTLRS AKLF
          380
```

```
>>sp|Q99259|DCE1_HUMAN Glutamate decarboxylase 1 OS=Homo
          10
EMBOSS CADAGGTSYKL
      :. : : . ::
sp|Q99 CGVAHGCTRKL
          40
          10
EMBOSS ADAGGTSYKLF
      : :: : : :
sp|Q99 ATAGTTVYGAF
          350
```

TCR diabetic 7: CIPGSEEYGNKLVFG

MAG: polyprotein, partial [Coxsackievirus A19] [AWU65853.1](#)

```
Query 7      EYGNKL--VFG 15
          +Y NKL +FG
Sbjct 1031    DYVNKLGM AFG 1041
```

hypothetical protein [Clostridium perfringens] [HAT4365449.1](#)

```
Query 6      EEY--GNKLVFG 15
          E Y GNKLVFG
Sbjct 739    EAYWQGNKLVFG 750
```

exo-alpha-sialidase NanH [Clostridium perfringens] [MDM0471704.1](#)

Query 1 CIPGSEEEYGNKL 12
 CIP EYGNKL
 Sbjct 333 CIP-YPEYGNKL 343

potassium-transporting ATPase subunit KdpC [Clostridium perfringens] [WP_096515864.1](#)

Query 3 PGSEEEYGNKLV 13
 P+SEEEY +KLV
 Sbjct 95 PASEEEY-EKLV 104

ferrous iron transport protein B [Clostridium tetani] [WP_130006490.1](#)

Query 7 EYGNKLVF 14
 EYGNK+ F
 Sbjct 555 EYGNKMMF 562

5'-nucleotidase C-terminal domain-containing protein [Clostridium tetani] [WP_023438975.1](#)

Query 6 EEYGNK 11
 EEYGNK
 Sbjct 226 EEYGNK 231

Chain A, Receptor-type tyrosine-protein phosphatase gamma [Homo sapiens] [2PBN_A](#)

Query 5 SEEEYGN 10
 SEEEYGN
 Sbjct 153 SEEEYGN 158

anti sigma factor C-terminal domain-containing protein [Clostridium botulinum] [HBJ1646806.1](#)

Query 5 SEEEYGNKLVF 14
 SEE+ KLVF
 Sbjct 227 SEEFSSKLVF 236

>>sp|Q16849|PTPRN_HUMAN Receptor-type tyrosine-protein p

EMBOSS PGSEEEYG

 sp|Q16 PAAEEYG
 470

protein-tyrosine phosphatase, partial [Homo sapiens] [CAA38070.1](#)

Query 4 GSEEEYGN 10
 GSEEEYGN
 Sbjct 366 GSEEEYGN 372

Crystal structure of Human PTPRZ D1 domain [Homo sapiens] [5AWX_A](#)

Query 4 GSEEEYGN 10
 GSEEEYGN
 Sbjct 143 GSEEEYGN 149

protein tyrosine phosphatase receptor type Z1, partial [Homo sapiens] [KAI2547656.1](#)

Query 4 GSEEEYGN 10
 GSEEEYGN
 Sbjct 285 GSEEEYGN 291

Insulin activator factor, partial [Homo sapiens] [AAB31986.1](#)

Query 6 EEYGNKL 12
EEYG KL
Sbjct 568 EEYG-KL 573

human diabetogenic TCR T1D3 in complex with DQ8-p8E9E peptide [Homo sapiens] [6DFX_G](#)
(Wang, et al., 2019)

Query 9 GNKLVFG 15
G KL+FG
Sbjct 98 GGKLIFG 104

Wang, Y., Sosinowski, T., Novikov, A., Crawford, F., White, J., Jin, N.,
Liu, Z., Zou, J., Neau, D., Davidson, H.W., Nakayama, M., Kwok, W.W.,
Gapin, L., Marrack, P., Kappler, J.W. and Dai, S.
TITLE How C-terminal additions to insulin B-chain fragments create
superagonists for T cells in mouse and human type 1 diabetes
JOURNAL Sci Immunol 4 (34) (2019)
PUBMED [30952805](#)

TCR diabetic 8: CASSQVRLAGGGEQFFG

polyprotein, partial [Coxsackievirus A13] [AGX00826.1](#)

Query 1 CASSQV 6
CAS+QV
Sbjct 185 CASNQV 190

BppU family phage baseplate upper protein [Clostridium perfringens] [HBI7084846.1](#)

Query 6 VRLAGGGE 13
VRLAGG E
Sbjct 560 VRLAGGSE 567

GIY-YIG nuclease family protein [Clostridium perfringens] [WP_164815721.1](#)

Query 8 LAGGGEQF 15
LA GGEQF
Sbjct 85 LAKGGEQF 92

myosin XVIIIIB, isoform CRA_c [Homo sapiens] [EAW59704.1](#)

Query 4 SQVRL-AGGGEQ 14
SQVRL AGGG Q
Sbjct 532 SQVRLPAGGGAQ 543

Query 7 RLAG-GGE 13
RLAG GGE
Sbjct 2045 RLAGDGGE 2052

```
>>sp|P01308|INS_HUMAN Insulin OS=Homo sapiens OX=9606 GN  (
      10
EMBOSS SQVRLAGG
      .:.:.:.:
sp|P01  GQVELGGG
      70
      10
EMBOSS CASSQVR--LAGGGEQFF
      :.:. :. :. :. :.
sp|P01  CGSHLVEALYLVCGERGFF
      40
```

```
>>sp|P47871|GLR_HUMAN Glucagon receptor OS=Homo
      10
EMBOSS ASSQVRLAGG
      .:.:. :.:.
sp|P47  SSAETPLAGG
      460
```

T-cell receptor beta V6-2J1.4, TCRBV6-2J1.4 {complementarity determining region 3} [human, peripheral T-lymphocytes, insulin-dependent diabetes mellitus patient GAD65.05, Peptide Partial, 25 aa] [Homo sapiens] [AAB46915.1](#)

```
Query  1  CASS-QVRLAGGGEQFFG  17
        CASS  R A G+E FFG
Sbjct  1  CASSPPGR-ADGDELFFG  17
```

T-cell receptor beta V5-2J2.1, TCRBV5-2J2.1 {complementarity determining region 3} [human, peripheral T-lymphocytes, insulin-dependent diabetes mellitus patient GAD65.05, Peptide Partial, 25 aa] [Homo sapiens] [AAB46921.1](#)

```
Query  1  CASSQVRL-AGGG--EQFFG  17
        CASS  L AGGG  EQFFG
Sbjct  1  CASS---LGAGGGGNEQFFG  17
```

TCR diabetic 9: CASSLGQGETEAFFG

polyprotein, partial [Coxsackievirus B3] [AAA42932.1](#)

Query 6 GQGETE 11
GQGE+E
Sbjct 8 GQGEIE 13

polyprotein, partial [Coxsackievirus B5] [ADN93440.1](#)

Query 4 SLGQGETEAFF 14
SL +GET/ +F
Sbjct 214 SLSNGETASMF 224

VP1, partial [Coxsackievirus A24] [AFV68047.1](#)

Query 11 EAFFG 15
EAFFG
Sbjct 26 EAFFG 30

LysM domain-containing protein [Clostridium perfringens] [WP_111936546.1](#)

Query 3 SSLGQGET 10
SSLGQG+T
Sbjct 190 SSLGQGDT 197

Crystal structure of myosin X motor domain with 2IQ motifs in pre-powerstroke state [Homo sapiens] [5I0I_C](#)

Query 4 SLGQGETEA 12
SLGQ TEA
Sbjct 37 SLGQNPTEA 45

Crystal structure of Myosin VIIa IQ5 in complex with Ca²⁺-CaM [Homo sapiens] [5WSV_A](#)

Query 4 SLGQGETEA 12
SLGQ TEA
Sbjct 43 SLGQNPTEA 51

T-cell receptor beta V5-2J1.1, TCRBV5-2J1.1 {complementarity determining region 3} [human, peripheral T-lymphocytes, insulin-dependent diabetes mellitus patient GAD65.05, Peptide Partial, 23 aa] [Homo sapiens] [AAB46914.1](#)

Query 1 CASSLGQGETEAFFG 15
CASS \++TEAFFG
Sbjct 1 CASSYEGADTEAFFG 15

TCR diabetic 10: CASRNLGLNTEAFFG

polyprotein, partial [Coxsackievirus B5] [CCW33423.1](#)

Sequence ID: Length: 1366Number of Matches: 1

```
Query 1    CASRNL 6
          CASRN+
Sbjct 348  CASRNM 353
```

Replication-associated recombination protein A [Clostridium perfringens] [MDO4535465.1](#)

Sequence ID: Length: 415Number of Matches: 1

```
Query 6    LGLNTEAFF 14
          L LNTE FF
Sbjct 221  LELNTESFF 229
```

aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme [Clostridium perfringens] [MBO3365597.1](#)

```
Query 2    ASRNLGLNTE 11
          A RNLGLN E
Sbjct 274  ARRNLGLNGE 283
```

```
>>sp|P06213|INSR_HUMAN Insulin receptor OS=Homo sapiens (
10
```

EMBOSS NLGLNTE

:::: ::

```
sp|P06 NLGLIEE
```

390

10

EMBOSS NLGLNTEAFFG

:... :: ::

```
sp|P06 NLAAELEANLG
```

380

```
>>sp|Q99259|DCE1_HUMAN Glutamate decarboxylase 1 OS=Homo
10
```

EMBOSS CASRNLGLNTEAFFG

: . :: :... ::

```
sp|Q99 CEKYNLWLHVDAWG
```

370

10

EMBOSS SRNLGLNTEAFF

:... ::

```
sp|Q99 TRKLGLKICGFL
```

40 50

10

EMBOSS ASRNLGLNTE

:. :... ::

```
sp|Q99 AGAALGFGTD
```

300

TCR diabetic 11: CASSFRRBTDYFG

P1, partial [Coxsackievirus A16] [AIW00805.1](#)

```
Query 1      CASSFRRBTDY 11
          CAS+ RR+T T
Sbjct 286    CAST-RRDTAT 295
```

AAA family ATPase [Clostridioides difficile] [HBY2661863.1](#)

```
Query 6      RRBTDYQY 13
          RR+TD+QY
Sbjct 118    RRDYDNQY 125
```

ethanolamine ammonia-lyase reactivating factor EutA, partial [Clostridioides difficile]
[WP_269807304.1](#)

```
Query 4      SFRRG--TDYQY 13
          SF+RG TDYQY
Sbjct 19      SFKRGEVTDYQY 30
```

```
>>sp|Q16849|PTPRN_HUMAN Receptor-type tyrosine-protein p (
      10
EMBOSS SFRRBTDYFG
      .:..... : :
sp|Q16 DFRRKVNKCYRG
      890      900
```

```
>>sp|Q99259|DCE1_HUMAN Glutamate decarboxylase 1 OS=Homo (
      10
EMBOSS SSFRRBTDYQY
      . :.. :....
sp|Q99 ARFRR-TETDF
      90
```

```
>>sp|P06213|INSR_HUMAN Insulin receptor OS=Homo
      10
EMBOSS CASSFRRBTDYQY
      : .. :.. :..
sp|P06 CKNS-RRQGCHQY
      300
```

myosin XVI [Homo sapiens] [KAI2569880.1](#)

```
Query 9      TDYQYF 14
          TD+QYF
Sbjct 714    TDIQYF 719
```


TCR DIA K2.12 CASSSDRLGNQPQHFpolyprotein, partial [Coxsackievirus A10] [CCC55386.1](#)

Query 2 ASSSDRLG 9
 A SS RLG
 Sbjct 33 APSSHRLG 40

hypothetical protein BN182_1230007 [Clostridioides difficile E9] [CCL59956.1](#)

Query 8 LGNQPQHF 15
 LGNQP HF
 Sbjct 31 LGNQPLHF 38

Restriction endonuclease [Clostridium perfringens] [EHK2335059.1](#)

Query 2 ASSSDRLGNQP 12
 ASSSDR G QP
 Sbjct 205 ASSSDRRG-QP 214

VPA1262 family protein [Clostridium perfringens] [MDM0720080.1](#)

Query 4 SSDRLGN 10
 SS+RLGN
 Sbjct 160 SSERLGN 166

unconventional myosin-Id isoform 4 [Homo sapiens] [NP_001398017.1](#)

Query 7 RLGNQPQ 13
 RL NQPQ
 Sbjct 896 RL-NQPQ 901

myosin ID, isoform CRA_c [Homo sapiens] [EAW80223.1](#)

Query 7 RLGNQPQ 13
 RL NQPQ
 Sbjct 973 RL-NQPQ 978

calcium-transporting ATPase type 2C member 2 isoform X2 [Homo sapiens] [XP_047290950.1](#)

Query 4 SSDRLGNQ 11
 S DRLG+Q
 Sbjct 267 SMDRLGKQ 274

>>sp|P06213|INSR_HUMAN Insulin receptor OS=Homo sapiens
 10

EMBOSS SDRLGNQPQ
 .. ::: :
 sp|P06 SECLGNCSQ
 240

>>sp|P01275|GLUC_HUMAN Pro-glucagon OS=Homo sapiens OX=9
 10

EMBOSS ASSSDRLGNQPQ
 ::::: ... /:
 sp|P01 ASQADPLSDPDQ
 40

```
>>sp|Q99259|DCE1_HUMAN Glutamate decarboxylase 1 OS=Homo (
      10
EMBOSS  SSSDRLGNQPQ
      ...  .: :::
sp|Q99  SGTTMVGYPQ
      550
```

T-cell receptor beta V23-2J1.5, TCRBV23-2J1.5 {complementarity determining region 3}
[human, peripheral T-lymphocytes, insulin-dependent diabetes mellitus patient GAD65.05,
Peptide Partial, 25 aa] [Homo sapiens] [AAB46923.1](#)

```
Query 1  CASS-SDR-LGNQPQHF 15
        CASS DR +G QPQHF
Sbjct 1  CASSLWDRGMG-QPQHF 16
```

TCR DIA K2.16 CASSQDRLRGVADTQYF

VP1, partial [Coxsackievirus A6] [QGF19190.1](#)

```
Query 6  DRLRGVADTQY 16
        DRLR A+T+Y
Sbjct 284 DRLRS-ATTDY 293
```

hypothetical protein, partial [Clostridium perfringens] [WP_198621907.1](#)

```
Query 2  ASSQDRLRGVA 12
        ASS DRLR A
Sbjct 5  ASSMDRLRAAA 15
```

N-acetylglucosamine-6-phosphate deacetylase [Clostridium perfringens] [NWJ14636.1](#)

```
Query 3  SSQDRLRGVADT 14
        SS +RL VA+T
Sbjct 98  SSKERLKDVAET 109
```

type I restriction endonuclease subunit R [Clostridium perfringens] [HAT4325355.1](#)

```
Query 6  DRLRGVAD 13
        DRLR+VA+
Sbjct 525 DRLRAVAE 532
```

DUF975 family protein [Clostridium perfringens] [WP_265869693.1](#)

```
Query 4  SQDRLRG 10
        SQD+LRG
Sbjct 10  SQDKLRG 16
```

Diacylglycerol O-acyltransferase [Clostridioides difficile] [VTR08062.1](#)

```
Query 2  ASSQ---DRLRGVAD 13
        AS Q DRLR VAD
Sbjct 242 ASQQWEIDRLRAVAD 256
```

ftsX-like permease family protein [Clostridioides difficile P28] [EQJ57339.1](#)

```
Query 8      LRGVADTQY 16
          LRGV DT+Y
Sbjct 443    LRGVDDTEY 451
```

ABC transporter permease [Clostridioides difficile] [MDB3323854.1](#)

