

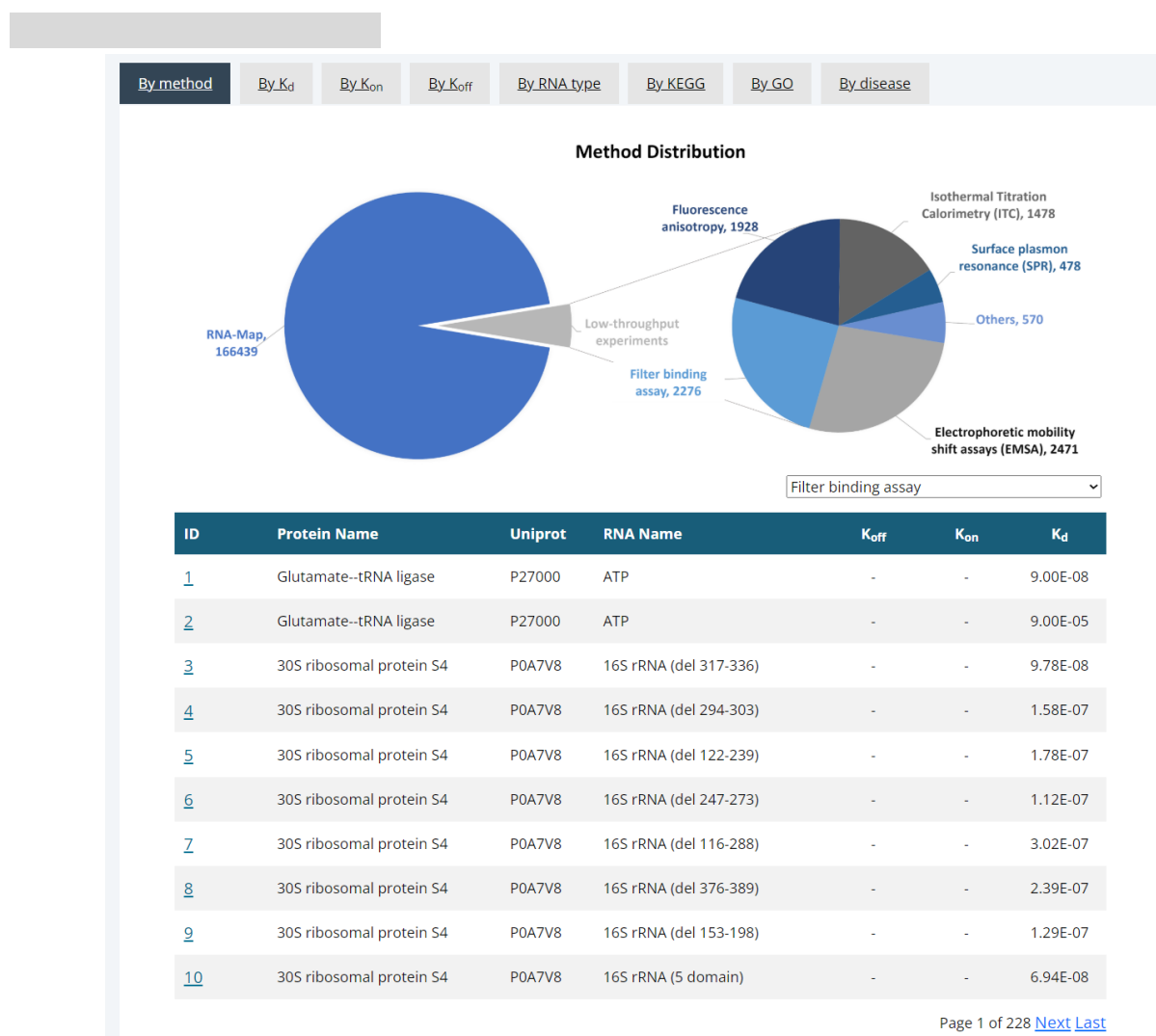
KDBI-RP User Manual

Browse KDBI-RP

Users can browse the database by clicking the "Browse" button on the homepage and then access specific data through multiple options.

