

download_uniprot
uniprot_id: Q8I2G6

download_uniprot
uniprot_id: Q8I5K4

create_features
fasta_basename: Q8I2G6

create_features
fasta_basename: Q8I5K4

alphafold_inference
fold: Q8I2G6

alphafold_inference
fold: Q8I2G6_Q8I5K4

alphafold_inference
fold: Q8I5K4

generate_report

all

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graph TD; A[download_uniprot<br/>uniprot_id: Q8I2G6] --> B[create_features<br/>fasta_basename: Q8I2G6]; A --> C[alphafold_inference<br/>fold: Q8I2G6]; B --> C; B --> D[alphafold_inference<br/>fold: Q8I2G6_Q8I5K4]; E[download_uniprot<br/>uniprot_id: Q8I5K4] --> F[create_features<br/>fasta_basename: Q8I5K4]; E --> G[alphafold_inference<br/>fold: Q8I5K4]; F --> D; F --> G; C --> H[generate_report]; D --> H; G --> H; H --> I[all];
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The flowchart illustrates a protein structure prediction pipeline. It starts with two parallel download steps for UniProt IDs Q8I2G6 and Q8I5K4. Each download leads to a 'create_features' step. The 'create_features' step for Q8I2G6 branches into two 'alphafold_inference' steps: one for the single fold 'Q8I2G6' and another for the combined fold 'Q8I2G6_Q8I5K4'. Similarly, the 'create_features' step for Q8I5K4 branches into two 'alphafold_inference' steps: one for the single fold 'Q8I5K4' and another for the combined fold 'Q8I2G6_Q8I5K4'. All three 'alphafold_inference' steps feed into a 'generate_report' step, which finally leads to the 'all' output.