```
Query 8      LRGVADTQY 16
          LRGV DT+Y
Sbjct 443    LRGVDDTEY 451
```

```
>>sp|Q99259|DCE1_HUMAN Glutamate decarboxylase 1 OS=Homo (
      10
EMBOSS LRGVADT
      :::: ..
sp|Q99 LRGVPDS
```

```
>>sp|P06213|INSR_HUMAN Insulin receptor OS=Homo sapiens
      10
EMBOSS RLRGVADTQY
      ::::: ..
sp|P06 RLRGLSPGNY
      920
      10
EMBOSS ASSQDRLRGVADTQ
      ..... :
sp|P06 GNARDIIKGEAETR
      1040      1050
```

TCR DIA K2.4 CASSQEADIQYF

polyprotein [Coxsackievirus B5] [UWT50257.1](#)

```
Query 3      SSQE-ADIQ 10
          SSQE +IQ
Sbjct 692    SSQEQSTIQ 700
```

polyprotein [Coxsackievirus B4] [APR72754.1](#)

```
Query 3      SSQE---ADIQYF 12
          S+QE +IQYF
Sbjct 1168    SDQEQLFNSIQYF 1180
```

polyprotein [Coxsackievirus B5] [AVJ35737.1](#)

```
Query 3      SSQE---ADIQYF 12
          S QE +IQYF
Sbjct 1171    SDQEQLFNSIQYF 1183
```