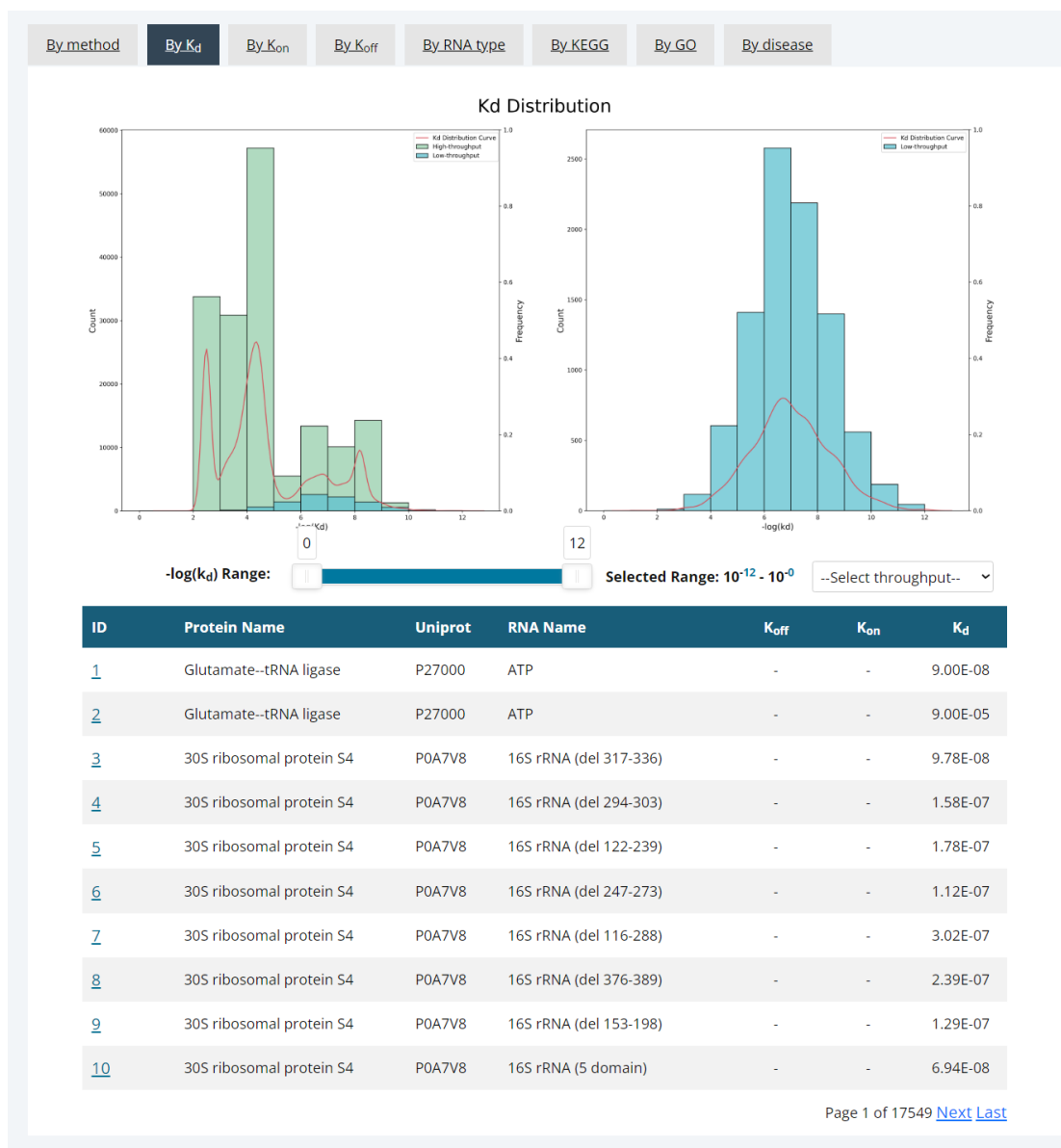
1. Browse KDBI-RP by Method

Users can browse KDBI-RP by assay method. The table will dynamically display corresponding data when the assay method is selected from the dropdown menu. Clicking on an ID will allow users to access detailed information for a single entry.



