

**Project Title:**

**Metagenomics Analysis**

**Name:**

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<p>1. Background and purpose of the project, relationship of the project with other projects</p> <p>In recent years, the human microbiome has become increasingly important due to its strong effect on host physiology. Metagenomic analysis is an effective method for comprehensively understanding the microbiome. However, it requires analyzing a vast amount of data due to the diversity of bacteria that make up the microbiome. This project aims to build a high-speed analysis environment using HOKUSAI to accelerate human microbiome research.</p>	<p>months with the conventional server environment.</p>
<p>2. Specific usage status of the system and calculation method</p> <p>We have used HPC portal resource and quota status page to estimate and calculate the usage.</p> <p>During this fiscal year, we used 1,039,417 compute hours (48%) out of total allocated 2,166,912 compute hours at BWMPD resource using the quick use account. For the priority account linked to the same project, we used 536,672 compute hours (74%) out of 720,000 compute hours.</p>	<p>5. Schedule and prospect for the future</p> <p>By applying the analysis environment established this fiscal year, we aim to accelerate research on human and animal microbiomes through metagenomic analysis and elucidate host-microbiome interactions.</p>
<p>3. Result</p> <p>Using large-scale human and animal gut microbiome metagenomic data (10Gbase/sample) obtained by various NGS, we built a pipeline for fast assembly, gene prediction, and annotation of metagenomic data.</p>	<p>6. If no job was executed, specify the reason.</p> <p>Not applicable</p>
<p>4. Conclusion</p> <p>Using Hokusai, we have created an environment that enables us to conduct large-scale metagenomic analysis rapidly, which would have taken several</p>	