# Score: 608.0

# Align Len: 446

# Identity: 115/446 (25.78%)

# Similarity: 116/446 (26.01%)

# Gap Count: 327/446 (73.32%)

VDJ 1 QVQLQQPGAELVRPGASVKLSCKASGYTFTSYWMNWVKQRPEQGLEWIGR 50

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PEAKS 1 EVQLQQPGAELVRPGASVKLSCKASGYTFTSYWMNWVKQRPEQGLEWIGR 50

VDJ 51 IDPYDSETHYNQKFKDKAILTVDKSSTTAYMQLSSLTSEDSAVYYCARWG 100

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

PEAKS 51 IDPYDSETHYNQKFKDKAILTVDKSSTTAYMQLSSLTSEDSAVYYCARWG 100

VDJ 101 TVE---WFFDYWGQGTTLTVSQ---------------------------- 119

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

PEAKS 101 TVEVSFRVFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCL 150

VDJ 120 -------------------------------------------------- 119

PEAKS 151 VKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSE 200

VDJ 120 -------------------------------------------------- 119

PEAKS 201 TVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVL 250

VDJ 120 -------------------------------------------------- 119

PEAKS 251 TITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFR 300

VDJ 120 -------------------------------------------------- 119

PEAKS 301 SVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI 350

VDJ 120 -------------------------------------------------- 119

PEAKS 351 PPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAQNYKNTQPIMDTD 400

VDJ 120 ---------------------------------------------- 119

PEAKS 401 GSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 446

# Score: 584.0

# Align Len: 221

# Identity: 113/221 (51.13%)

# Similarity: 113/221 (51.13%)

# Gap Count: 108/221 (48.87%)

VDJ 1 DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSYNQENYLAWYQQKPGQSP 50

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

PEAKS 1 DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSYNQENYLAWYQQKPGQSP 50

VDJ 51 KLLVYFASTRESGVPDRFIGSGSGTDFTLTISSVQAEDLADYFCQQHYST 100

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

PEAKS 51 KLLVYFASTRESGVPDRFIGSGSGTDFTLTISSVQAEDLADYFCQQHYST 100

VDJ 101 PFTFGSGTKLEIK------------------------------------- 113

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

PEAKS 101 PFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDI 150

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

PEAKS 151 NVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTC 200

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

PEAKS 201 EATHKTSTSPIVKSFNRNECF 221

# Score: 643.0

# Align Len: 443

# Identity: 118/443 (26.64%)

# Similarity: 118/443 (26.64%)

# Gap Count: 324/443 (73.14%)

VDJ 1 QVQLQQPGAELVRPGASVKLSCKASGYTFTSYWMNWVKQRPEQGLEWIGR 50

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

Fusion 1 QVQLQQPGAELVRPGASVKLSCKASGYTFTSYWMNWVKQRPEQGLEWIGR 50

VDJ 51 IDPYDSETHYNQKFKDKAILTVDKSSTTAYMQLSSLTSEDSAVYYCARWG 100

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

Fusion 51 IDPYDSETHYNQKFKDKAILTVDKSSTTAYMQLSSLTSEDSAVYYCARWG 100

VDJ 101 TVEWFFDYWGQGTTLTVSQ------------------------------- 119

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Fusion 101 TVEWFFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKG 150

VDJ 120 -------------------------------------------------- 119

Fusion 151 YFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVT 200

VDJ 120 -------------------------------------------------- 119

Fusion 201 CNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTIT 250

VDJ 120 -------------------------------------------------- 119

Fusion 251 LTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVS 300

VDJ 120 -------------------------------------------------- 119

Fusion 301 ELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPP 350

VDJ 120 -------------------------------------------------- 119

Fusion 351 KEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTNGSY 400

VDJ 120 ------------------------------------------- 119

Fusion 401 FVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 443

# Score: 584.0

# Align Len: 220

# Identity: 113/220 (51.36%)

# Similarity: 113/220 (51.36%)

# Gap Count: 107/220 (48.64%)

VDJ 1 DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSYNQENYLAWYQQKPGQSP 50