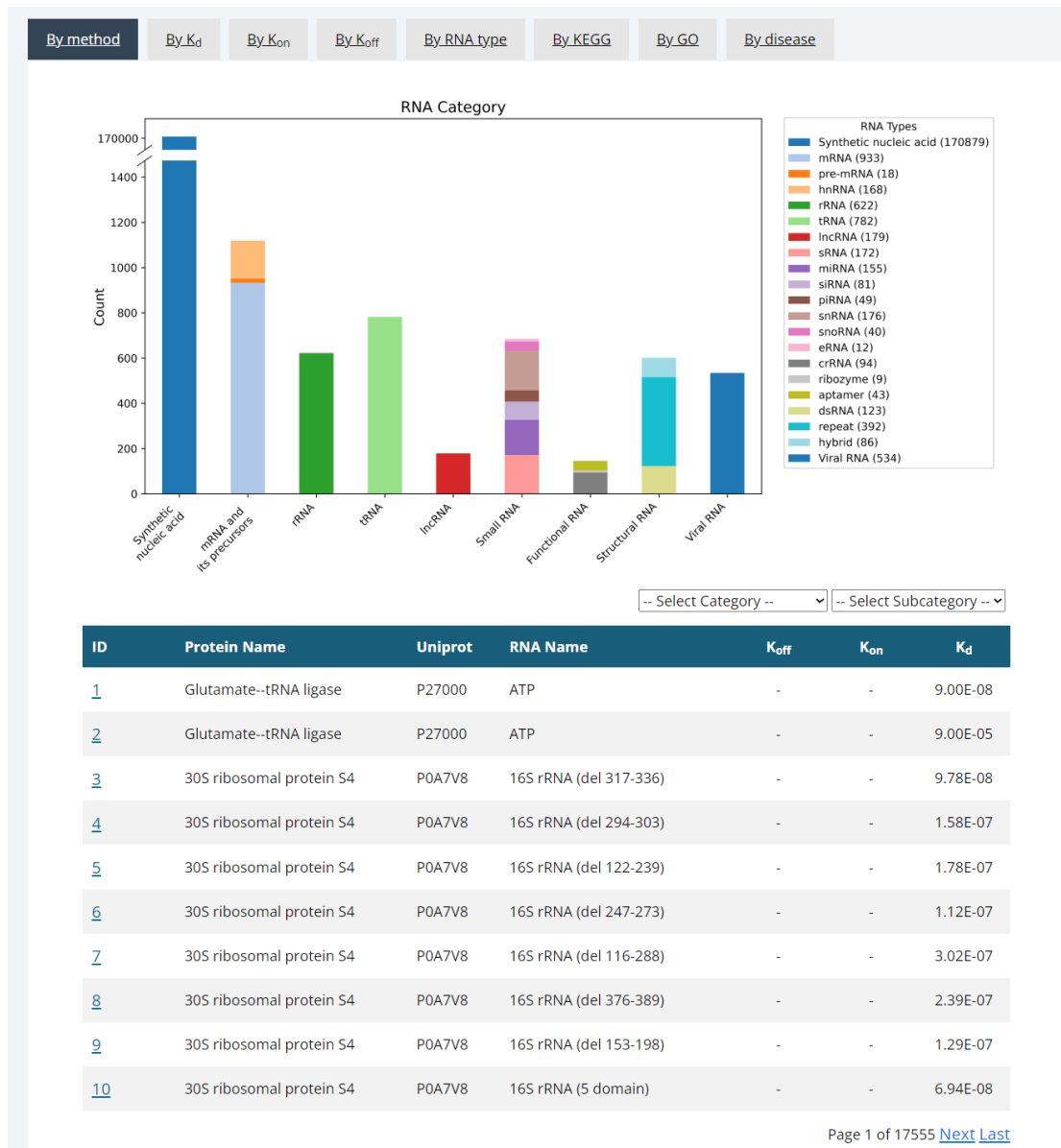
2. Browse KDBI-RP by $K_d/k_{on}/k_{off}$

Users can browse KDBI-RP by kinetic parameters. The range of kinetic parameters can be selected using a slider, and users can choose the experimental throughput from the dropdown menu. A table with corresponding data will be dynamically displayed below. Clicking on an ID will allow users to access detailed information for a single entry.