```
>>sp|Q16849|PTPRN_HUMAN Receptor-type tyrosine-protein p
                        10
EMBOSS  CASSQ-EADIQ
      ::::: :::::
sp|Q16  CATAQGEGNIK
      730
```

TCR Heart 2.1 CASSQDVAGLGFFGPolyprotein, Coxsackievirus A13, [WAB71078.1](#)

| | | | |
|---------------|-----|--------------|-----|
| TCR Heart 2.1 | 3 | SSQDVAGLGFFG | 14 |
| | | SSQD AG +++G | |
| CoxA13 | 805 | SSQD-AGAAYYG | 815 |

Spore germination protein YndE, *Streptococcus pneumoniae*, [CKI08002.1](#)
 hypothetical protein, *Streptococcus anginosus*, [MCW1043024.1](#)

| | | | |
|---------------|----|----------|----|
| TCR Heart 2.1 | 7 | VAGLGFFG | 14 |
| | | VAG+GFFG | |
| S.pneumoniae | 57 | VAGIGFFG | 64 |
| S.anginosus | 66 | IAGLGFF | 72 |

ABC transporter ATP-binding protein, *Streptococcus sanguinis*, [WP_002923689.1](#)

| | | | |
|---------------|-----|---------|-----|
| TCR Heart 2.1 | 4 | SQDVAGL | 10 |
| | | SQDVAGL | |
| S.sanguinis | 220 | SQDVAGL | 226 |

tail fiber domain-containing protein, *Streptococcus pneumoniae*, [MDG7249185.1](#)

| | | | |
|---------------|----|-------------|----|
| TCR Heart 2.1 | 4 | SQDVAGLGFFG | 14 |
| | | SQDVA FFG | |
| S.pneumoniae | 35 | SQDVA--NFFG | 43 |

myosin XVA, isoform CRA_b, *Homo sapiens*, [EAW55664.1](#)unconventional myosin-XV isoform X4, *Homo sapiens*, [XP_024306549.1](#)

| | | | |
|----------------|------|---------|------|
| Heart 2.1 | 5 | QDVAGLG | 11 |
| | | Q VAGLG | |
| Myosin | 551 | QAVAGLG | 557 |
| Unconv. Myosin | 1992 | QAVAGLG | 1998 |

laminin, alpha 1, isoform CRA_d, partial, *Homo sapiens*, [EAX01631.1](#)

| | | | |
|-----------|------|----------|------|
| Laminin | 2028 | DVAGL | 2032 |
| | | DVAGL | |
| Heart 2.1 | 6 | DVAGLGFF | 13 |
| | | DV GL F+ | |
| Laminin | 2831 | DVEGL-FY | 2837 |

collagen type IV alpha 2 chain, *Homo sapiens*, [KAI2569886.1](#)

| | | | |
|---------------|------|---------|------|
| Collagen | 1116 | GLKGFFG | 1122 |
| | | GL GFFG | |
| TCR Heart 2.1 | 9 | GL-GFFG | 14 |
| TCR Heart 2.1 | 9 | GLGFFG | 14 |
| | | GLGF+G | |
| Collagen | 232 | GLGFYG | 237 |

Chain C, Troponin I, *Homo sapiens*, [1JIE_C](#)Chain U, Troponin I, cardiac muscle, *Homo sapiens*, [6KN7_U](#)

| | | | |
|---------------|----|-------|----|
| TCR Heart 2.1 | 8 | AGLGF | 12 |
| | | AGLGF | |
| Troponin | 46 | AGLGF | 50 |

insulin isoform U2 [Homo sapiens] [QMS45322.1](#)

Sequence ID: Length: 198 Number of Matches: 1

Query 3 SSQDVAGL 10
S +DVAGL
Sbjct 54 SREDVAGL 61

TCR Heart 2.2 CASSQDVAGLAFFG (2 clones)

TCR Heart 2.2 4 SQDVAGL 10
SQDVAGL
S.sanguinis 220 SQDVAGL 226
ABC transporter ATP-binding protein **Streptococcus sanguinis**, WP_004192995.1

DUF1275 family protein **Streptococcus agalactiae**, [MCD0152263.1](#)

S.agal. 68 VAGLAFF 74
VAGLAFF
TCR Heart 2.2 7 VAGLAFFG 14
VA LAFFG
S.sanguinis 54 VASLAFFG 61
type II CAAX endopeptidase protein **Streptococcus sanguinis**, WP_223313500.1

TCR Heart 2.20 5 QDVAGLAFF 13
Q +AGLAFF
S.pneumoniae 42 QGAAGLAFF 50
Uncharacterised Protein (DUF2627) **Streptococcus pneumoniae**, COC68514.1

TCR Heart 2.2 7 VAGLA-FFG 14
VAGLA FFG
S.pneumoniae 12 VAGLAVFFG 20
sugar ABC transporter permease **Streptococcus pneumoniae**, COI72814.1

TCR Heart 2.2 3 SSQDVAGLAFFG 14
SSQD AG A++G
CoxA13 805 SSQD-AGAAYYG 815
polyprotein **Coxsackievirus A13**, WAB71078.1

collagen alpha-1(XVII) chain, Homo sapiens, [NP_000485.3](#)

Heart 2.2 2 ASSQDVAG 9
ASSQ+V+G
Collagen 198 ASSQSVSG 205

plasma membrane calcium-transporting ATPase 2 isoform 3, Homo sapiens, [NP_001317540.1](#)

Heart 2.2 4 SQDVAGL 10
SQDVA L
Ca+ transp. 1122 SQDVANL 1128

ryanodine receptor 1 isoform X4, Homo sapiens, [XP_047295158.1](#)

Heart 2.2 5 QDVAGLAFF 13
QDV+ L FF

Ryanodine rec. 1205 QDVSSLRFF 1213

T cell receptor beta chain, partial [Homo sapiens] [AAG15724.1](#)

Query 1 CASSQDVAG 9
CASSQDV G
Sbjct 10 CASSQDVQG 18

Slachta, C.A., Jeevanandam, V., Goldman, B., Lin, W.L. and
Platsoucas, C.D.

TITLE Coronary arteries from human cardiac allografts with chronic rejection contain oligoclonal T cells: persistence of identical clonally expanded TCR transcripts from the early post-transplantation period (endomyocardial biopsies) to chronic rejection (coronary arteries)

JOURNAL J. Immunol. 165 (6), 3469-3483 (2000)

T cell receptor beta chain, partial [Homo sapiens] [BAC01027.1](#)

Query 1 CASSQDYRAADTRFFG 16
CASSQD +ADT +FG
Sbjct 3 CASSQD-SGADTQYFG 17

Saito, M., Higuchi, I., Saito, A., Izumo, S., Usuku, K., Bangham, C.R.
and Osame, M.

TITLE Molecular analysis of T cell clonotypes in muscle-infiltrating lymphocytes from patients with human T lymphotropic virus type 1 polymyositis

JOURNAL J. Infect. Dis. 186 (9), 1231-1241 (2002)

C4-dicarboxylate-binding periplasmic protein, Streptococcus pneumoniae], [CJL99217.1](#)

TCR Heart 2.3 2 ASSQRFQ----GRA 11
A++QRFQ GRA
S.pneumoniae 116 AAAQRFQQSDKGRA 129

T-cell receptor beta V17-1J1.2, TCRBV17.1J1.2 {complementarity determining region 3}
[human, peripheral T-lymphocytes, insulin-dependent diabetes mellitus patient GAD65.05,
Peptide Partial, 21 aa] [Homo sapiens]

Sequence ID: [AAB46922.1](#) Length: 21 Number of Matches: 1

Range 1: 1 to 13 [GenPeptGraphics](#) Next Match Previous Match

Alignment statistics for match #1

| | Score | Expect | Identities | Positives | Gaps |
|---------|------------------|--------|------------|------------|-----------|
| | 20.2 bits(40) | 481 | 10/15(67%) | 10/15(66%) | 3/15(20%) |
| Query 1 | CASSQRFQGRAY-FG | 14 | | | |
| | CASS+R QG +Y FG | | | | |
| Sbjct 1 | CASSNR-QG-GYTFFG | 13 | | | |

TCR Heart 2.4 CASSALRGVYFFG (1 clone)polyprotein, partial, Coxsackievirus B5, [CCW33418.1](#)

| | | | |
|---------------|------|------------|------|
| CoxB5 & CoxB4 | 1143 | SAALLR-HYF | 1151 |
| | | S+ALR YF | |

| | | | |
|---------------|---|-------------|----|
| TCR Heart 2.4 | 1 | CASSALRGVYF | 11 |
| | | CA+ GVYF | |

| | | | |
|---------------|-----|-------------|-----|
| CoxB5 & CoxB4 | 341 | CAT----GVYF | 347 |
|---------------|-----|-------------|-----|

polyprotein, partial, Coxsackievirus B4, [AAV69735.1](#)polyprotein, partial, Coxsackievirus A9, [AAF27790.1](#)polyprotein, partial, Coxsackievirus A13, [CAC08130.1](#)

| | | | |
|---------------|---|-------------|----|
| TCR Heart 2.4 | 1 | CASSALRGVYF | 11 |
| | | CA+ A GVYF | |

| | | | |
|----------------|-----|-------------|-----|
| CoxA9 & CoxA13 | 173 | CACRA--GVYF | 181 |
|----------------|-----|-------------|-----|

homoserine O-succinyltransferase, Streptococcus pneumoniae, [MXQ48449.1](#)homoserine O-succinyltransferase, Streptococcus agalactiae, [WP_017769226.1](#)

| | | | |
|---------------|---|--------------|----|
| TCR Heart 2.4 | 2 | ASSALRGVYFFG | 13 |
| | | ASS LR VY FG | |

| | | | |
|-------------------------|-----|--------------|-----|
| S.pneumoniae & S. agal. | 223 | ASSDLREVYSFG | 234 |
|-------------------------|-----|--------------|-----|

PolC-type DNA polymerase III [Streptococcus pyogenes] [WP_136307060.1](#)

| | | | |
|---------------|---|---------|----|
| TCR Heart 2.4 | 5 | ALRGVYF | 11 |
| | | ALRG+YF | |

| | | | |
|------------|------|---------|------|
| S.pyogenes | 1298 | ALRGAYF | 1304 |
|------------|------|---------|------|

alpha/beta hydrolase-fold protein, Streptococcus pneumoniae, [WP_221073517.1](#)

| | | | |
|---------------|---|-------------|----|
| TCR Heart 2.4 | 5 | ALRGVY---FF | 12 |
| | | ALRGVY FF | |

| | | | |
|--------------|-----|-------------|-----|
| S.pneumoniae | 168 | ALRGVYDARFF | 178 |
|--------------|-----|-------------|-----|

myosin IG, isoform CRA_e, Homo sapiens, [EAW61072.1](#)unconventional myosin 1G valine form, partial, Homo sapiens, [AAK58092.1](#)

| | | | |
|---------------|---|--------------|----|
| TCR Heart 2.4 | 5 | EGF---DRDHLF | 13 |
| | | EGF +RD+LF | |

| | | | |
|----------------|-----|--------------|-----|
| Unconv. Myosin | 497 | EGFIDKNRDFLF | 508 |
|----------------|-----|--------------|-----|

actin filament-associated protein 1 isoform X5, Homo sapiens, [XP_016864025.1](#)

| | | | |
|---------------|---|------------|----|
| TCR Heart 2.4 | 3 | SSEGFD-RDH | 11 |
| | | SS GFD +DH | |

| | | | |
|--------------|----|------------|----|
| Actin-assoc. | 40 | SSKGFDVKDH | 49 |
|--------------|----|------------|----|

glutamate receptor, metabotropic 8, isoform CRA_d, Homo sapien, [EAW83624.1](#)

| | | | |
|---------------|---|----------|---|
| TCR heart 2.4 | 2 | ASSEGFD | 9 |
| | | AS +GFDR | |

| | | | |
|----------|-----|----------|-----|
| Glut Rec | 336 | ASIDGFDR | 343 |
|----------|-----|----------|-----|

laminin subunit alpha-5 isoform X6, Homo sapiens, [XP_054179422.1](#)

| | | | |
|---------------|---|------------|---|
| TCR Heart 2.4 | 1 | CASSAL--RG | 8 |
| | | CA SAL RG | |

| | | | |
|---------|---|------------|----|
| Laminin | 6 | CAGSALCVRG | 15 |
|---------|---|------------|----|

myosin-reactive immunoglobulin heavy chain variable region, partial [Homo sapiens]

[AAD56259.1](#)

| | | | |
|-------|----|-------------|-----|
| Query | 1 | CA---SSEGFD | 8 |
| | | CA SSE+FD | |
| Sbjct | 96 | CARGDSSEAFD | 106 |

TCR Heart 2.5 CASSEGFD RDH LFG (1 Clone)

Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatC, *Streptococcus pneumoniae*,

[WP_088834616.1](#)

| | | | |
|---------------|----|-------------|----|
| TCR Heart 2.5 | 5 | EGFDRDH L F | 13 |
| | | EG DRDH L F | |
| S.pneumoniae | 69 | EGIDRDH L F | 77 |

NAD-dependent deacetylase, *Streptococcus pneumoniae*, [VTQ32396.1](#)

| | | | |
|---------------|----|------------|----|
| TCR Heart 2.5 | 2 | ASSEGFD RD | 10 |
| | | A+ EGFD RD | |
| S.pneumoniae | 76 | ATPEGFD RD | 84 |

Predicted integral membrane protein, *Streptococcus pneumoniae*, [COE84929.1](#)

| | | | |
|---------------|----|-------------|----|
| TCR Heart 2.5 | 5 | EGFDRDH L F | 13 |
| | | EG++RD+L F | |
| S.pneumoniae | 37 | EGYERDQ L F | 45 |

hypothetical protein , *Streptococcus agalactiae*, [WP_001255838.1](#)

hypothetical protein, *Streptococcus pyogenes*, [WP_136107756.1](#)

| | | | |
|----------------------|----|-------------|----|
| TCR Heart 2.5 | 4 | SEGFD RDH L | 12 |
| | | SEG D+DHL | |
| S.pyogenes & S.agal. | 71 | SEGLDKDHL | 79 |

LytTR family DNA-binding domain-containing protein, *Streptococcus sanguinis*,

[WP_176798752.1](#)

| | | | |
|---------------|---|-------------|----|
| TCR Heart 2.5 | 6 | GFDRDH--L F | 13 |
| | | GFDR+H L F | |

S.sanguinis 75 GFDREHKTLF 84

myosin IG, isoform CRA_e, Homo sapiens, [EAW61072.1](#)

TCR Heart 2.5 5 EGF---DRDHLEF 13
EGF +RD+LEF

Myosin 291 EGFIDKNRDFLEF 302

myosin ID, isoform CRA_e, partial, Homo sapiens, [EAW80225.1](#)

TCR Heart 2.5 1 CASS---EGFDRD 10
CAS+ E FDRD

Myosin 506 CASDKILE-FDRD 517

actin filament-associated protein 1 isoform X5, Homo sapiens, [XP_016864025.1](#)

TCR Heart 2.5 3 SSEGFD-RDH 11
SS GFD +DH

Actin filament 40 SSKGFDVKDH 49

Chain A, Metabotropic glutamate receptor 8, Homo sapiens, [6BSZ_A](#)

TCR Heart 2.5 2 ASSEGFD 9
AS +GFDR

Glutamate rec. 300 ASIDGFDR 307

acetylcholine-specific T-cell receptor beta chain, partial [Homo sapiens] [AAB25007.1](#)

Query 1 CASS-EGF 7
CASS EG+

Sbjct 4 CASSLEGY 11

myosin-reactive immunoglobulin heavy chain variable region, partial [Homo sapiens] [AAD56259.1](#)

Query 1 CA---SSEGFD 8
CA SSE+FD

Sbjct 96 CARGDSSEAFD 106

TCR Heart 2.6 CASSQGLGYTFFG (1 CLONE)VP1, partial, Coxsackievirus A16, [AIW00798.1](#)

| | | | |
|-----------|-------|---------|-----|
| CoxA16 | 34 | ASSHGLG | 40 |
| | | ASS+GLG | |
| TCR Heart | 2.6 2 | ASSQGLG | 8 |
| | | ASSQGL | |
| CoxB1 | 329 | ASSQGL | 334 |

Polyprotein, Coxsackievirus B1, [ABV64405.1](#)polyprotein, partial, Coxsackievirus A11, [WAB71058.1](#)polyprotein, partial, Coxsackievirus A15, [BAZ95882.1](#)polyprotein, partial, Human enterovirus, [QRG33074.1](#)

| | | | |
|-----------------|-----|-----------|-----|
| TCR Heart 2.6 | 2 | ASSQGLGYT | 10 |
| | | AS+Q LGYT | |
| CoxA11 & CoxA15 | 430 | ASEQRLGYT | 438 |

putative arabinose transporter, Streptococcus pneumoniae, [CJR70294.1](#)Purine efflux pump PbuE, Streptococcus pneumoniae, [CVN64787.1](#)

Sequence ID: Length: 396Number of Matches: 1

| | | | |
|---------------|-----|-----------|-----|
| TCR Heart 2.6 | 5 | QGLGYTFFG | 13 |
| | | +GLGY+FFG | |
| S.pneumoniae | 245 | HGLGYVFFG | 253 |

LLM class flavin-dependent oxidoreductase, Streptococcus pyogenes, [WP_136274362.1](#)

| | | | |
|---------------|-----|--------|-----|
| TCR Heart 2.6 | 6 | GLGYTF | 11 |
| | | GLGYTF | |
| S.pyogenes | 177 | GLGYTF | 182 |

myosin XV variant, partial, Homo sapiens, [BAD92660.1](#)

| | | | |
|---------------|-----|---------|-----|
| TCR Heart 2.6 | 3 | SSQGLGY | 9 |
| | | SS GLGY | |
| Myosin | 659 | SSPGLGY | 665 |

glutamate ionotropic receptor NMDA type subunit 2A, partial, Homo sapiens, [KAI2577129.1](#)

| | | | |
|---------------|-----|---------------|-----|
| TCR Heart 2.6 | 2 | ASSQGL-GYTFF | 12 |
| | | A S GL GY+FF | |
| Glut. Rec. | 107 | ARSLGLTG YDFF | 118 |

axonemal dynein, partial, Homo sapiens, [AAC27542.1](#)

| | | | |
|---------------|----|------------|----|
| TCR Heart 2.6 | 4 | SQG--LGYTF | 11 |
| | | SQG LGYTF | |
| Dynein | 86 | SQGRKLGYTF | 95 |

TCR Heart 2.7 CASSQDRGQGFFFG (1 CLONE)

radical SAM peptide maturase, CXXX-repeat target family, *Streptococcus pneumoniae*,
[MDG8229751.1](#)

| | | | |
|---------------------|-----|---------|----|
| TCR Heart 2.7 | 1 | CASSQDR | 7 |
| | | CASS+DR | |
| <i>S.pneumoniae</i> | 411 | CASEDR | 41 |

zinc metalloprotease ZmpD, *Streptococcus pneumoniae*, [WP_000054783.1](#)

| | | | |
|---------------------|-----|--------|-----|
| TCR Heart 2.7 | 6 | DRGQGF | 11 |
| | | DRGQGF | |
| <i>S.pneumoniae</i> | 452 | DRGQGF | 457 |

bacteriocin immunity protein, *Streptococcus pneumoniae*, [WP_061756112.1](#)

| | | | |
|---------------------|----|---------|----|
| TCR Heart 2.7 | 2 | ASSQDRG | 8 |
| | | ASSQ+RG | |
| <i>S.pneumoniae</i> | 78 | ASSQERG | 84 |

hypothetical protein, *Streptococcus pyogenes*, [WP_136022607.1](#)

| | | | |
|-------------------|-----|-------------|-----|
| TCR Heart 2.7 | 2 | ASSQ-DRG-QG | 10 |
| | | ASSQ DRG QG | |
| <i>S.pyogenes</i> | 159 | ASSQDRGHQG | 169 |

GHKL domain-containing protein, *Streptococcus agalactiae*, [WP_047201031.1](#)

| | | | |
|---------------------|----|---------------|----|
| TCR Heart 2.7 | 2 | ASS--QDRGQGFF | 12 |
| | | ASS +DRG GF+ | |
| <i>S.agalactiae</i> | 56 | ASSKGEDRGLGFY | 68 |

filamin A, alpha (actin binding protein 280), isoform CRA_d,,Homo sapiens, [EAW72747.1](#)

| | | | |
|---------------|------|--------|------|
| TCR Heart 2.7 | 5 | QDRGQG | 10 |
| | | QDRG+G | |
| Filamin | 1310 | QDRGDG | 1315 |

unconventional myosin-VIIb isoform X5, Homo sapiens, [XP_016859658.1](#)

| | | | |
|---------------|------|-------------|------|
| TCR Heart 2.7 | 4 | SQ----DRGQG | 10 |
| | | SQ DRGQG | |
| Mysoin | 1435 | SQVMASDRGQG | 1445 |

T-cell receptor beta V12-1J2.6, TCRBV12-1J2.6 {complementarity determining region 3}
 [human, peripheral T-lymphocytes, insulin-dependent diabetes mellitus patient GAD65.05,
 Peptide Partial, 28 aa] [Homo sapiens] [AAB46918.1](#)

| | | | |
|-------|---|------------|----|
| Query | 1 | CASSQDRGQG | 10 |
| | | CASS + GQG | |
| Sbjct | 1 | CASSVEPGQG | 10 |

T cell receptor beta chain, partial [Homo sapiens] [BAC01026.1](#)

| | | | |
|-------|---|------------------|----|
| Query | 1 | CASSQDRGQ--GFFFG | 14 |
| | | CASSQDRGQ G+ FG | |
| Sbjct | 3 | CASSQDRGQVYGYTFG | 18 |

Saito,M., Higuchi,I., Saito,A., Izumo,S., Usuku,K., Bangham,C.R.