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

Fusion 1 DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSYNQENYLAWYQQKPGQSP 50

VDJ 51 KLLVYFASTRESGVPDRFIGSGSGTDFTLTISSVQAEDLADYFCQQHYST 100

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

Fusion 51 KLLVYFASTRESGVPDRFIGSGSGTDFTLTISSVQAEDLADYFCQQHYST 100

VDJ 101 PFTFGSGTKLEIK------------------------------------- 113

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

Fusion 101 PFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDI 150

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

Fusion 151 NVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTC 200

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

Fusion 201 EATHKTSTSPIVKSFNRNEC 220

# Score: 627.0

# Align Len: 443

# Identity: 116/443 (26.19%)

# Similarity: 116/443 (26.19%)

# Gap Count: 324/443 (73.14%)

VDJ 1 QVQLQQPGAELVRPGASVKLSCKASGYTFTSYWMNWVKQRPEQGLEWIGR 50

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

Stitch 1 QVQLQQPGAELVRPGASVKLSCKASGYTFTSYWMNWVKQRPEQGLEWIGR 50

VDJ 51 IDPYDSETHYNQKFKDKAILTVDKSSTTAYMQLSSLTSEDSAVYYCARWG 100

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Stitch 51 IDPYDSETHYNQKFKDKAILTVDKSSTTAYMQLSSLTSEDSAVYYCARWG 100

VDJ 101 TVEWFFDYWGQGTTLTVSQ------------------------------- 119

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Stitch 101 TVEWVKDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKG 150

VDJ 120 -------------------------------------------------- 119

Stitch 151 YFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVT 200

VDJ 120 -------------------------------------------------- 119

Stitch 201 CNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTIT 250

VDJ 120 -------------------------------------------------- 119

Stitch 251 LTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFRSVS 300

VDJ 120 -------------------------------------------------- 119

Stitch 301 ELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPP 350

VDJ 120 -------------------------------------------------- 119

Stitch 351 KEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSY 400

VDJ 120 ------------------------------------------- 119

Stitch 401 FVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 443

# Score: 584.0

# Align Len: 220

# Identity: 113/220 (51.36%)

# Similarity: 113/220 (51.36%)

# Gap Count: 107/220 (48.64%)

VDJ 1 DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSYNQENYLAWYQQKPGQSP 50

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

Stitch 1 DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSYNQENYLAWYQQKPGQSP 50

VDJ 51 KLLVYFASTRESGVPDRFIGSGSGTDFTLTISSVQAEDLADYFCQQHYST 100

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

Stitch 51 KLLVYFASTRESGVPDRFIGSGSGTDFTLTISSVQAEDLADYFCQQHYST 100

VDJ 101 PFTFGSGTKLEIK------------------------------------- 113

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

Stitch 101 PFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDI 150

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

Stitch 151 NVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTC 200

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

Stitch 201 EATHKTSTSPIVKSFNRNEC 220

# Score: 2360.0

# Align Len: 446

# Identity: 439/446 (98.43%)

# Similarity: 441/446 (98.88%)

# Gap Count: 3/446 (0.67%)

Fusion 1 QVQLQQPGAELVRPGASVKLSCKASGYTFTSYWMNWVKQRPEQGLEWIGR 50

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PEAKS 1 EVQLQQPGAELVRPGASVKLSCKASGYTFTSYWMNWVKQRPEQGLEWIGR 50

Fusion 51 IDPYDSETHYNQKFKDKAILTVDKSSTTAYMQLSSLTSEDSAVYYCARWG 100

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PEAKS 51 IDPYDSETHYNQKFKDKAILTVDKSSTTAYMQLSSLTSEDSAVYYCARWG 100

Fusion 101 TVE---WFFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCL 147

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

PEAKS 101 TVEVSFRVFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCL 150

Fusion 148 VKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSE 197

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

PEAKS 151 VKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSE 200

Fusion 198 TVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVL 247

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

PEAKS 201 TVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVL 250

Fusion 248 TITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFR 297

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

PEAKS 251 TITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFR 300

Fusion 298 SVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI 347

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

PEAKS 301 SVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI 350

Fusion 348 PPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTD 397

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PEAKS 351 PPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAQNYKNTQPIMDTD 400