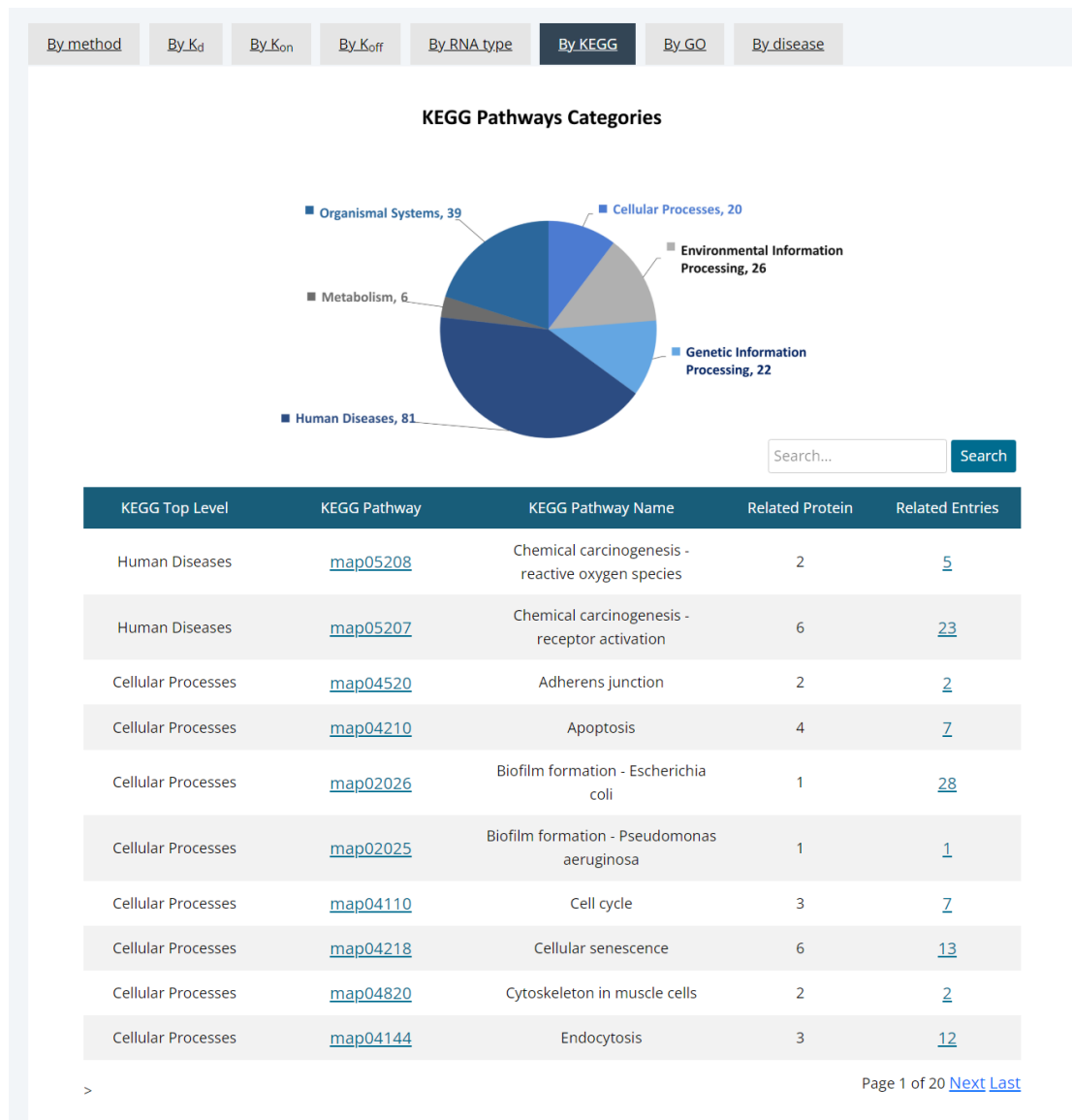
3. Browse KDBI-RP by RNA Type

Users can browse KDBI-RP by RNA type. Selecting the RNA category and subclass from the dropdown menu will dynamically display the corresponding data in a table. Clicking on an ID will allow users to access detailed information for a single entry.



4. Browse KDBI-RP by KEGG Pathway

Users can browse KDBI-RP by KEGG pathway. The search box allows users to perform a fuzzy search by pathway name or ID, and related data will be dynamically displayed in the table below. Clicking on a KEGG Pathway will access the corresponding pathway. Users can also click "Related Entries" to view a new webpage containing specific entries for the matched pathway.



5. Browse KDBI-RP by Gene Ontology

Users can browse KDBI-RP by GO pathway. From the dropdown menu, users can select the GO type, and the search box allows fuzzy matching of pathway names or IDs. Related data will be dynamically displayed in the table below. Clicking on a GO Category will access the corresponding pathway category, or clicking on a GO Term will access the specific pathway. Users can also click "Related Entries" to view a new webpage with specific entries for the matched pathway.

