# Score: 640.0

# Align Len: 444

# Identity: 120/444 (27.03%)

# Similarity: 120/444 (27.03%)

# Gap Count: 324/444 (72.97%)

VDJ 1 EVQLQQSGPELVNPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGG 50

||||||||||||||||||||||||||||||||||||||||||||||||||

PEAKS 1 EVQLQQSGPELVNPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGG 50

VDJ 51 INPNNGDTIYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVFYCAREG 100

||||||||||||||||||||||||||||||||||||||||||||||||||

PEAKS 51 INPNNGDTIYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVFYCAREG 100

VDJ 101 DYYVSSYGYWGQGTTLTVSS------------------------------ 120

||||||||||||||||||||

PEAKS 101 DYYVSSYGYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVK 150

VDJ 121 -------------------------------------------------- 120

PEAKS 151 GYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETV 200

VDJ 121 -------------------------------------------------- 120

PEAKS 201 TCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTI 250

VDJ 121 -------------------------------------------------- 120

PEAKS 251 TLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFRSV 300

VDJ 121 -------------------------------------------------- 120

PEAKS 301 SELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPP 350

VDJ 121 -------------------------------------------------- 120

PEAKS 351 PKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAQNYKNTQPIMDTDGS 400

VDJ 121 -------------------------------------------- 120

PEAKS 401 YFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 444

# Score: 486.5

# Align Len: 219

# Identity: 98/219 (44.75%)

# Similarity: 100/219 (45.66%)

# Gap Count: 114/219 (52.05%)

VDJ 1 DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQQKPGQSP 50

||||||||||||||||||||||||||||||||||||||||||||||||||

PEAKS 1 DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQQKPGQSP 50

VDJ 51 KLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSF 100

||||||||||||||||||||||||||||||||||||||||||||..

PEAKS 51 KLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCGT---- 96

VDJ 101 PLTFGAGTKLELK------------------------------------- 113

..||.:||:

PEAKS 97 ----ANGTAVELRTNAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDIN 142

VDJ 114 -------------------------------------------------- 113

PEAKS 143 VKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCE 192

VDJ 114 ------------------- 113

PEAKS 193 ATHKTSTSPIVKSFNRNEC 211

# Score: 640.0

# Align Len: 444

# Identity: 120/444 (27.03%)

# Similarity: 120/444 (27.03%)

# Gap Count: 324/444 (72.97%)

VDJ 1 EVQLQQSGPELVNPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGG 50

||||||||||||||||||||||||||||||||||||||||||||||||||

Fusion 1 EVQLQQSGPELVNPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGG 50

VDJ 51 INPNNGDTIYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVFYCAREG 100

||||||||||||||||||||||||||||||||||||||||||||||||||

Fusion 51 INPNNGDTIYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVFYCAREG 100

VDJ 101 DYYVSSYGYWGQGTTLTVSS------------------------------ 120

||||||||||||||||||||

Fusion 101 DYYVSSYGYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVK 150

VDJ 121 -------------------------------------------------- 120

Fusion 151 GYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETV 200

VDJ 121 -------------------------------------------------- 120

Fusion 201 TCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTI 250

VDJ 121 -------------------------------------------------- 120

Fusion 251 TLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFRSV 300

VDJ 121 -------------------------------------------------- 120

Fusion 301 SELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPP 350

VDJ 121 -------------------------------------------------- 120

Fusion 351 PKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGS 400

VDJ 121 -------------------------------------------- 120

Fusion 401 YFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 444

# Score: 583.0

# Align Len: 220

# Identity: 113/220 (51.36%)

# Similarity: 113/220 (51.36%)

# Gap Count: 107/220 (48.64%)

VDJ 1 DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQQKPGQSP 50

||||||||||||||||||||||||||||||||||||||||||||||||||

Fusion 1 DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQQKPGQSP 50

VDJ 51 KLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSF 100

||||||||||||||||||||||||||||||||||||||||||||||||||

Fusion 51 KLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSF 100

VDJ 101 PLTFGAGTKLELK------------------------------------- 113

|||||||||||||

Fusion 101 PLTFGAGTKLELKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDI 150

VDJ 114 -------------------------------------------------- 113

Fusion 151 NVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTC 200

VDJ 114 -------------------- 113

Fusion 201 EATHKTSTSPIVKSFNRNEC 220

# Score: 640.0

# Align Len: 445

# Identity: 120/445 (26.97%)

# Similarity: 120/445 (26.97%)

# Gap Count: 325/445 (73.03%)

VDJ 1 EVQLQQSGPELVNPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGG 50

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 1 EVQLQQSGPELVNPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGG 50

VDJ 51 INPNNGDTIYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVFYCAREG 100

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 51 INPNNGDTIYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVFYCAREG 100

VDJ 101 DYYVSSYGYWGQGTTLTVSS------------------------------ 120

||||||||||||||||||||

Stitch 101 DYYVSSYGYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVK 150

VDJ 121 -------------------------------------------------- 120

Stitch 151 GYFPEPVTVTWNSGSLSSGVHTFPAVLASLDLYTLSSSVTVPSSTWPSET 200

VDJ 121 -------------------------------------------------- 120

Stitch 201 VTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLT 250

VDJ 121 -------------------------------------------------- 120

Stitch 251 ITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRS 300

VDJ 121 -------------------------------------------------- 120

Stitch 301 VSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIP 350

VDJ 121 -------------------------------------------------- 120

Stitch 351 PPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDG 400

VDJ 121 --------------------------------------------- 120

Stitch 401 SYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 445

# Score: 583.0

# Align Len: 220

# Identity: 113/220 (51.36%)

# Similarity: 113/220 (51.36%)

# Gap Count: 107/220 (48.64%)

VDJ 1 DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQQKPGQSP 50

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 1 DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQQKPGQSP 50