Fusion 398 GSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 443

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

PEAKS 401 GSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 446

# Score: 1154.0

# Align Len: 221

# Identity: 220/221 (99.55%)

# Similarity: 220/221 (99.55%)

# Gap Count: 1/221 (0.45%)

Fusion 1 DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSYNQENYLAWYQQKPGQSP 50

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

PEAKS 1 DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSYNQENYLAWYQQKPGQSP 50

Fusion 51 KLLVYFASTRESGVPDRFIGSGSGTDFTLTISSVQAEDLADYFCQQHYST 100

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PEAKS 51 KLLVYFASTRESGVPDRFIGSGSGTDFTLTISSVQAEDLADYFCQQHYST 100

Fusion 101 PFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDI 150

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

PEAKS 101 PFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDI 150

Fusion 151 NVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTC 200

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

PEAKS 151 NVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTC 200

Fusion 201 EATHKTSTSPIVKSFNRNEC- 220

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

PEAKS 201 EATHKTSTSPIVKSFNRNECF 221

# Score: 2382.0

# Align Len: 443

# Identity: 441/443 (99.55%)

# Similarity: 441/443 (99.55%)

# Gap Count: 0/443 (0.00%)

Fusion 1 QVQLQQPGAELVRPGASVKLSCKASGYTFTSYWMNWVKQRPEQGLEWIGR 50

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Stitch 1 QVQLQQPGAELVRPGASVKLSCKASGYTFTSYWMNWVKQRPEQGLEWIGR 50

Fusion 51 IDPYDSETHYNQKFKDKAILTVDKSSTTAYMQLSSLTSEDSAVYYCARWG 100

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

Stitch 51 IDPYDSETHYNQKFKDKAILTVDKSSTTAYMQLSSLTSEDSAVYYCARWG 100

Fusion 101 TVEWFFDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKG 150

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

Stitch 101 TVEWVKDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKG 150

Fusion 151 YFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVT 200

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

Stitch 151 YFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVT 200

Fusion 201 CNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTIT 250

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

Stitch 201 CNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTIT 250

Fusion 251 LTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFRSVS 300

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

Stitch 251 LTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFDSTFRSVS 300

Fusion 301 ELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPP 350

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

Stitch 301 ELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPP 350

Fusion 351 KEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSY 400

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

Stitch 351 KEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSY 400

Fusion 401 FVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 443

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

Stitch 401 FVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 443

# Score: 1154.0

# Align Len: 220

# Identity: 220/220 (100.00%)

# Similarity: 220/220 (100.00%)

# Gap Count: 0/220 (0.00%)

Fusion 1 DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSYNQENYLAWYQQKPGQSP 50

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

Stitch 1 DIVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSYNQENYLAWYQQKPGQSP 50

Fusion 51 KLLVYFASTRESGVPDRFIGSGSGTDFTLTISSVQAEDLADYFCQQHYST 100

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

Stitch 51 KLLVYFASTRESGVPDRFIGSGSGTDFTLTISSVQAEDLADYFCQQHYST 100

Fusion 101 PFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDI 150

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

Stitch 101 PFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDI 150

Fusion 151 NVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTC 200

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

Stitch 151 NVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTC 200

Fusion 201 EATHKTSTSPIVKSFNRNEC 220

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

Stitch 201 EATHKTSTSPIVKSFNRNEC 220