 and Osame,M.

TITLE Molecular analysis of T cell clonotypes in muscle-infiltrating lymphocytes from patients with human T lymphotropic virus type 1 polyomyositis
JOURNAL J. Infect. Dis. 186 (9), 1231-1241 (2002)

T cell receptor beta chain, partial [Homo sapiens] [AAG15721.1](#)

Query 1 CASSQDRGQGFFFG 14
CASSQ RG+ FFG
Sbjct 10 CASSQGRGE-LFFG 22

Slachta,C.A., Jeevanandam,V., Goldman,B., Lin,W.L. and Platsoucas,C.D.
Coronary arteries from human cardiac allografts with chronic rejection contain oligoclonal T cells: persistence of identical clonally expanded TCR transcripts from the early post-transplantation period (endomyocardial biopsies) to chronic rejection (coronary arteries)
JOURNAL J. Immunol. 165 (6), 3469-3483 (2000)

TCR Heart 2.8 CASSQDGVANQRSFFG (1 CLONE)

curlin minor subunit CsgB, Streptococcus pneumoniae, [CJK66416.1](#)

TCR Heart 2.8 4 SQDGVANQ 11
SQDGV NQ
S.pneumoniae 142 SQDGVSNQ 149

alpha/beta hydrolase-fold protein, partial, Streptococcus sanguinis, [WP_142999620.1](#)

TCR Heart 2.8 8 VANQRSFFG 16
V+NQRS FG
S.sanguin. 56 VTNQRSIFG 64

short-chain dehydrogenase oxidoreductase, Streptococcus pneumoniae, [CGF85861.1](#)

TCR Heart 2.8 7 GVANQRS 13
GVANQRS
S.pneumoniae 13 GVANQRS 19

Eco57I restriction-modification methylase domain-containing protein, Streptococcus anginosus, [WP_264339775.1](#)

TCR Heart 2.8 3 SSQDGVANQ 11
SS+DGVAN+
S.anginosus 606 SSDDGVANE 614

Tfp pilus assembly protein FimV, Streptococcus pneumoniae, [CJL37375.1](#)

TCR Heart 2.8 2 ASSQDGVANQ 11
ASS+ GVAN+
S.pneumoniae 402 ASSEGGVANE 411

Uncharacterised protein, *Streptococcus pneumoniae*, [COQ53279.1](#)

| | | | |
|---------------------|-----|-------------|-----|
| TCR Heart 2.8 | 4 | SQDGVANQRSF | 14 |
| | | SQDGV +QR F | |
| <i>S.pneumoniae</i> | 505 | SQDGVFEQRHF | 515 |

Dynein axonemal heavy chain 5 isoform X7, *Homo sapiens*, [XP_054207919.1](#)

| | | | |
|---------------|------|-------|------|
| Dynein | 3189 | QDGVA | 3193 |
| | | QDGVA | |
| TCR Heart 2.8 | 5 | QDGVA | 9 |
| | | QDGVA | |
| Myosin | 656 | QDGVA | 660 |

human Myosin 1c, *Homo sapiens*, [4BYF_A](#)

Laminin, alpha 1, isoform CRA_a, partial, *Homo sapiens*, [EAX01628.1](#)

| | | | |
|---------------|------|--------|------|
| TCR Heart 2.8 | 3 | SSQDGV | 8 |
| | | SSQ+GV | |
| Laminin | 2674 | SSQNGV | 2679 |

Laminin subunit alpha-5 isoform X7, *Homo sapiens*, [XP_054179424.1](#)

| | | | |
|---------------|-----|------------------|-----|
| TCR Heart 2.8 | 1 | CASSQDGVANQRSFFG | 16 |
| | | CAS++DG | FFG |
| Laminin | 808 | CASCKDG-----FFG | 817 |

TCR Heart 2.9 CASSATGAGTGEFFG (1 CLONE)

polyprotein, partial, Coxsackievirus B4, [WDE31181.1](#)

| | | | |
|---------------|----|---------|----|
| TCR Heart 2.9 | 2 | AS-SATG | 7 |
| | | AS SATG | |
| CoxB4 | 15 | ASLSATG | 21 |

dihydrodipicolinate synthase, *Streptococcus pneumoniae*, [CJL82484.1](#)

dihydrodipicolinate synthase family protein, *Streptococcus agalactiae*, [MCQ3823083.1](#)

| | | | |
|---------------------|---|-----------------|----|
| TCR Heart 2.9 | 2 | ASS--ATGAGTGEFF | 14 |
| | | AS A+G GTGEFF | |
| <i>S.pneumoniae</i> | 5 | ASALFAAG-GTGEFF | 18 |

Serine transporter, *Streptococcus pneumoniae*, [COE01047.1](#)

| | | | |
|---------------------|----|-------------------|-----|
| TCR Heart 2.9 | 2 | ASSAT-G--AGTGEFFG | 15 |
| | | A SAT G A TGE+FG | |
| <i>S.pneumoniae</i> | 87 | AGSATDGILAVTGEYFG | 103 |

portal protein, *Streptococcus pneumoniae*, [VSZ18930.1](#)

| | | | |
|---------------------|-----|---------|-----|
| TCR Heart 2.9 | 6 | TGAGTGE | 12 |
| | | TGAGTGE | |
| <i>S.pneumoniae</i> | 174 | TGAGTGE | 180 |

anaerobic ribonucleoside triphosphate reductase, *Streptococcus pneumoniae*, [CJL47967.1](#)

| | | | |
|---------------------|----|-----------|----|
| TCR Heart 2.9 | 5 | ATGAGTGEF | 13 |
| | | A+GA+TGEF | |
| <i>S.pneumoniae</i> | 34 | AAGAATGEF | 42 |

myosin ID, isoform CRA_b, partial, *Homo sapiens*, [EAW80222.1](#)

| | | | |
|---------------|-----|---------------|-----|
| TCR Heart 2.9 | 3 | SSATGAGTGEFFG | 15 |
| | | SSATGA | FG |
| Myoson | 950 | SSATGA-----FG | 957 |
| TCR Heart 2.9 | 7 | GAGTGE | 12 |
| | | GAGT+E | |
| Myosin | 440 | GAGTAE | 445 |

filamin A, alpha (actin binding protein 280), isoform CRA_d, *Homo sapiens*, [EAW72747.1](#)

| | | | |
|---------------|-----|--------|-----|
| TCR Heart 2.9 | 7 | GAGTGE | 12 |
| | | GAGTGE | |
| Filamin | 410 | GAGTGE | 415 |
| TCR Heart 2.9 | 7 | GAGTGE | 12 |
| | | GAG+GE | |
| Filamin | 509 | GAGSGE | 514 |

TCR Heart 2-10 CASSQDYRAADTRFFG (1 clone)

VP1 protein, partial, Coxsackievirus A13, [CAD98887.1](#), [M1Q4H9](#);

Coxsackie virus A18 [B2X7L9](#)

| | | | |
|-----------------|----|--------|----|
| TCR Heart 2-10: | 6 | DYRAAD | 11 |
| | | DY+AAD | |
| CoxA13, CoxA18 | 84 | DYKAAD | 89 |

polyprotein, partial, Coxsackievirus A13, [UBM82731.1](#)

| | | | |
|----------------|-----|---------|-----|
| TCR Heart 2.10 | 2 | ASSQDYR | 8 |
| | | ASS+DYR | |
| CoxA13 | 286 | ASSEDYR | 292 |

Polyprotein, Cocksackievirus A6, [AVQ94429.1](#)

| | | | |
|----------------|----|----------------|----|
| TCR Heart 2.10 | 2 | ASSQDYRAAD-TRF | 14 |
| | | AS QD+ A D T+F | |
| CoxA6 | 41 | ASRQDF-AQDPTKF | 53 |

chorismate binding enzyme para-aminobenzoate synthetase, *Streptococcus pneumoniae*, [CJD24034.1](#)

| | | | |
|---------------------|-----|----------|-----|
| TCR Heart 2.10 | 1 | CASSQDYR | 8 |
| | | CA +QDYR | |
| <i>S.pneumoniae</i> | 425 | CAANQDYR | 432 |

tRNA 2-selenouridine synthase, *Streptococcus pneumoniae*, [VTQ31256.1](#)

| | | | |
|---------------------|---|-------------|----|
| TCR Heart 2.10 | 5 | QDYRA---ADT | 12 |
| | | QDYRA ADT | |
| <i>S.pneumoniae</i> | 8 | QDYRALLIADT | 18 |

single-stranded DNA-binding protein, *Streptococcus anginosus*, [RGY85239.1](#)

| | | | |
|--------------------|----|------------|----|
| TCR Heart 2.10 | 2 | ASSQDYRAAD | 11 |
| | | A+S DY+AAD | |
| <i>S.anginosus</i> | 31 | ATSRDYKAA | 40 |

hypothetical protein, partial, *Streptococcus pyogenes*, [WP_216353496.1](#)

| | | | |
|-------------------|----|------------------|----|
| TCR Heart 2.10 | 2 | ASSQD----YRAADTR | 13 |
| | | A S+D YRAA+TR | |
| <i>S.pyogenes</i> | 61 | AASDDFASRYRAAQTR | 76 |

unc-45 myosin chaperone B, *Homo sapiens*, [KAI4048879.1](#)

| | | | |
|------------------|----|--------|----|
| TCR Heart 2.10 | 5 | QDYRAA | 10 |
| | | QDY+AA | |
| Myosin chaperone | 20 | QDYKAA | 25 |

collagen type VI alpha 3 chain, partial, *Homo sapiens*, [KAI2527606.1](#)

| | | | |
|----------------|-----|-----------|-----|
| TCR Heart 2.10 | 3 | SSQDYRAAD | 11 |
| | | SS YRAA+ | |
| Collagen VI | 539 | SSAGYRAAE | 547 |

outer dynein arm-docking complex subunit 2 isoform 2, *Homo sapiens*, [NP_001276950.1](#)

| | | | |
|----------------|-----|------------|-----|
| TCR Heart 2.10 | 1 | CASSQDYRAA | 10 |
| | | CAS+++YRAA | |
| Dynein | 184 | CASEENYRAA | 193 |

TCR Heart 2-11 CASSQDRGGGAGFG (1 clone)polyprotein, partial, Coxsackievirus A1, [UBM82506.1](#)

| | | | |
|----------------|-----|---------|-----|
| CoxA1 | 424 | GAGFG | 428 |
| | | GAGFG | |
| TCR Heart 2.11 | 8 | GGGAGFG | 14 |
| | | GGGAG | |
| CoxA20 | 1 | GGGAG | 5 |

polyprotein, partial [Coxsackievirus A20] [AEG42513.1](#)molecular chaperone DnaJ, Streptococcus pneumoniae, [MTV44814.1](#)phage portal protein, lambda family [Streptococcus pneumoniae] [VTQ34062.1](#), 23-29

| | | | |
|----------------|-----|-------------|-----|
| S.pneumoniae | 5 | GGGAGFG | 11 |
| | | GGGAGFG | |
| TCR Heart 2.11 | 4 | SQDRGGGAGFG | 14 |
| | | SQD+ GAGFG | |
| S.pneumoniae | 303 | SQDKNQGAGFG | 313 |

ribonucleotide-diphosphate reductase subunit alpha, Streptococcus pneumoniae, [CKH96652.1](#)radical SAM peptide maturase, CXXX-repeat target family, Streptococcus pneumoniae, [MDG8229751.1](#)putative transcriptional regulator, Streptococcus pneumoniae, [VSE37131.1](#)

| | | | |
|----------------|-----|---------|-----|
| TCR Heart 2.11 | 1 | CASSQDR | 7 |
| | | CASS+DR | |
| S.pneumoniae | 411 | CASSEDR | 417 |

Transcription termination factor Rho, Streptococcus pneumoniae, [CVM18608.1](#)

| | | | |
|----------------|------|-----------|------|
| S.pneumoniae | 134 | ASDQDRSGG | 143 |
| | | AS+QDR GG | |
| TCR Heart 2.11 | 2 | ASSQDRGGG | 9 |
| | | ASSQ+RG | |
| S.pneumoniae | 1598 | ASSQNRG | 1607 |

phage hyaluronidase. Streptococcus pneumoniae, [CVQ11983.1](#)amino acid ABC transporter periplasmic protein, Streptococcus pneumoniae, [CJK97637.1](#)

| | | | |
|----------------|----|-----------|----|
| TCR Heart 2.11 | 5 | QDRGGGAGF | 13 |
| | | QDR G AGF | |
| S.pneumoniae | 56 | QDRNGEAGF | 64 |

unconventional myosin-VIIb isoform X1-8, Homo sapiens. [XP_047300396.1](#)

| | | | |
|----------------|-----|-----------------|-----|
| TCR Heart 2.11 | 4 | SQ----DRGGGAGFG | 14 |
| | | SQ DRG GAG+G | |
| S.pneumoniae | 259 | SQVMASDRGQGAGMG | 273 |

F-actin-uncapping protein LRRC16A isoform X17, Homo sapiens, [XP_054211808.1](#)

| | | | |
|----------------|------|--------------|------|
| TCR Heart 2.11 | 3 | SSQDR--GGGAG | 14 |
| | | SS +R GGGAG | |
| S.pneumoniae | 1181 | SSVERSDGGGAG | 1199 |

myosin light chain kinase 2, skeletal muscle, isoform CRA_d, Homo sapiens, [EAW76417.1](#)

| | | | |
|----------------|----|-----------------|----|
| TCR Heart 2.11 | 3 | SSQ-----DRGGG | 10 |
| | | SSQ DRGGG | |
| S.pneumoniae | 72 | SSQGPKEGEGDRGGG | 85 |

myosin-reactive immunoglobulin heavy chain variable region, partial [Homo sapiens]

[AAD56255.1](#)

Query 1 CASSQDRGGG 10
CA SQ GGG
Sbjct 96 CARSQ--GGG 103

T cell receptor beta chain, partial [Homo sapiens] [BAC01026.1](#)

Query 1 CASSQDRG 8
CASSQDRG
Sbjct 3 CASSQDRG 10

Saito,M., Higuchi,I., Saito,A., Izumo,S., Usuku,K., Bangham,C.R.
and Osame,M.

TITLE Molecular analysis of T cell clonotypes in muscle-infiltrating
lymphocytes from patients with human T lymphotropic virus type 1
polymyositis

JOURNAL J. Infect. Dis. 186 (9), 1231-1241 (2002)

TCR Heart 2-12 CASSQDYRAAYFG (2 clones)

polyprotein, Coxsackievirus A13, [URT60091.1](#)

TCR Heart 2.12 2 ASSQDY 7
A+SQDY
TCR Heart 2.12 2 ASSQDYR 8
ASS+DYR

CoxA13 286 ASSEDYR 292

polyprotein, partial, Coxsackievirus A13, Sequence ID: [UBM82731.1](#)

Polyprotein, Coxsackievirus A13] [WAB71078.1](#)

TCR Heart 2.12 3 SSQDYRAAYFG 13
SSQD AAY+G
CoxA13 805 SSQDAGAAYYG 815

TCR Heart 2-12 1 CASSQDYR 8
CA++QDYR

S.pneumoniae 425 CAANQDYR 432

aminodeoxychorismate synthase component I, Streptococcus pneumoniae, [WP_050282022.1](#)

TCR Heart 2-12 4 SQDYRA-----AYFG 13
SQD+RA AYFG

S.anginosus 197 SQDHRAAIAFLAYFG 211

ABC transporter ATP-binding protein **Streptococcus anginosus** WP_223351257.1

TCR Heart 2-12 5 QDY-RAAYF 12
+DY RAAYF

S.pyogenes & S.agal. 15 EDYERAAAYF 23

AAA family ATPase, partial Streptococcus pyogenes, [WP_031499689.1](#)

ATP-dependent Clp protease, ATP-binding protein ClpE, Streptococcus agalactiae, [VFA67960.1](#), 32-40

outer dynein arm-docking complex subunit 2 isoform X1, Homo sapiens, [XP_024303817.1](#)

Sequence ID: Length: 1107Number of Matches: 1

TCR Heart 2.12 1 CASSQDYRAA 10
CAS+++YRAA

Dynein 659 CASEENYRAA 668

unc-45 myosin chaperone B, Homo sapiens, [KAI4048880.1](#)

TCR Heart 2.12 5 QDYRAA 10
QDY+AA

Myosin chaperone 20 QDYKAA 25

TCR Heart 2.13 CASSPRTGRYEQYF (6 clones)

VP1, partial Coxsackievirus A16, [QNL13216.1](#)

TCR Heart 2.13 2 ASSPRTG 6
ASSPR G

CoxA16 34 ASSPRLG 42

VP1, Coxsackievirus A14, [AAD40501.1](#)

CoxA14 121 CASSSRT 127
CASS RT

TCR Heart 2.13 1 CASSPRTGRQY 11
CA+ +RTGR+Y

CoxA6 & CoxA16 341 CAELARTGREY 351

RNA-dependent RNA polymerase Coxsackievirus A6 [ALB73117.1](#)

And polyprotein Coxsackievirus A16, [AKN89892.1](#), 2072-2082

Uncharacterised protein Streptococcus pyogenes, [QBX28410.1](#), 2-7,

And type 11 methyltransferase Streptococcus pneumoniae, [CKH25746.1](#), 211-216,

And transcriptional regulatory protein Streptococcus pneumoniae, [COF52299.1](#)

S.pyogenes & S.pneumoniae 157 SPRTGR 162
SPRTGR

TCR Heart 2.13 2 ASSPRTGRQY 11
A SP+TGR Y

S.pneumoniae 36 APSPHTGRPY 45

hypothetical protein, Streptococcus pneumoniae, [MDG7107425.1](#)

transcriptional regulatory protein, *Streptococcus pneumoniae*, [COF52299.1](#)

| | | | |
|---------------------|-----|-------------|-----|
| TCR Heart 2.13 | 4 | SPRTGR---YE | 11 |
| | | SPRTGR YE | |
| <i>S.pneumoniae</i> | 157 | SPRTGRSILYE | 167 |

collagen type VI alpha 6, partial, *Homo sapiens*, [CAO81741.1](#)

| | | | |
|----------------|-----|----------|-----|
| TCR Heart 2.13 | 4 | SPRTGRQY | 11 |
| | | SPRTG+ Y | |
| Collagen | 299 | SPRTGKAY | 306 |

capping protein regulator and myosin 1 linker 1, partial [*Homo sapiens*]

Sequence ID: [KAI2541054.1](#) Length: 932 Number of Matches: 2

| | | | |
|-----------------|-----|-----------|-----|
| TCR Heart 2.13 | 3 | SSPRTGRQY | 11 |
| | | SSP++GR+Y | |
| Myosin 1 linker | 750 | SSPQAGRRY | 758 |

F-actin-uncapping protein LRRC16A isoform X17, *Homo sapiens*, [XP_054211808.1](#)

| | | | |
|-------------------------|------|-----------|------|
| TCR Heart 2.13 | 3 | SSPRTGRQY | 11 |
| | | SSP++GR+Y | |
| F-actin uncapping prot. | 1130 | SSPQAGRRY | 1138 |

TCR Heart 2.14 CASSPRTGRYEQYF (1 Clone)

VP1, partial, Coxsackievirus A14, [AAD40501.1](#)

| | | | |
|----------------|-----|---------|-----|
| TCR Heart 2.14 | 1 | CASSPRT | 7 |
| | | CASS RT | |
| CoxA14 | 121 | CASSSRT | 127 |

Membrane dipeptidase (Peptidase family M19), *Streptococcus pneumoniae*, [CJF66504.1](#)

| | | | |
|---------------------|-----|----------|-----|
| TCR Heart 2.14 | 6 | RTGRYEQY | 13 |
| | | R GRYEQY | |
| <i>S.pneumoniae</i> | 268 | RLGRYEQY | 275 |

Carbohydrate diacid regulator, *Streptococcus pneumoniae*, [COC58580.1](#)

| | | | |
|---------------------|-----|--------|-----|
| TCR Heart 2.14 | 8 | GRYEQY | 13 |
| | | GRYEQY | |
| <i>S.pneumoniae</i> | 168 | GRYEQY | 173 |

transcriptional regulatory protein, *Streptococcus pneumoniae*, [COF52299.1](#)

| | | | |
|---------------------|-----|-------------|-----|
| TCR Heart 2.14 | 4 | SPRTGR---YE | 11 |
| | | SPRTGR YE | |
| <i>S.pneumoniae</i> | 157 | SPRTGRSILYE | 167 |

ABC transporter ATP-binding protein/permease, *Streptococcus pyogenes*, [WP_011184891.1](#)

TCR Heart 2.14 7 TGRYEQYF 14
 TGRYEQ F
S.pyogenes 226 TGRYEQEF 233

T-cell receptor beta chain junction region=TCR V beta 3 J beta 2.7 [human, inclusion body myositis patient 8, muscle-infiltrating lymphocytes, Peptide Partial, 23 aa] [Homo sapiens] [AAB32012.1](#)

Query 1 CASSPRTG-RYEQYF 14
 CASS R G YEQYF
 Sbjct 1 CASS-RQGLPYEQYF 14
 O'Hanlon, T.P., Dalakas, M.C., Plotz, P.H. and Miller, F.W.
 TITLE The alpha beta T-cell receptor repertoire in inclusion body
 myositis: diverse patterns of gene expression by
 muscle-infiltrating lymphocytes
 JOURNAL J. Autoimmun. 7 (3), 321-333 (1994)
 PUBMED 7916906

TCR Heart 2.15 CASSQDVGQLTNYEQYF (1 CLONE)

polyprotein, partial, Coxsackievirus B5, [CCW33402.1](#)

TCR Heart 2.15 7 VGQLTNY 13
 VGQ+TNY
CoxB5 1088 VGQVTNY 1094

polyprotein, partial, Coxsackievirus B5, [CCW33402.1](#)

TCR Heart 2.15 2 ASSQ-DVGQL-TNYEQYF 17
 A SQ D QL +N QYF
CoxB5 599 APSQSDQEQLFSN-VQYF 615

Uncharacterized conserved protein, *Streptococcus pneumoniae*, [CKF69883.1](#)

TCR Heart 2.15 9 QLTNYEQY 16
 QLTNYEQY
S.pneumoniae 115 QLTNYEQY 122

Uncharacterised protein, *Streptococcus pneumoniae*, [CKH22399.1](#)

TCR Heart 2.15 11 TNYEQY 16
 TNYEQY
S.pneumoniae 126 TNYEQY 131

threonine dehydratase, *Streptococcus pneumoniae*, [VOI57995.1](#)