VDJ 51 KLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSF 100

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 51 KLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSF 100

VDJ 101 PLTFGAGTKLELK------------------------------------- 113

|||||||||||||

Stitch 101 PLTFGAGTKLELKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDI 150

VDJ 114 -------------------------------------------------- 113

Stitch 151 NVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTC 200

VDJ 114 -------------------- 113

Stitch 201 EATHKTSTSPIVKSFNRNEC 220

# Score: 2388.0

# Align Len: 444

# Identity: 443/444 (99.77%)

# Similarity: 444/444 (100.00%)

# Gap Count: 0/444 (0.00%)

Fusion 1 EVQLQQSGPELVNPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGG 50

||||||||||||||||||||||||||||||||||||||||||||||||||

PEAKS 1 EVQLQQSGPELVNPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGG 50

Fusion 51 INPNNGDTIYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVFYCAREG 100

||||||||||||||||||||||||||||||||||||||||||||||||||

PEAKS 51 INPNNGDTIYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVFYCAREG 100

Fusion 101 DYYVSSYGYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVK 150

||||||||||||||||||||||||||||||||||||||||||||||||||

PEAKS 101 DYYVSSYGYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVK 150

Fusion 151 GYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETV 200

||||||||||||||||||||||||||||||||||||||||||||||||||

PEAKS 151 GYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETV 200

Fusion 201 TCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTI 250

||||||||||||||||||||||||||||||||||||||||||||||||||

PEAKS 201 TCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTI 250

Fusion 251 TLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFRSV 300

||||||||||||||||||||||||||||||||||||||||||||||||||

PEAKS 251 TLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFRSV 300

Fusion 301 SELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPP 350

||||||||||||||||||||||||||||||||||||||||||||||||||

PEAKS 301 SELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPP 350

Fusion 351 PKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGS 400

|||||||||||||||||||||||||||||||||||:||||||||||||||

PEAKS 351 PKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAQNYKNTQPIMDTDGS 400

Fusion 401 YFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 444

||||||||||||||||||||||||||||||||||||||||||||

PEAKS 401 YFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 444

# Score: 1035.5

# Align Len: 220

# Identity: 203/220 (92.27%)

# Similarity: 205/220 (93.18%)

# Gap Count: 9/220 (4.09%)

Fusion 1 DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQQKPGQSP 50

||||||||||||||||||||||||||||||||||||||||||||||||||

PEAKS 1 DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQQKPGQSP 50

Fusion 51 KLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSF 100

||||||||||||||||||||||||||||||||||||||||||||..

PEAKS 51 KLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCGT---- 96

Fusion 101 PLTFGAGTKLELKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDI 150

..||.:|| |.:||||||||||||||||||||||||||||||||||

PEAKS 97 ----ANGTAVEL-RTNAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDI 141

Fusion 151 NVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTC 200

||||||||||||||||||||||||||||||||||||||||||||||||||

PEAKS 142 NVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTC 191

Fusion 201 EATHKTSTSPIVKSFNRNEC 220

||||||||||||||||||||

PEAKS 192 EATHKTSTSPIVKSFNRNEC 211

# Score: 2370.0

# Align Len: 445

# Identity: 442/445 (99.33%)

# Similarity: 443/445 (99.55%)

# Gap Count: 1/445 (0.22%)

Fusion 1 EVQLQQSGPELVNPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGG 50

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 1 EVQLQQSGPELVNPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGG 50

Fusion 51 INPNNGDTIYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVFYCAREG 100

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 51 INPNNGDTIYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVFYCAREG 100

Fusion 101 DYYVSSYGYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVK 150

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 101 DYYVSSYGYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVK 150

Fusion 151 GYFPEPVTVTWNSGSLSSGVHTFPAVLQS-DLYTLSSSVTVPSSTWPSET 199

|||||||||||||||||||||||||||.| ||||||||||||||||||||

Stitch 151 GYFPEPVTVTWNSGSLSSGVHTFPAVLASLDLYTLSSSVTVPSSTWPSET 200

Fusion 200 VTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLT 249

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 201 VTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLT 250

Fusion 250 ITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFRS 299

||||||||||||||||||||||||||||||||||||||||||||:|||||

Stitch 251 ITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRS 300

Fusion 300 VSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIP 349

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 301 VSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIP 350

Fusion 350 PPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDG 399

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 351 PPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDG 400

Fusion 400 SYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 444

|||||||||||||||||||||||||||||||||||||||||||||

Stitch 401 SYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 445

# Score: 1153.0

# Align Len: 220

# Identity: 220/220 (100.00%)

# Similarity: 220/220 (100.00%)

# Gap Count: 0/220 (0.00%)

Fusion 1 DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQQKPGQSP 50

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 1 DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQQKPGQSP 50

Fusion 51 KLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSF 100

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 51 KLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYSF 100

Fusion 101 PLTFGAGTKLELKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDI 150

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 101 PLTFGAGTKLELKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDI 150

Fusion 151 NVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTC 200

||||||||||||||||||||||||||||||||||||||||||||||||||

Stitch 151 NVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTC 200

Fusion 201 EATHKTSTSPIVKSFNRNEC 220

||||||||||||||||||||

Stitch 201 EATHKTSTSPIVKSFNRNEC 220