[By method](#)
[By K_d](#)
[By K_{on}](#)
[By K_{off}](#)
[By RNA type](#)
[By KEGG](#)
[By GO](#)
[By disease](#)

Molecular Function Categories

Molecular Function Categories

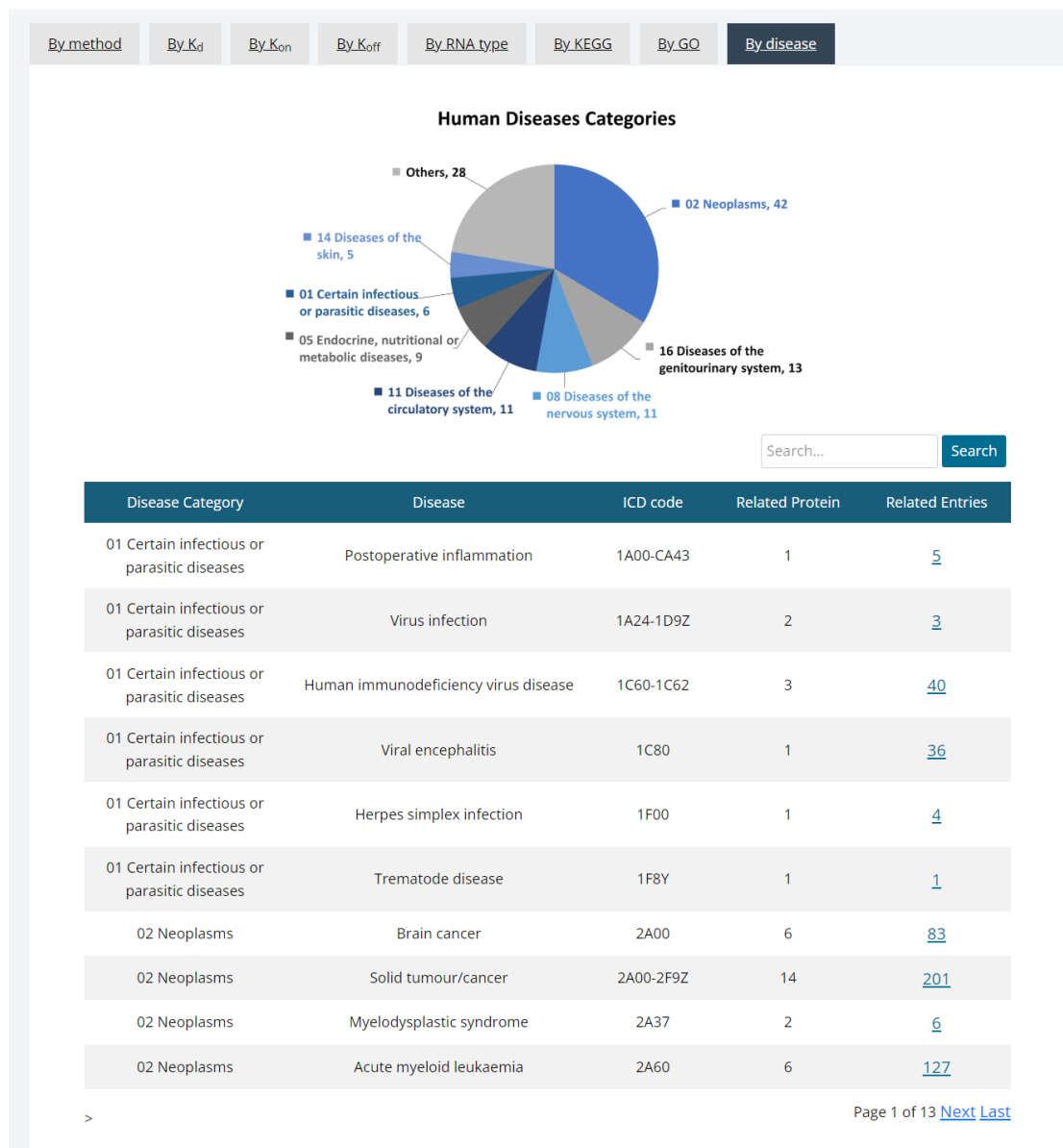
GO type	GO Category	GO Category Description	GO Term	GO Term Description	Related Protein	Related Entries
MF	GO:0140657	ATP-dependent activity	GO:0008186	ATP-dependent activity, acting on RNA	5	27
MF	GO:0140657	ATP-dependent activity	GO:0140545	ATP-dependent protein disaggregase activity	1	4
MF	GO:0140657	ATP-dependent activity	GO:0043139	5'-3' DNA helicase activity	2	11
MF	GO:0140657	ATP-dependent activity	GO:0032574	5'-3' RNA helicase activity	2	11
MF	GO:0140657	ATP-dependent activity	GO:0036121	double-stranded DNA helicase activity	2	11
MF	GO:0140657	ATP-dependent activity	GO:0008094	ATP-dependent activity, acting on DNA	1	6
MF	GO:0140657	ATP-dependent activity	GO:0043138	3'-5' DNA helicase activity	2	53
MF	GO:0140657	ATP-dependent activity	GO:0033679	3'-5' DNA/RNA helicase activity	2	53
MF	GO:0140657	ATP-dependent activity	GO:1990518	single-stranded 3'-5' DNA helicase activity	1	17
MF	GO:0005488	binding	GO:0071889	14-3-3 protein binding	4	32