```
TCR Heart 2.15      5      QDVGQLTNYE---QY  16
                      Q  VGQLT  YE    QY
S.pneumoniae      241    QKVGQLT-YEATRQY  254
```

putative PKS biosynthesis protein, *Streptococcus pneumoniae*, [CJR91720.1](#)

```
TCR Heart 2.15      2      ASSQDVGQLTN-YEQ  15
                      AS  Q+V  QL++  YEQ
S.pneumoniae      129    ASAQNVVQLDDVYEQ  143
```

T cell receptor beta chain, partial [*Homo sapiens*] [ABR67593.1](#)

```
Query 1  CASSQDVGQLTNYEQYF  17
          CASS DVG  T  YEQYF
Sbjct 1  CASSLDVG--TAYEQYF  15
```

Menezes,C.A.S., Sullivan,A.K., Falta,M.T., Mack,D.G., Freed,B.M.,
Rocha,M.O.C., Gollob,K.J., Fontenot,A.P. and Dutra,W.O.

TITLE Oligoclonal Expansions among Specific V Expressing T Cells in
Human Chagas Disease

JOURNAL Unpublished

[https://www.ncbi.nlm.nih.gov/protein/ABR67593.1?report=genbank&log\\$=protalign
&blast_rank=1&RID=G3M26FPY016](https://www.ncbi.nlm.nih.gov/protein/ABR67593.1?report=genbank&log$=protalign&blast_rank=1&RID=G3M26FPY016) (accessed 13 Sep 2023)

T cell receptor beta chain, partial [*Homo sapiens*] [ABR67597.1](#)

```
Query 1  CASSQDVGQLTNYEQYF  17
          CASS D G  TNYEQYF
Sbjct 1  CASSLDVG--TNYEQYF  15
```

Menezes,C.A.S., Sullivan,A.K., Falta,M.T., Mack,D.G., Freed,B.M.,
Rocha,M.O.C., Gollob,K.J., Fontenot,A.P. and Dutra,W.O.

TITLE Oligoclonal Expansions among Specific V Expressing T Cells in
Human

Chagas Disease

JOURNAL Unpublished

[https://www.ncbi.nlm.nih.gov/protein/ABR67593.1?report=genbank&log\\$=protalign
&blast_rank=1&RID=G3M26FPY016](https://www.ncbi.nlm.nih.gov/protein/ABR67593.1?report=genbank&log$=protalign&blast_rank=1&RID=G3M26FPY016) (accessed 13 Sep 2023)

TCR Heart 2.16 CASSQGGAGAYEQYF (1 CLONE)

carboxymuconolactone decarboxylase family protein, *Streptococcus anginosus*,

[WP_003026283.1](#)

| | | | |
|----------------|-----|--------|-----|
| TCR Heart 2.16 | 10 | AYEQYF | 15 |
| | | AYEQYF | |
| S.angino. | 133 | AYEQYF | 138 |

D-alanyl-lipoteichoic acid biosynthesis protein DltD, *Streptococcus pneumoniae*,

[WP_061652184.1](#)

| | | | |
|----------------|-----|-------------|-----|
| TCR Heart 2.16 | 5 | QGGAGAYEQYF | 15 |
| | | QGGA+ ++QYF | |
| S.pneumoniae | 101 | QGGAASFNQYF | 111 |

salivaricin A modification enzyme, *Streptococcus pyogenes*, [VGW66486.1](#)

| | | | |
|----------------|----|--------|----|
| TCR Heart 2.16 | 9 | GAYEQY | 14 |
| | | GAYEQY | |
| S.pyogenes | 24 | GAYEQY | 29 |

actin related protein 2/3 complex subunit 1B, partial, *Homo sapiens*, [KAI2546845.1](#)

| | | | |
|-----------------------|-----|-------------|-----|
| TCR Heart 2.16 | 2 | ASSQGG--AGA | 10 |
| | | ASS+GG AGA | |
| Actin-related protein | 309 | ASSEGGAAGA | 319 |

intermediate dynein chain, *Homo sapiens*, [CAC17464.1](#)

dynein axonemal heavy chain 9 isoform X4, *Homo sapiens*, [XP_016879783.1](#), 2370-4

| | | | |
|----------------|-----|-------|-----|
| TCR Heart 2.16 | 11 | YEQYF | 15 |
| | | YE+YF | |
| Dynein | 130 | YEEYF | 134 |

myosin-reactive immunoglobulin heavy chain variable region, partial [*Homo sapiens*]

[AAD56255.1](#)

Sequence ID: Length: 125Number of Matches: 1

| | | | |
|-------|----|---------|-----|
| Query | 1 | CASSQGG | 7 |
| | | CA SQGG | |
| Sbjct | 96 | CARSQGG | 102 |

T cell receptor beta chain, partial [*Homo sapiens*] [ABR67596.1](#)

| | | | |
|-------|---|-----------------|----|
| Query | 1 | CASSQGGAGAYEQYF | 15 |
| | | CASS G/ YEQYF | |
| Sbjct | 1 | CASSLDGGSSYEQYF | 15 |

Menezes,C.A.S., Sullivan,A.K., Falta,M.T., Mack,D.G., Freed,B.M.,
Rocha,M.O.C., Gollob,K.J., Fontenot,A.P. and Dutra,W.O.

TITLE Oligoclonal Expansions among Specific V Expressing T Cells in
Human Chagas Disease

JOURNAL Unpublished

[https://www.ncbi.nlm.nih.gov/protein/ABR67593.1?report=genbank&log\\$=protalign&blast_rank=1&RID=G3M26FPY016](https://www.ncbi.nlm.nih.gov/protein/ABR67593.1?report=genbank&log$=protalign&blast_rank=1&RID=G3M26FPY016) (accessed 13 Sep 2023)

TCR Heart 2.17 CASSQEPPGTRAYHDYEQYF (1 CLONE)

hypothetical protein, *Streptococcus anginosus*, [WP_167702630.1](#)

| | | | |
|--------------------|----|----------|----|
| TCR Heart 2.17 | 12 | AYHDYEQY | 19 |
| | | AYHD+EQY | |
| <i>S.anginosus</i> | 31 | AYHDHEQY | 38 |

YtxH domain-containing protein, *Streptococcus pneumoniae*, WP_275584198.

Tn916 ORF15 signal peptide containing protein, *Streptococcus pneumoniae*, [SNF13786.1](#)

| | | | |
|---------------------|-----|----------------------|-----|
| TCR Heart 2.17 | 2 | ASS-QEPPGTR--AYHDYEQ | 18 |
| | | ASS QE P TR YHD EQ | |
| <i>S.pneumoniae</i> | 588 | ASSVQERPTTRQEQYHD-EQ | 606 |

Protein of uncharacterised function (DUF2515), *Streptococcus pneumoniae*, [COE47240.1](#)

| | | | |
|---------------------|-----|-------------|-----|
| TCR Heart 2.17 | 9 | GTRAYHDYEQY | 19 |
| | | G+RA DYEQY | |
| <i>S.pneumoniae</i> | 253 | GSRA--DYEQY | 261 |

Enterotoxin 40 kDa subunit, *Streptococcus pneumoniae*, [CJV90557.1](#)

| | | | |
|---------------------|----|----------|----|
| TCR Heart 2.17 | 12 | AYHDYEQY | 19 |
| | | AY+DYE+Y | |
| <i>S.pneumoniae</i> | 46 | AYNDYEEY | 53 |

hypothetical protein, *Streptococcus anginosus*, [MCW1065389.1](#)

| | | | |
|--------------------|----|----------------|----|
| TCR Heart 2.17 | 7 | PPGTRAYHD---YE | 17 |
| | | PP +RAYHD YE | |
| <i>S.anginosus</i> | 20 | PP-ARAYHDTVIYE | 32 |

F-actin binding protein, isoform CRA_e, *Homo sapiens*, [EAW60185.1](#)

| | | | |
|-----------------------|-----|---------|-----|
| Actin-binding protein | 279 | SQEPPPG | 285 |
| | | SQE PPG | |
| TCR Heart 2.17 | 4 | SQEPPGT | 10 |
| | | Q+PPGT | |
| Actin-binding protein | 39 | QDPPGT | 44 |

TCR Heart 2.18 CASSRSEREQYEQYF (1 CLONE)

hypothetical protein, *Streptococcus sanguinis*, [WP_002895342.1](#)

```
Sbjct      588 REEYEQY 594
              RE+YEQY
Query    5    RSEREQYEQY 14
              R+E EQY+
Sbjct    588 REEYEQYD 595
```

Phosphoribulokinase, *Streptococcus anginosus*, [WP_270736522.1](#)

```
Query    8    REQYEQYF 15
              REQYE Y+
Sbjct   164 REQYERYYY 171
```

Phosphoribulokinase/Uridine kinase family protein, *Streptococcus anginosus*, [ETI82303.1](#)

```
Query    4    SRSEREQYEQYF 15
              SR R+QYE+Y+
Sbjct    49    SR--RQQYEHYY 58
```

Myosin heavy chain, myosin-1, myosin-2, myosin-3, myosin-13, *Homo sapiens*,
[CAA31492.1](#), [NP_003793.2](#), [CAA32167.1](#), [AAD29948](#), [XP_054172208.1](#),
[NP_005954.3](#), [AAI14546.1](#), [EAW90006.1](#)

```
Query    3    SSRSE----REQYEQ 13
              SSR + REQYE+
Sbjct   1339 SSRHDCDLLREQYEE 1353
```

cardiac alpha-myosin heavy chain & myosin-6, *Homo sapiens*, [CAA79675.1](#), [NP_002462.2](#)

```
Query    8    REQYEQ 13
              REQYE+
Sbjct   1346 REQYEE 1351
```

myosin IC, isoform CRA_a, *Homo sapiens*, [EAW90619.1](#)

```
Query    6    SEREQYE-----QYF 15
              SE+E+YE QYF
Sbjct   255 SEQEEYEAEGLAWEVPVQYF 273
```

actin nucleation promoting factor, partial, *Homo sapiens*, [ABX71502.1](#)

```
Query    4    SRSEREQYEQ-----YF 15
              S S REQ EQ YF
Sbjct   162 SISKREQLQEQVQYF 178
```

dynein axonemal heavy chain 17 isoform X4, *Homo sapiens*, [XP_024306782.1](#)

```
Query    6    SEREQYEQYF 15
              S RE YE YF
Sbjct   2342 SPRELYELYF 2351
```

TCR Heart 2.19 CASSQDGGYTYEQYF (1 CLONE)polyprotein, partial, Coxsackievirus B5, [CCW33713.1](#)

| | | | |
|----------------|-----|---------|-----|
| TCR Heart 2.19 | 3 | SSQDGGY | 9 |
| | | SS+D+GY | |
| CoxB5 | 142 | SSKDAGY | 148 |

VP1, partial, Coxsackievirus A6, [AFV68079.1](#)

| | | | |
|----------------|----|---------|----|
| TCR Heart 2.19 | 4 | SQDGGYT | 10 |
| | | SQD GYT | |
| CoxA6 | 46 | SQD-GYT | 51 |

capsid protein, partial, Coxsackievirus A8, [QMU95405.1](#)

| | | | |
|----------------|----|-------------|----|
| TCR Heart 2.19 | 5 | QDGGYT---YE | 12 |
| | | QDGG T YE | |
| CoxA8 | 19 | QDGG-TNKGYE | 28 |

pyridine nucleotide-disulfide oxidoreductase, *Streptococcus pneumoniae*, [COF02052.1](#)

| | | | |
|----------------|----|-----------|----|
| TCR Heart 2.19 | 6 | DGGYT-YEQ | 13 |
| | | DGGYT YEQ | |
| S.pneumoniae | 90 | DGGYTAYEQ | 98 |

Bacterial capsule synthesis protein PGA_cap, *Streptococcus pneumoniae*, [CVY82333.1](#)

| | | | |
|----------------|-----|------------|-----|
| TCR Heart 2.19 | 3 | SSQDGGYTYE | 12 |
| | | S+Q+GGYT+E | |
| S.pneumoniae | 347 | SDQNGGYTFE | 356 |

Uncharacterized protein conserved in bacteria, *Streptococcus pneumoniae*, [CKF14060.1](#)

| | | | |
|----------------|----|---------|----|
| TCR Heart 2.19 | 9 | YTYEQYF | 15 |
| | | YTY+QYF | |
| S.pneumoniae | 49 | YTYSQYF | 55 |

bacitracin transport ATP-binding protein BcrA, *Streptococcus pneumoniae*, [CVN40703.1](#)

| | | | |
|----------------|-----|--------|-----|
| TCR Heart 2.19 | 8 | GYTYEQ | 13 |
| | | GYTYEQ | |
| S.pneumoniae | 245 | GYTYEQ | 250 |

ABC transporter ATP-binding protein, *Streptococcus pneumoniae*, [VTF11396.1](#)

| | | | |
|----------------|-----|----------|-----|
| TCR Heart 2.19 | 5 | QDGGYTYE | 12 |
| | | Q+GG+TYE | |
| S.pneumoniae | 132 | QEGGFYE | 139 |

myosin X, *Homo sapiens*, [KAI2537022.1](#)

| | | | |
|----------------|-----|------------|-----|
| TCR Heart 2.19 | 4 | SQDGGYTYEQ | 13 |
| | | S DG Y+Y+Q | |
| Myosin | 423 | SPDGDYDYDQ | 432 |

type X collagen, partial, Homo sapiens, [AAA61221.1](#)

```
TCR Heart 2.19      9   YTYEQY   14
                      YTY++Y
Collagen            77   YTYDEY   82
```

acetylcholine-specific T-cell receptor beta chain, partial [Homo sapiens] [AAB25007.1](#)

```
Query 1  CASSQDGGYTYEQYF 15
          CASS +G YT E +F
Sbjct 4  CASSLEG-YTGELFF 17
```

T cell receptor beta chain, partial [Homo sapiens] [ABR67596.1](#)

```
Query 1  CASSQDGGYTYEQYF 15
          CASS DGG +YEQYF
Sbjct 1  CASSLDGGSSYEQYF 15
```

Menezes,C.A.S., Sullivan,A.K., Falta,M.T., Mack,D.G., Freed,B.M.,
Rocha,M.O.C., Gollob,K.J., Fontenot,A.P. and Dutra,W.O.
TITLE Oligoclonal Expansions among Specific V Expressing T Cells in
Human Chagas Disease
[https://www.ncbi.nlm.nih.gov/protein/ABR67596.1?report=genbank&log\\$=protalign
&blast_rank=1&RID=G47HCJ6X013](https://www.ncbi.nlm.nih.gov/protein/ABR67596.1?report=genbank&log$=protalign&blast_rank=1&RID=G47HCJ6X013) (accessed 13 Sep 2023)

T cell receptor beta chain, partial [Homo sapiens] [ABR67594.1](#)

Sequence ID: Length: 17Number of Matches: 1

```
Query 1  CASSQDGGYTYEQYF 15
          CASS D G TYEQYF
Sbjct 1  CASSLDQGTTYEQYF 15
```

Menezes,C.A.S., Sullivan,A.K., Falta,M.T., Mack,D.G., Freed,B.M.,
Rocha,M.O.C., Gollob,K.J., Fontenot,A.P. and Dutra,W.O.
TITLE Oligoclonal Expansions among Specific V Expressing T Cells in
Human Chagas Disease
JOURNAL Unpublished
[https://www.ncbi.nlm.nih.gov/protein/ABR67594.1?report=genbank&log\\$=protalign
&blast_rank=9&RID=G47HCJ6X013](https://www.ncbi.nlm.nih.gov/protein/ABR67594.1?report=genbank&log$=protalign&blast_rank=9&RID=G47HCJ6X013) (accessed 13 Sep 2023)

T cell receptor beta chain, partial [Homo sapiens] [ABR67598.1](#)

