**H9C12WT-HC**

64.8% identity in 122 residues overlap; Score: 369.0; Gap frequency: 4.1%

Reference 1 QVQLKQSGPGLLQPSQRLSITCTVSGFSLGRYGVH---WIRQSPGKGLEWLGVIWRGGTT

Assembly 1 QVQLKQSGPGLLQPSQRLSLTCTVSGFSIGRGGGGSGGFIRQSPGKGLEWIGVIWRRGST

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\* \*\* \* \*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\* \* \*

Reference 58 DYNAVFMSRLSINKDDSKSQVFFTMNSLRPDDTAIYYCAR--QGSNFPLAYWGQGTLVTV

Assembly 61 CYNPSLKSLVNISLDTSKNQVSLSLSAVQEADLAVYFPQRGQQSGNFPLAYWGQGTLVTV

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Reference 116 SA

Assembly 121 SA

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**H9C12WT-LC**

67.0% identity in 112 residues overlap; Score: 330.0; Gap frequency: 5.4%

Reference 1 NIVMTQTPKFLLVSIGDSITITCKASQSVTNDAA-----WYQKKPGQSPQLLIYQASTRY

Assembly 2 NLVMTQTPKFLLVTPGEPATITLRSSQSLLNENGYNYKYWYQKKPGQSPQLLIYQASTRA

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Reference 56 TGVPDRFSGSGYGTDFTFTISAVQAEDLAVYFCHQDYSSPLTFGAGTKLELK

Assembly 62 SGVPDRFGSPRYGTGGSDFISRVQAEDLAVPECHQDLQSP-TFGAGTKLEIK

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**Umab-HC**

88.2% identity in 119 residues overlap; Score: 519.0; Gap frequency: 2.5%

Reference 1 EVQLVQSGAEVKKPGESLKISCKGSGYSFTTYWLGWVRQMPGKGLDWIGIMSPVDSDIRY

Assembly 1 EVQLVQSGAEVKKPGESLKISGHGSGYSFTTYWIGWVRQMPNK-LDWLGIMSPVDSDLRY

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\* \* \*\*\* \*\*\*\*\*\*\*\*\* \*\*

Reference 61 SPSFQGQVTMSVDKSITTAYLQWNSLKASDTAMYYCARRRPGQGYFDFWGQGTLVTVSS

Assembly 60 SPSFQGQVTMSVDKSITTAYLQWNSLKASDTAMYYHAQRP--QFPFDFWGQGTLVTVSS

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**Umab-LC**

92.5% identity in 107 residues overlap; Score: 506.0; Gap frequency: 0.0%

Reference 1 DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPS

Assembly 1 DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPS

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Reference 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNIYPYTFGQGTKLEIK

Assembly 61 RFSGSGSGPDLTLTITLLLPEDFATYYQCQYNLYPYTFGQGTKLEIK

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**PGDM1400-HC**

61.6% identity in 146 residues overlap; Score: 339.0; Gap frequency: 18.5%

Reference 4 LVQSGPEVRKPGTSVKVSCKAPGNTLKTYDLHWVRSVPGQGLQWMGWISHEGDKK----V

Assembly 3 LLQQPEELVKP-SQEKVSCKAPGNTLTTYDIHWVRQVPGQGLQWMGWISHEGDKKKLRKV

\* \* \* \*\* \*\*\*\*\*\*\*\*\*\*\* \*\*\* \*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*

Reference 60 IVERFKAKVTIDWD----RSTNTAYLQLSGLTSGDTAVYYCAKGSKHRLRDYALYDDDGA

Assembly 62 LVERFKFTTSTPAAGLGVASTSTAYLQLSLSTSGDTAVYYCAK-------DLADVD----

\*\*\*\*\* \*\* \*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\* \* \* \*

Reference 116 LNWAVDVDYLSNLEFWGQGTAVTVSS

Assembly 111 ----VDVDA---LEFWGQGTAVTVSS

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**PGDM1400-LC**

96.4% identity in 112 residues overlap; Score: 571.0; Gap frequency: 0.0%

Reference 1 DFVLTQSPHSLSVTPGESASISCKSSHSLIHGDRNNYLAWYVQKPGRSPQLLIYLASSRA

Assembly 1 DFVLTQSPHSLSVTPGESASISCKSSHSLLHGDRSNYLAWYVQKPGRSPQLLIDLASERA

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\* \*\*

Reference 61 SGVPDRFSGSGSDKDFTLKISRVETEDVGTYYCMQGRESPWTFGQGTKVDIK

Assembly 61 SGVPDRFSGSGSDKDFTLKISRVETEDVGTYYCMQGRESPWTFGQGTKVDIK

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