```
Query 1  CASSQDGGYTYEQYF 15
          CASS D G YEQYF
Sbjct 1  CASSLDSGTSYEQYF 15
```

Menezes,C.A.S., Sullivan,A.K., Falta,M.T., Mack,D.G., Freed,B.M.,
Rocha,M.O.C., Gollob,K.J., Fontenot,A.P. and Dutra,W.O.
TITLE Oligoclonal Expansions among Specific V Expressing T Cells in
Human Chagas Disease
JOURNAL Unpublished
[https://www.ncbi.nlm.nih.gov/protein/ABR67594.1?report=genbank&log\\$=protalign
&blast_rank=9&RID=G47HCJ6X013](https://www.ncbi.nlm.nih.gov/protein/ABR67594.1?report=genbank&log$=protalign&blast_rank=9&RID=G47HCJ6X013) (accessed 13 Sep 2023)

TCR Heart 7.1 CASSPVEPNMTEAFFG (1 CLONE)

Nucleotidyl transferase of uncharacterised function (DUF1814), *Streptococcus pneumoniae*, [CJD10567.1](#)

| | | | |
|---------------------|-----|----------|-----|
| TCR Heart 7.1 | 9 | NMTEAFFG | 16 |
| | | NMTE FFG | |
| <i>S.pneumoniae</i> | 303 | NMTEMFFG | 310 |

TrkH family potassium uptake protein, *Streptococcus pneumoniae*, [MTV64622.1](#)

| | | | |
|---------------------|----|----------|----|
| TCR Heart 7.1 | 8 | PNMTEAFF | 15 |
| | | PNM++AFF | |
| <i>S.pneumoniae</i> | 24 | PNMIDAFF | 31 |

degenerate transposase, *Streptococcus pyogenes*, [VGQ37628.1](#)

| | | | |
|-------------------|----|---------|----|
| TCR Heart 7.1 | 10 | MTEAFFG | 16 |
| | | MTE FFG | |
| <i>S.pyogenes</i> | 12 | MTESFFG | 18 |

ryanodine receptor 2 (cardiac), isoform CRA_b, *Homo sapiens*, [EAW70070.1](#)

| | | | |
|----------------|------|-----------|------|
| Ryanodine rec. | 3342 | DMSEA | 3346 |
| | | +M+EA | |
| TCR Heart 7.1 | 6 | VEPNMTEAF | 14 |
| | | VEP+M+ /F | |
| Ryanodine rec. | 2447 | VEPDMSAGF | 2455 |

cardiac-enriched FHL2-interacting protein X2 (hypertrophy), *Homo sapiens*, [XP_016871108.1](#)

| | | | |
|----------------------------------|-----|-------|-----|
| TCR Heart 7.1 | 5 | PVEPN | 9 |
| | | PVEPN | |
| Cardiac FHL2-interacting protein | 284 | PVEPN | 288 |

myosin XIX, *Homo sapiens*, [KAI2582507.1](#)

| | | | |
|---------------|----|--------------|----|
| TCR Heart 7.1 | 3 | SSPVEPNMTEAF | 14 |
| | | SSPV M EAF | |
| Myosin | 41 | SSPV---M-EAF | 48 |

TCR Heart 7.2 CASSTLTGPTEAFFG (1 CLONE)

AMP-binding protein, partial;*Streptococcus pneumoniae*, [WP_142998241.1](#)Length

| | | | |
|---------------------|----|-------------|----|
| TCR Heart 7.2 | 3 | SSTLTGPTEAF | 13 |
| | | S TLTGP++AF | |
| <i>S.pneumoniae</i> | 32 | SATLTGPSSAF | 42 |

Putative transposase InsK for insertion sequence element IS150, *Streptococcus agalactiae*, [AKI94966.1](#)

| | | | |
|---------------|----|---------|----|
| TCR Heart 7.2 | 9 | PTEAFFG | 15 |
| | | PTE FFG | |
| S.agalac. | 12 | PTESFFG | 18 |

hypothetical protein, partial, *Streptococcus pneumoniae*, [WP_196301310.1](#)

Sequence ID: Length: 77Number of Matches: 1

| | | | |
|---------------|----|---------|----|
| TCR Heart 7.2 | 3 | SSTLTGP | 9 |
| | | SSTLTGP | |
| S.pneumoniae | 33 | SSTLTGP | 39 |

DnaD domain protein, *Streptococcus sanguinis*, [WP_126435224.1](#)

| | | | |
|---------------|----|--------------|-----|
| TCR Heart 7.2 | 4 | STLTGPTEAFFG | 15 |
| | | STLT +E FFG | |
| S.sanguinis | 96 | STLT--AEEFFG | 105 |

Chain A, Collagen alpha-1(XX) chain, *Homo sapiens*, [2EE3_A](#)

| | | | |
|---------------|----|--------|----|
| TCR Heart 7.2 | 3 | SSTLTG | 8 |
| | | SSTLTG | |
| Collagen | 86 | SSTLTG | 91 |

Collagen alpha-1(VII) chain isoform X7, *Homo sapiens*, [XP_054201152.1](#)

| | | | |
|---------------|------|---------|------|
| TCR Heart 7.2 | 6 | LTGPTEA | 12 |
| | | LTGPT A | |
| Collagen | 2219 | LTGPTGA | 2225 |

myosin, heavy polypeptide 14, isoform CRA_a, *Homo sapiens*, [EAW71838.1](#)

| | | | |
|---------------|----|-------|----|
| TCR Heart 7.2 | 7 | TGPTE | 11 |
| | | TGPTE | |
| Myosin | 43 | TGPTE | 47 |

cardiomyopathy associated 5, *Homo sapiens*, [EAW95839.1](#)

| | | | |
|------------------------|-----|--------|-----|
| TCR Heart 7.2 | 1 | CASSTL | 6 |
| | | CASST+ | |
| Cardiomyopathy protein | 252 | CASSTM | 257 |

TCR Heart 7.3 CASSQVLDNYGY (1 CLONE)

polyprotein, partial, Coxsackievirus A13, [AGX00826.1](#)

| | | | |
|---------------|-----|--------|-----|
| TCR Heart 7.3 | 1 | CASSQV | 6 |
| | | CAS+QV | |
| CoxA13 | 185 | CASNQV | 190 |

YfhO family protein, *Streptococcus agalactiae*, [WP_150417292.1](#)

Sequence ID: Length: 859 Number of Matches: 1

| | | | |
|---------------------|-----|----------|-----|
| TCR Heart 7.3 | 1 | CASSQVLD | 8 |
| | | C SSQVLD | |
| <i>S.agalactiae</i> | 527 | CSSSQVLD | 534 |

histidine--tRNA ligase, *Streptococcus mutans*, [NLQ79294.1](#)

| | | | |
|-----------------|----|-----------|----|
| TCR Heart 7.3 | 4 | SQVLDNYGY | 12 |
| | | S +LDNYGY | |
| <i>S.mutans</i> | 30 | SRLLDNYGY | 38 |
| <i>S.mutans</i> | 20 | SRLLDNYGY | 28 |

ATP phosphoribosyltransferase regulatory subunit, *Streptococcus mutans*, [WP_179957260.1](#)

LCP family protein, *Streptococcus anginosus*, [WP_195323471.1](#)

| | | | |
|--------------------|----|----------|----|
| TCR Heart 7.3 | 5 | QVLDNYGY | 12 |
| | | QVL+N+GY | |
| <i>S.anginosus</i> | 61 | QVLENFGY | 68 |

Protein of uncharacterised function (DUF2845), *Streptococcus pneumoniae*, [CJL33301.1](#)

| | | | |
|---------------------|----|----------|----|
| TCR Heart 7.3 | 6 | QVLDNYGY | 12 |
| | | +VLD+YGY | |
| <i>S.pneumoniae</i> | 58 | EVLDEYGY | 65 |

single-stranded-DNA-specific exonuclease RecJ, *Streptococcus pneumoniae*, [WP_057546754.1](#)

| | | | |
|---------------------|-----|---------|-----|
| TCR Heart 7.3 | 4 | SQVLDNY | 10 |
| | | SQVL+NY | |
| <i>S.pneumoniae</i> | 428 | SQVLENY | 434 |
| <i>S.pneumoniae</i> | 4 | QVLDNY | 9 |

hypothetical protein, *Streptococcus pneumoniae*, [WP_061630890.1](#)

histidyl-tRNA synthetase, *Streptococcus pneumoniae*, [CJK96554.1](#)

| | | | |
|---------------------|----|----------|----|
| TCR Heart 7.3 | 5 | QVLDNYGY | 12 |
| | | Q+LD+YGY | |
| <i>S.pneumoniae</i> | 31 | QLLDSYGY | 38 |

Myosin IE, *Homo sapiens*, [KAI2574451.1](#)

| | | | |
|---------------|-----|---------|-----|
| TCR Heart 7.3 | 6 | VLDNYGY | 12 |
| | | VLD YG+ | |
| Myosin | 106 | VLDIYGF | 112 |
| Myosin | 385 | VLDIYGF | 391 |

Myosin IB, isoform CRA_b, *Homo sapiens*, [EAX10840.1](#)

unconventional myosin-VIIb isoform X7, *Homo sapiens*, [XP_054198142.1](#)

| | | | |
|---------------|-----|-------|-----|
| TCR Heart 7.3 | 4 | SQVLD | 8 |
| | | SQVLD | |
| Myosin | 760 | SQVLD | 764 |

TCR Heart 7.4 CASSQDSGRVYSRYGY (1 CLONE)polyprotein, partial, Coxsackievirus A17, [AGF90750.1](#), [AAF43589.1](#)

| | | | |
|---------------|----|---------------|----|
| TCR Heart 7.4 | 3 | SSQDSGRVYSRYG | 15 |
| | | S+QDSG +Y YG | |
| CoxA17 | 19 | STQDSGAAY--YG | 29 |
| CoxA17 | 56 | STQDSGAAY--YG | 66 |

replication initiation factor domain-containing protein, *Streptococcus agalactiae*,
[WP_047205410.1](#)

| | | | |
|--------------------|----|---------|-----|
| TCR Heart 7.4 | 10 | VYSRYGY | 16 |
| | | VYSRYGY | |
| <i>S.agalactae</i> | 97 | VYSRYGY | 103 |

transcriptional regulator, *Streptococcus pneumoniae*, [CWE88364.1](#)

| | | | |
|---------------------|-----|-----------|-----|
| TCR Heart 7.4 | 9 | RVYSRYGY | 16 |
| | | R+YSRYGY | |
| <i>S.pneumoniae</i> | 206 | RAYSYRYGY | 213 |

helicase-exonuclease AddAB subunit AddA, *Streptococcus sanguinis*, [WP_002906286.1](#)

| | | | |
|--------------------|-----|----------|-----|
| TCR Heart 7.4 | 10 | VYSRYGY | 16 |
| | | V+SYRYGY | |
| <i>S.sanguinis</i> | 133 | VFSRYGY | 139 |

ZmpA/ZmpB/ZmpC family metallo-endopeptidase, *Streptococcus sanguinis*, [WP_268701444.1](#)

| | | | |
|--------------------|------|-------------|------|
| TCR Heart 7.4 | 6 | DSGRVYSRYGY | 16 |
| | | DSGR Y+R GY | |
| <i>S.sanguinis</i> | 2390 | DSGR-YTRNGY | 2399 |

Cardiomyopathy-associated protein 3 (Xin actin-binding protein 2) [A4UGR9.2](#)

| | | | |
|------------------------|------|---------|------|
| TCR Heart 7.4 | 5 | QDSGRVY | 11 |
| | | Q+SGRV+ | |
| Cardiomyopathy protein | 3310 | QESGRVF | 3316 |

Myosin Vc pre-powerstroke state, *Homo sapiens*, [5HMP_A](#)

| | | | |
|---------------|-----|-------|-----|
| TCR Heart 7.4 | 11 | YSRYG | 15 |
| | | YSRYG | |
| Myosin | 692 | YSRYG | 696 |

Collagen type XXVII alpha 1 chain, partial, *Homo sapiens*, [KAI4008170.1](#)

| | | | |
|---------------|-----|--------|-----|
| TCR Heart 7.4 | 4 | SQDSGR | 9 |
| | | SQDSGR | |
| Collagen | 198 | SQDSGR | 203 |

Collagen-like cementum protein, *Homo sapiens*, [ULE28343.1](#)

| | | | |
|---------------|-----|------------|-----|
| TCR Heart 7.4 | 4 | SQDSGRVYSR | 13 |
| | | SQ +GRV SR | |
| Cementum | 134 | SQGTGRVSSR | 143 |

Dynein cytoplasmic 1 intermediate chain 2, *Homo sapiens*, [KAI2525768.1](#)

| | | | |
|---------------|----|---------|----|
| TCR Heart 7.4 | 2 | ASSQDSG | 8 |
| | | A SQDSG | |
| Dynein | 93 | AGSQDSG | 99 |

myosin-reactive immunoglobulin heavy chain variable region, partial [Homo sapiens]
[AAD56255.1](#)

Query 1 CASSQDSGRV 10
 CA SQ GR+
 Sbjct 96 CARSQGGGRI 105

T cell receptor beta chain, partial [Homo sapiens] [BAC01026.1](#)

Query 1 CASSQDSGRVYSRYGY 16
 CASSQD G V YGY
 Sbjct 3 CASSQDRGQV---YGY 15

Saito,M., Higuchi,I., Saito,A., Izumo,S., Usuku,K., Bangham,C.R.
 and Osame,M.

TITLE Molecular analysis of T cell clonotypes in muscle-infiltrating
 lymphocytes from patients with human T lymphotropic virus type 1
 polymyositis

JOURNAL J. Infect. Dis. 186 (9), 1231-1241 (2002)

T cell receptor beta chain, partial [Homo sapiens] [BAC01001.1](#)

Query 1 CASSQDSGRVYSRYGY 16
 CASSQDSG GY
 Sbjct 3 CASSQDSG-----GY 12

Saito,M., Higuchi,I., Saito,A., Izumo,S., Usuku,K., Bangham,C.R.
 and Osame,M.

TITLE Molecular analysis of T cell clonotypes in muscle-infiltrating
 lymphocytes from patients with human T lymphotropic virus type 1
 polymyositis

JOURNAL J. Infect. Dis. 186 (9), 1231-1241 (2002)

Heart 7.5 CASSQDKGAYFG (1 CLONE)

VP1 protein, partial, Coxsackievirus A18, [CAD98894.1](#)

CoxA18 25 STQDTGAAYYG 35
 S+QD G AY+G
 TCR Heart 7.5 3 SSQDKG-AYFG 12
 SSQD G AY+G
 CoxA13 805 SSQDAGAAAYYG 815

Polyprotein, Coxsackievirus A13, [WAB71078.1](#)

Polyprotein, Coxsackievirus A13, [WAB71078.1](#)

| | | | |
|---------------|------|----------|------|
| CoxA13 | 6 | SSQKVGA | 12 |
| | | SSQ /GA | |
| TCR Heart 7.5 | 2 | ASSQDKGA | 9 |
| | | AS ++KG | |
| CoxA13 | 1336 | ASLEEKG | 1342 |

Polyprotein, Coxsackievirus B2, [ANQ31694.1](#)

| | | | |
|---------------|------|--------|------|
| TCR Heart 7.5 | 6 | DKGSYF | 11 |
| | | DKG+YF | |
| CoxB2 | 2084 | DKGEYF | 2089 |

Polyprotein, Coxsackievirus B2, [ANQ31694.1](#)

| | | | |
|---------------|---|---------|----|
| TCR Heart 7.5 | 3 | SSQDKGA | 9 |
| | | SSQ/\GA | |
| CoxB2 | 6 | SSQKTGA | 12 |

AAA family ATPase, Streptococcus anginosus, [WP_220432070.1](#)

AAA family ATPase, Streptococcus agalactiae, [WP_199267360.1](#)

| | | | |
|---------------|-----|-------------|-----|
| TCR Heart 7.5 | 3 | SSQDK--GAYF | 11 |
| | | SS+DK GAYF | |
| S.anginosus | 523 | SSEDKRLGAYF | 533 |
| S.agalactiae | 510 | SSEDKRMGAYF | 520 |

ATPase family (AAA), Streptococcus pneumoniae, [VSL20909.1](#)

Dam family site-specific DNA-(adenine-N6)-methyltransferase, Streptococcus pneumoniae, [WP_241003538.1](#)

| | | | |
|---------------|-----|--------|-----|
| TCR Heart 7.5 | 6 | DKGAYF | 11 |
| | | DKGAYF | |
| S.pneumoniae | 655 | DKGAYF | 660 |

T-cell receptor beta chain, partial [Homo sapiens] [BAC01027.1](#)

| | | | |
|-------|---|-----------------|----|
| Query | 1 | CASSQDKGA---YFG | 12 |
| | | CASSQD GA YFG | |
| Sbjct | 3 | CASSQDSGADTQYFG | 17 |

Saito,M., Higuchi,I., Saito,A., Izumo,S., Usuku,K., Bangham,C.R.
and Osame,M.

TITLE Molecular analysis of T cell clonotypes in muscle-infiltrating
lymphocytes from patients with human T lymphotropic virus type 1
polymyositis

JOURNAL J. Infect. Dis. 186 (9), 1231-1241 (2002)

| | |
|-------|---|
| TITLE | Molecular analysis of T cell clonotypes in muscle-infiltrating lymphocytes from patients with human T lymphotropic virus type 1 |
|-------|---|

polymyositis
JOURNAL J. Infect. Dis. 186 (9), 1231-1241 (2002)

T cell receptor beta chain, partial [Homo sapiens] [AAG15755.1](#)

Query 1 CASSQDRGQGFNEQFFG 17
CASS DRG +NEQFFG
Sbjct 8 CASSPDRG--YNEQFFG 22

Slachta, C.A., Jeevanandam, V., Goldman, B., Lin, W.L. and
Platsoucas, C.D.

TITLE Coronary arteries from human cardiac allografts with chronic
rejection contain oligoclonal T cells: persistence of identical
clonally expanded TCR transcripts from the early
post-transplantation period (endomyocardial biopsies) to chronic
rejection (coronary arteries)

JOURNAL J. Immunol. 165 (6), 3469-3483 (2000)

T cell receptor beta chain, partial [Homo sapiens] [AAG15782.1](#)

Query 1 CASSQDRGQGFNEQFFG 17
CASS D GQG NEQFFG
Sbjct 8 CASSLDPGQGRNEQFFG 24

Slachta, C.A., Jeevanandam, V., Goldman, B., Lin, W.L. and
Platsoucas, C.D.

TITLE Coronary arteries from human cardiac allografts with chronic
rejection contain oligoclonal T cells: persistence of identical
clonally expanded TCR transcripts from the early
post-transplantation period (endomyocardial biopsies) to chronic
rejection (coronary arteries)

JOURNAL J. Immunol. 165 (6), 3469-3483 (2000)

TCR Heart 7.7 CASSQNIGASGNEQFFG (1 CLONE)polyprotein, partial, Coxsackievirus A1, [WBR19182.1](#)polyprotein, partial, Coxsackievirus A19, [WBR19366.1](#)

TCR Heart 7.7 5 QNIGASG 11

QNI+ASG

CoxA1, CoxA19

16 QNIAASG 22

polyprotein, partial, Coxsackievirus B4, [AAK59941.1](#)

TCR Heart 7.7 2 ASSQNIGASGNEQFF 16

A SQ SG+EQ+F

CoxB4

64 APSQ----SGQEQLF 74

Polyprotein, Coxsackievirus B2, [ANQ31694.1](#)

TCR Heart 7.7 3 SSQNIG-----ASGN 12

SSQ++G ASGN

CoxB4

6 SSQKTGAHETSLSASGN 22

H3 ,Streptococcus pneumoniae, [CVM61464.1](#)

TCR Heart 7.7 2 ASSQNIGASGNEQ 14

A S++I AS+NEQ

S.pneumoniae

506 AGSEEISASANEQ 518

outer membrane biogenesis protein BamB, Streptococcus pneumoniae, [CJR72959.1](#)

TCR Heart 7.7 4 SQNIGASGF 12

SQN GASGF

S.pneumoniae

47 SQNNGASGF 55

phospholipase D-like domain-containing protein, Streptococcus sanguinis, [WP_004186649.1](#)

TCR Heart 7.7 3 SSQNIGASGFF 13

SSQN G+SG+F

S.sanguinis

312 SSQNFGTSGWF 322

thioester reductase domain-containing protein, Streptococcus sanguinis, [WP_002924092.1](#)

TCR Heart 7.7 4 SQNI---GASGFFG 14

SQNI GA+GF G

S.sanguinis

173 SQNIFMTGATGFLG 186

signal recognition particle-docking protein FtsY, Streptococcus pneumoniae, [CVP51044.1](#)

TCR Heart 7.7 5 QNIGAS--GFF 13

QNIGA GFF

S.pneumoniae

109 QNIGAGFRGFF 119

Quinol oxidase subunit 1, Streptococcus pneumoniae, [COQ48439.1](#)

TCR Heart 7.7 9 ASGFFG 14

ASGFFG

S.pneumoniae

11 ASGFFG 16

Cardiomyopathy-associated protein 3 (xin actin-binding 2), Homo sapiens, [KAI2525625.1](#)

TCR Heart 7.7 7 IGAS--GNEQFF 16

I AS GN QFF

Cardiomyopathy protein

1513 IDASERGNVQFF 1524

anti-acetylcholine receptor immunoglobulin kappa light chain variable region, partial [Homo sapiens] [AAK61521.1](#)

```
Query 1 CASSQNIGAS 10
      C \SQ+IG+S
Sbjct 23 CQASQDIGTS 32
```

T-cell receptor beta V6-2J1.4, TCRBV6-2J1.4 {complementarity determining region 3} [human, peripheral T-lymphocytes, insulin-dependent diabetes mellitus patient [GAD65.05](#), Peptide Partial, 25 aa] [Homo sapiens] [AAB46915.1](#)

Sequence ID: Length: 25Number of Matches: 1

```
Query 1 CASSQNIG-ASGNEQFFG 17
      CASS G A+G+E FFG
Sbjct 1 CASSPP-GRADGDELFFG 17
Weiss,U., Manfras,B.J., Terjung,D., Eiermann,T., Wolpl,A.,
      Loliger,C., KuhnI,P. and Boehm,B.O.
TITLE In vitro stimulation with glutamic acid decarboxylase (GAD65)
leads to an oligoclonal response of peripheral T-cells in an IDDM patient
JOURNAL Scand. J. Immunol. 42 (6), 673-678 (1995)
```

TCR Heart 7.8 CASSQDWQNCYFG (1 CLONE)

Polyprotein, Coxsackievirus B5, [QQL13745.1](#)

```
TCR Heart 7.8 2 ASSQDWQNC 10
      A+S+DWQNC
CoxB5 874 ATSHDWQNC 882
      A+S DWQNC
CoxB3 & CoxB4 874 ATSADWQNC 882
```

polyprotein, Coxsackievirus B3, [AAV34212.1](#)

polyprotein, Coxsackievirus B4, [QKZ25342.1](#)

polyprotein, Echovirus E11, [WIL60493.1](#)

```
TCR Heart 7.8 5 QDWQNC 10
      QDWQNC
Ecovirus E11 887 QDWQNC 892
```

MFS transporter, Streptococcus sanguinis, [WP_176798328.1](#)

```
TCR Heart 7.8 3 SSQDWQ 8
      SSQDWQ
S.sanguinis 198 SSQDWQ 203
```

Domain of uncharacterised function (DU1801), Streptococcus pneumoniae, [CVY52767.1](#)

```
TCR Heart 7.8 4 SQDWQNCY 11
      SQ WQ+CY
S.pneumoniae 17 SQ-WQDCY 23
```

SidA/IucD/PvdA family monooxygenase, *Streptococcus pneumoniae*, [MXQ49484.1](#)

| | | | |
|---------------------|-----|----------|-----|
| TCR Heart 7.8 | 4 | SQDWQNCY | 11 |
| | | SQ+WQ | CY |
| <i>S.pneumoniae</i> | 117 | SQEWQ-CY | 123 |

cholinergic receptor nicotinic delta subunit, *Homo sapiens*, [KAI2527445.1](#)

| | | | |
|------------------------|-----|-------|-----|
| Acetylcholine receptor | 161 | DWQNC | 165 |
| | | DWQNC | |
| TCR Heart 7.8 | 6 | DWQNC | 10 |
| | | DWQNC | |
| Acetylcholine receptor | 28 | DWQNC | 32 |

acetylcholine receptor epsilon subunit, extracellular domain, *Homo sapiens*, [AAB46913.1](#)**unconventional myosin-XVI isoform X5, *Homo sapiens*, [XP_054230245.1](#)**

| | | | |
|---------------|------|-----------|------|
| TCR Heart 7.8 | 1 | CASSQDWQN | 8 |
| | | C + QDWQ+ | |
| Myosin | 1194 | CEEGQDWQS | 1201 |

T cell receptor beta chain, partial [*Homo sapiens*] [ABR67605.1](#)

| | | | |
|-------|---|------------------|----|
| Query | 1 | CASSQDW--QNCYFG | 13 |
| | | CASSQD Q YFG | |
| Sbjct | 2 | CASSQDSTDTQ--YFG | 15 |

Menezes,C.A.S., Sullivan,A.K., Falta,M.T., Mack,D.G., Freed,B.M.,
Rocha,M.O.C., Gollob,K.J., Fontenot,A.P. and Dutra,W.O.

TITLE Oligoclonal Expansions among Specific V Expressing T Cells in
Human Chagas Disease

JOURNAL Unpublished

TCR Heart 7.9 CASSYGYEQYF (1 CLONE)IS3 family transposase, *Streptococcus pneumoniae*, [WP_088849926.1](#)

| | | | |
|---------------|-----|---------|-----|
| TCR Heart 7.9 | 5 | YGYEQYF | 11 |
| | | YGYEQ F | |
| S.pneumoniae | 404 | YGYEQNF | 410 |

isochorismatase family protein, *Streptococcus dysgalactiae*, [WP_192942422.1](#)

| | | | |
|---------------|-----|---------|-----|
| TCR Heart 7.9 | 5 | YGYEQYF | 11 |
| | | YGY+QYF | |
| S. pneum. | 142 | YGYDQYF | 148 |

T cell receptor beta chain variable region, partial [Homo sapiens] [AAW33959.1](#)

| | | | |
|-------|----|----------------|----|
| Query | 1 | CASS--YG-YEQYF | 11 |
| | | CASS YG YEQYF | |
| Sbjct | 38 | CASSLTYPYEQYF | 51 |

Ellis,N.M., Li,Y., Hildebrand,W., Fischetti,V.A. and
Cunningham,M.W.

TITLE T cell mimicry and epitope specificity of cross-reactive T cell
clones from rheumatic heart disease

JOURNAL J. Immunol. 175 (8), 5448-5456 (2005)

TCR Heart 7.10 CASSQGAEP LQYEQYF (1 CLONE)VP1, partial, Coxsackievirus A6, [WCB86769.1](#)

| | | | |
|----------------|-----|-------|-----|
| TCR Heart 7.10 | 10 | LQYEQ | 14 |
| | | LQYEQ | |
| CoxA6 | 112 | LQYEQ | 116 |

polyprotein, partial, Coxsackievirus A1, [WBR19198.1](#)

| | | | |
|----------------|-----|--------|-----|
| TCR Heart 7.10 | 9 | PLQYEQ | 14 |
| | | PLQY+Q | |
| CoxA1 | 303 | PLQYSQ | 308 |

phage protein, *Streptococcus pyogenes*, [VGT93048.1](#)

| | | | |
|----------------|---|----------|----|
| TCR Heart 7.10 | 9 | PLQYEQYF | 16 |
| | | PLQY QYF | |
| S.pyogenes | 7 | PLQY-QYF | 13 |

aquaporin Z, *Streptococcus pneumoniae*, [COI98568.1](#)

| | | | |
|----------------|-----|----------|-----|
| TCR Heart 7.10 | 9 | PLQYEQYF | 16 |
| | | PL YEQYF | |
| S.pneumoniae | 263 | PL-YEQYF | 269 |

phosphoribosylaminoimidazole synthetase, Streptococcus pneumoniae, [CWH83385.1](#)

| | | | |
|----------------|----|--------------|-----|
| TCR Heart 7.10 | 5 | QGAEPLQYEQYF | 16 |
| | | QGAEPL YF | |
| S.pneumoniae | 95 | QGAEPL----YF | 102 |

exonuclease domain-containing protein, Streptococcus pyogenes, [WP_227868769.1](#)

| | | | |
|----------------|-----|---------|-----|
| TCR Heart 7.10 | 9 | PLQYEQY | 15 |
| | | PLQYE+Y | |
| S.pyogenes | 323 | PLQYEDY | 329 |

Exodeoxyribonuclease V beta chain, Streptococcus pneumoniae, [CVQ41851.1](#)

| | | | |
|----------------|------|---------|------|
| TCR Heart 7.10 | 8 | EPLQYEQ | 14 |
| | | EPLQ+EQ | |
| S.pneumoniae | 1091 | EPLQFEQ | 1097 |

C-5 cytosine-specific DNA methylase protein, Streptococcus pneumoniae NP127, [EHE51824.1](#)

| | | | |
|----------------|----|-----------------|----|
| TCR Heart 7.10 | 1 | CASSQGAEPLQY-EQ | 14 |
| | | C SSQG +QY EQ | |
| S.pneumoniae | 86 | CPSSQG---MQYSEQ | 9 |

Myosin IC, isoform CRA_a, Homo sapiens, [EAW90619.1](#)

| | | | |
|----------------|-----|---------|-----|
| TCR Heart 7.10 | 6 | GAEPLQY | 12 |
| | | G+EP+QY | |
| Myosin | 714 | GSEPIQY | 720 |

Myosin MYO9A, partial, Homo sapiens, [SPT35772.1](#)

| | | | |
|----------------|------|---------------|------|
| Myosin | 1326 | SSQGSLELLSYEE | 1338 |
| | | SSQG+ E L+YE+ | |
| TCR Heart 7.10 | 3 | SSQGA-EPLQYEQ | 14 |
| | | SSQG+ E L+YE+ | |
| Myosin | 1267 | SSQGSLELLSYEE | 1279 |

unconventional myosin-IXa isoform X15, Homo sapiens, [XP_047288533.1](#)**collagen alpha-1(II) chain isoform X4 [Homo sapiens] [XP_016874320.1](#)**

| | | | |
|-------|------|----------|------|
| Query | 6 | GAEPLQY | 12 |
| | | G +PLQY | |
| Sbjct | 1050 | GPDPPLQY | 1056 |
| | | | |
| Query | 4 | SQGAEPLQ | 11 |
| | | S GA+ LQ | |
| Sbjct | 527 | SPGAQGLQ | 534 |

collagen alpha-1(II) chain isoform X4 [Homo sapiens] [XP_016874320.1](#)

| | | | |
|-------|------|----------|------|
| Query | 6 | GAEPLQY | 12 |
| | | G +PLQY | |
| Sbjct | 1050 | GPDPPLQY | 1056 |
| | | | |
| Query | 4 | SQGAEPLQ | 11 |
| | | S GA+ LQ | |
| Sbjct | 527 | SPGAQGLQ | 534 |

laminin A chain, partial [Homo sapiens] [CAA41418.1](#)

| | | | |
|-------|-----|------------------|-----|
| Query | 3 | SSQGAE--PLQ-YEQY | 15 |
| | | S+Q AE LQ YE+Y | |
| Sbjct | 620 | STQ-AEGLSLQPYEEY | 634 |

dynein axonemal heavy chain 9 isoform X4 [Homo sapiens] [XP_016879783.1](#)

```
Query 12      YEQYF 16
          YE+YF
Sbjct 2370    YEHYF 2374
```

```
Query 1      CASSQGAEPL 10
          CA S  AE L
Sbjct 46     CAGSAEAEQL 55
```

TCR Heart 7.11 CASSQDKNYESQYF (1 CLONE)

M protein, Streptococcus pyogenes, [WP_128888759.1](#)

```
TCR Heart 7.11      4      SQDKNYESQY 12
                      S++ NYEQY
S.pyogenes          73     SHNNNNYESQY 81
```

bifunctional metallophosphatase/5'-nucleotidase, Streptococcus agalactiae, [WP_000726931.1](#)

```
TCR Heart 7.11      7      KNYEQY 12
                      KNYEQY
S.agalactiae        218    KNYEQY 223
```

dynein axonemal intermediate chain 7 isoform X11, Homo sapiens, [XP_047285034.1](#)

```
TCR Heart 7.11      5      QDKNYESQY 12
                      QDKN  QY
Dynein              158    QDKNIIQY 165
```

TCR Heart 7.12 CASSFNREAYEQYF (1 CLONE)anthranilate synthase component I, *Streptococcus pneumoniae*, [CJK74717.1](#)

| | | | |
|---------------------|-----|------------|-----|
| TCR Heart 7.12 | 3 | SSFNREAYEQ | 12 |
| | | SSF+RE YEQ | |
| <i>S.pneumoniae</i> | 219 | SSFSREDYEQ | 228 |

hypothetical protein, *Streptococcus sanguinis*, [WP_149565477.1](#)

| | | | |
|--------------------|----|---------------|----|
| TCR Heart 7.12 | 3 | SSFNREAY--EQY | 13 |
| | | SSF+RE+Y +QY | |
| <i>S.sanguinis</i> | 84 | SSFSRESYTTQQY | 96 |

DnaB-like helicase C-terminal domain-containing protein, *Streptococcus pneumoniae*,
[WP_078712880.1](#)

| | | | |
|---------------------|-----|-----------|-----|
| TCR Heart 7.12 | 3 | SSFNREAYE | 11 |
| | | SSFNR+ YE | |
| <i>S.pneumoniae</i> | 563 | SSFNRDNYE | 571 |

DNA cytosine methyltransferase, partial, *Streptococcus pneumoniae*, [WP_168970539.1](#)

| | | | |
|---------------------|----|---------|----|
| TCR Heart 7.12 | 8 | EAYEQYF | 14 |
| | | EAYEQ+F | |
| <i>S.pneumoniae</i> | 10 | EAYEQFF | 16 |

dynein, cytoplasmic 1, intermediate chain 1, isoform CRA_b, *Homo sapiens*, [EAW76752.1](#)

| | | | |
|----------------|-----|-----------|-----|
| TCR Heart 7.12 | 4 | SFNREAYEQ | 12 |
| | | SFNR+ Y++ | |
| Dynein | 223 | SFNRQFYDE | 231 |

dynein axonemal heavy chain 17 isoform X4, *Homo sapiens*, [XP_024306782.1](#)

| | | | |
|----------------|------|----------|------|
| TCR Heart 7.12 | 7 | REAYEQYF | 14 |
| | | RE+YE YF | |
| Dynein | 2344 | RELYELYF | 2351 |

T cell receptor beta chain, partial [*Homo sapiens*] [AAG15792.1](#)

| | | | |
|-------|---|----------------|----|
| Query | 1 | CASSFNREAYEQYF | 14 |
| | | CASSF+R +YEQYF | |
| Sbjct | 8 | CASSFRR-GYEQYF | 20 |

Slachta, C.A., Jeevanandam, V., Goldman, B., Lin, W.L. and
Platsoucas, C.D.

TITLE Coronary arteries from human cardiac allografts with chronic rejection contain oligoclonal T cells: persistence of identical clonally expanded TCR transcripts from the early post-transplantation period (endomyocardial biopsies) to chronic rejection (coronary arteries)

JOURNAL J. Immunol. 165 (6), 3469-3483 (2000)

TCR Heart 7.13 CASSSGLAGYEQYF

VP1, partial, Coxsackievirus A12, [QWM97587.1](#)

| | | | |
|----------------|----|---------|----|
| CoxA12 | 34 | SRSGLAG | 40 |
| | | S SGLAG | |
| TCR Heart 7.13 | 3 | SSSGLAG | 9 |
| | | S SGLAG | |
| CoxA5 | 8 | SRSGLAG | 14 |

capsid protein, partial, Coxsackievirus A5, [QMU95395.1](#)

Polyprotein, Coxsackievirus B1, [P08291](#)

| | | | |
|----------------|-----|--------|-----|
| TCR Heart 7.13 | 2 | ASSSGL | 7 |
| | | ASS+GL | |
| CoxB1 | 599 | ASSQGL | 604 |

Dipeptidase, Streptococcus agalactiae 138P, [AHN30202.1](#)

| | | | |
|----------------|-----|---------|-----|
| TCR Heart 7.13 | 8 | AGYEQYF | 14 |
| | | AGYEQYF | |
| S.agalactiae | 281 | AGYEQYF | 287 |

DNA repair protein RecO, Streptococcus pneumoniae, [CJD30205.1](#)

| | | | |
|----------------|-----|-----------|-----|
| TCR Heart 7.13 | 6 | GLAGYEQYF | 14 |
| | | GL G++QYF | |
| S.pneumoniae | 130 | GLSGFDQYF | 138 |

carbohydrate ABC transporter permease, Streptococcus pneumoniae, [MTW00257.1](#)

| | | | |
|----------------|----|------------|----|
| TCR Heart 7.13 | 1 | CASSSGLAGY | 10 |
| | | CA+SS LAGY | |
| S.pneumoniae | 71 | CATSS-LAGY | 79 |

membrane protein BUG1, Streptococcus pneumoniae, [CJC53609.1](#)

| | | | |
|----------------|-----|-----------|-----|
| S.pneumoniae | 246 | GLSSYDQYF | 254 |
| | | GL Y+QYF | |
| TCR Heart 7.13 | 6 | GLAGYEQYF | |
| | | GL Y+QYF | |
| | | GL Y+QYF | |
| S.pneumoniae | 583 | GLSSYDQYF | 591 |

Putative membrane protein ydgH, Streptococcus pneumoniae, [CJO25202.1](#)

collagen alpha-3(IV) chain isoform X6, Homo sapiens, [XP_054196411.1](#)

| | | | |
|----------------|-----|-----------|-----|
| TCR Heart 7.13 | 1 | CASSSGLAG | 9 |
| | | CA+S GL G | |
| Collagen | 422 | CAGSPGLPG | 430 |

T cell receptor beta chain, partial [Homo sapiens] [BAC01046.1](#)

| | | | |
|-------|---|-----------------|----|
| Query | 1 | CASSSGLAG-YEQYF | 12 |
| | | CASS+GLAG +QYF | |
| Sbjct | 3 | CASSAGLAGGVTQYF | 17 |

Saito,M., Higuchi,I., Saito,A., Izumo,S., Usuku,K., Bangham,C.R.
and Osame,M.

TITLE Molecular analysis of T cell clonotypes in muscle-infiltrating
lymphocytes from patients with human T lymphotropic virus type 1
polymyositis

JOURNAL J. Infect. Dis. 186 (9), 1231-1241 (2002)

T cell receptor beta chain, partial [Homo sapiens] [ABR67600.1](#)

Query 1 CASSSGLAG--YEQYF 12

CASSSGLAG EQ+F

Sbjct 1 CASSSGLAGVSDEQFF 16

Menezes,C.A.S., Sullivan,A.K., Falta,M.T., Mack,D.G., Freed,B.M.,
Rocha,M.O.C., Gollob,K.J., Fontenot,A.P. and Dutra,W.O.

TITLE Oligoclonal Expansions among Specific V Expressing T Cells in
Human Chagas Disease

JOURNAL Unpublished

[https://www.ncbi.nlm.nih.gov/protein/ABR67600.1?report=genbank&log\\$=protalign
&blast_rank=6&RID=G3Z8ZE1D016](https://www.ncbi.nlm.nih.gov/protein/ABR67600.1?report=genbank&log$=protalign&blast_rank=6&RID=G3Z8ZE1D016) (accessed 13 Sep 2023)

TCR Heart 7.14 CASSQDRGQYEQYF (1 CLONE)

Chain F, The heavy chain of fab 9B5, Coxsackievirus A16, [7YMS_F](#)

TCR Heart 7.14 1 CASSQDRGQYEQYF 14

CA RG+YE+YF

CoxA16 96 CA----RGDYENYF 105

6S rRNA methyltransferase GidB, *Streptococcus pneumoniae*, [VSH22310.1](#)

TCR Heart 7.14 3 SSQDRGQYEQYF 14

SSQ++ Q+E YF

S.pneumoniae 18 SSQQKEQFERYF 29

Uncharacterized protein conserved in bacteria, *Streptococcus pneumoniae*, [CJS00925.1](#)

TCR Heart 7.14 6 DRGQYEQY 13

D +QYEQY

S.pneumoniae 215 DQAQYEQY 222

hypothetical protein, *Streptococcus pyogenes*, [AJW83682.1](#)

TCR Heart 7.14 3 SSQDRGQY----EQY 13

SS+DR++Y EQY

S.pyogenes 22 SSED RANYQALKEQY 36

Cardiac peroxidase, Homo sapiens, [AAX70929.1](#)

| | | | |
|--------------------|------|------------|------|
| TCR Heart 7.14 | 2 | ASSQDRGQYE | 11 |
| | | A ++D GQYE | |
| Cardiac peroxidase | 478 | AAQHDQGQYE | 487 |
| TCR Heart 7.14 | 1 | CASSQDRGQY | 10 |
| | | CA++ +RGQ+ | |
| Cardiac peroxidase | 1299 | CADCRSRGQF | 1308 |

T cell receptor beta chain, partial [Homo sapiens] [BAC01026.1](#)

| | | | |
|-------|---|-------------|----|
| Query | 1 | CASSQDRGQQY | 11 |
| | | CASSQDRGQ Y | |
| Sbjct | 3 | CASSQDRGQVY | 13 |

Saito,M., Higuchi,I., Saito,A., Izumo,S., Usuku,K., Bangham,C.R.
and Osame,M.

TITLE Molecular analysis of T cell clonotypes in muscle-infiltrating
lymphocytes from patients with human T lymphotropic virus type 1
polymyositis

JOURNAL J. Infect. Dis. 186 (9), 1231-1241 (2002)

TCR Heart 7.15 CASSQDLQGRIEYQYF**Polyprotein, Coxsackievirus B2, [Q9YLG5](#)**

| | | | |
|-----------------|-----|---------|-----|
| TCR Heart 7-15: | 3 | SSQDLQG | 9 |
| | | SSQ+ QG | |
| CoxB2 | 676 | SSQTSQG | 682 |

Polyprotein, Coxsackievirus B1, [SPS68029.1](#)

| | | | |
|----------------|-----|--------|-----|
| TCR Heart 7.15 | 2 | ASSQDL | 7 |
| | | ASSQ L | |
| CoxB1 | 329 | ASSQGL | 334 |

Polyprotein, Coxsackievirus A9, [P21404](#)

| | | | |
|----------------|-----|----------|-----|
| TCR Heart 7-15 | 4 | SQD--LQG | 9 |
| | | SQD LQG | |
| CoxA9 | 675 | SQDNKLQG | 683 |

transposase, partial, Streptococcus sanguinis, [WP_196757391.1](#)

| | | | |
|----------------|----|-------------|----|
| TCR Heart 7.15 | 4 | SQDLQGRYEY | 14 |
| | | SQDL RYE Y | |
| S.sanguinis | 29 | SQDLRNRYELY | 39 |

chloride channel protein, *Streptococcus pyogenes*, [WP_136111792.1](#)

| | | | |
|----------------|-----|-----------|-----|
| TCR Heart 7.15 | 7 | LQGRYE-QY | 14 |
| | | LQGRYE QY | |
| S.pyogenes | 230 | LQGRYEIQY | 238 |

GNAT family N-acetyltransferase, partial, *Streptococcus pneumoniae*, [WP_142325397.1](#)

Sequence ID: Length: 142 Number of Matches: 1

| | | | |
|----------------|-----|-------------|-----|
| TCR Heart 7.15 | 4 | SQDLQGRYEQY | 14 |
| | | SQDLQG +EY+ | |
| S.pneumoniae | 131 | SQDLQGNFESY | 141 |

Glycosyltransferase, *Streptococcus pneumoniae*, [WP_235977465.1](#)

| | | | |
|----------------|----|-------------|----|
| TCR Heart 7.15 | 7 | LQGR-Y-EQYF | 15 |
| | | LQGR Y EQYF | |
| S.pneumoniae | 84 | LQGRMYIEQYF | 94 |

FtsK/SpoIIIE domain-containing protein, *Streptococcus aginosus*, [WP_229045148.1](#)

| | | | |
|----------------|-----|--------|-----|
| TCR Heart 7.15 | 10 | RYEQYF | 15 |
| | | RYEQYF | |
| S.aginosus | 190 | RYEQYF | 195 |

myosin-9, *Homo sapiens*, [NP_002464.1](#)

| | | | |
|----------------|------|----------|------|
| TCR Heart 7.15 | 6 | DLQGRYEQ | 13 |
| | | DLQGR EQ | |
| Myosin | 1572 | DLQGRDEQ | 1579 |

POTE-2 alpha-actin, *Homo sapiens*, [ABP57734.1](#)

| | | | |
|----------------|-----|---------------|-----|
| TCR Heart 7.15 | 3 | SSQDLQG---RQY | 12 |
| | | SSQDL+G R+Y | |
| Actin | 332 | SSQDLSGQTAREY | 344 |

TCR Heart 7.16 CASSQDKNYESQYF (1 CLONE)

NADH-quinone oxidoreductase subunit L, *Streptococcus pneumoniae*, [COR59093.1](#)

| | | | |
|----------------|-----|-----------|-----|
| TCR Heart 7.16 | 6 | DKNYESQYF | 13 |
| | | DKNY QYF | |
| S.pneumoniae | 140 | DKNYRQYF | 147 |

M protein, *Streptococcus pyogenes*, [WP_128888759.1](#)

| | | | |
|----------------|----|------------|----|
| TCR Heart 7.16 | 4 | SQDKNYESQY | 12 |
| | | S++ NYESQY | |
| S.pyogenes | 73 | SHNNNYESQY | 81 |

bifunctional metallophosphatase/5'-nucleotidase, *Streptococcus agalactiae*, [WP_000726933.1](#)

| | | | |
|----------------|-----|---------|-----|
| TCR Heart 7.16 | 7 | KNYESQY | 12 |
| | | KNYESQY | |
| S.agalactiae | 218 | KNYESQY | 223 |

dynein axonemal intermediate chain 7 isoform X11, Homo sapiens, [XP_047285034.1](#)

| | | | |
|----------------|-----|----------|-----|
| TCR Heart 7.16 | 5 | QDKNYEQY | 12 |
| | | QDKN QY | |
| Dynein | 158 | QDKNIIQY | 165 |

T cell receptor beta chain, partial [Homo sapiens] [ABR67597.1](#)

| | | | |
|-------|---|-----------------|----|
| Query | 1 | CASSQD--KNYEQYF | 13 |
| | | CASS D NYEQYF | |
| Sbjct | 1 | CASSLDSGTNYEQYF | 15 |

Menezes,C.A.S., Sullivan,A.K., Falta,M.T., Mack,D.G., Freed,B.M.,
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TITLE Oligoclonal Expansions among Specific V Expressing T Cells in
Human Chagas Disease

JOURNAL Unpublished

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