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6. Browse KDBI-RP by Disease

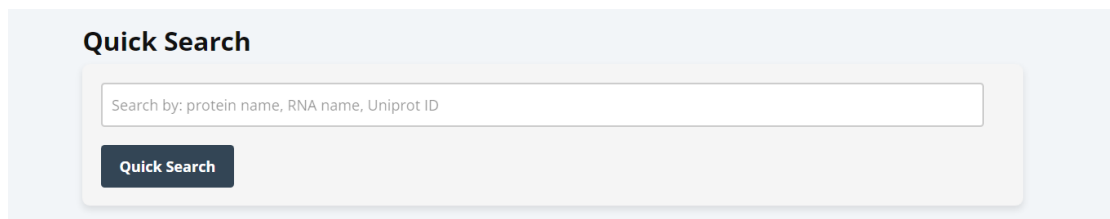
Users can browse KDBI-RP by disease. The search box allows users to perform a fuzzy search by disease name, and related data will be dynamically displayed in the table below. Users can click "Related Entries" to view a new webpage containing specific entries for the matched disease.



Search KDBI-RP

1. Simple Search

Users can search protein names, RNA names, and UNIPROT IDs through the simple search feature located at the top of the page or on the search page. After clicking the "Search" button, a new page will display the matching entries.



The image shows a 'Quick Search' form. It has a title 'Quick Search' in bold. Below the title is a search input field with the placeholder text 'Search by: protein name, RNA name, Uniprot ID'. Below the input field is a dark blue button with the text 'Quick Search' in white.

2. Advanced Search

Users can perform an advanced search on the search page by selecting protein information, RNA information, PubMed ID, methodology, throughput, kinetic parameters, structure, and other categories (19 subcategories in total). After clicking the "Search" button, a new page will display the matching entries.

Advanced Search

Protein Name	RNA Name
Protein Sequence	RNA Sequence
Protein Uniprot	RNA Type
	ALL
Protein Source	RNA Source
Protein Taxonomy	RNA Taxonomy
Protein Mutation	RNA Mutation
ALL	ALL
Method	PubMed ID
ALL	
Throughput	☐ K_d / $-\log(K_d)$ range from to
ALL	☐ K_{on} / $\log(K_{on})$ range from to
☐ K_{off} / $-\log(K_{off})$ range from to	
☐ Complex Structure	

Advanced Search

Download Data

Users can freely and easily download data from KDBI-RP. On the download page, users can download the entire database in CSV, JSON, or XLSX formats. On the search result page, a download button is provided at the bottom, allowing users to download the filtered data of interest. On each detail page, the 3D structure of protein monomers and complexes, as well as the predicted 2D and 3D structures of RNA, are available for download.

Download Protein-RNA Interaction Data

Below you can find various datasets related to protein-RNA interactions. You can download them in multiple formats that suit your research needs.



CSV Format

Download the dataset in CSV format for easy use in spreadsheets or data analysis tools.

[Download CSV](#)



JSON Format

Get the dataset in JSON format for easy integration with applications and scripts.

[Download JSON](#)



Excel Format

Download the dataset as an Excel file for advanced analysis and reporting.

[Download Excel](#)

Detail Page Description

The detail page is organized into six sections: protein information, RNA information, data source, kinetics information, structural information, and related entries.

1. Protein Information

This section provides comprehensive information about proteins, including their name, species, Uniprot ID, sequence, mutation details, and region information (for fragments of existing proteins). Additionally, it integrates cross-references to five major categories of external databases: Nucleic Acid Sequence and Gene Databases, Domain and Functional Classification Databases, Protein-Protein Interaction Databases, Gene Ontology and Pathway Databases, Disease and Drug Databases. Entries are matched via Uniprot IDs, and users can explore detailed information through expandable dropdown menus across 16 linked databases.

2. RNA Information

The RNA section includes data such as RNA name, species of origin, RNA type, sequence information (including complementary strand sequences for double-stranded RNAs), and mutation details. Additionally, RNA sequences are cross-referenced with external databases, including PDB, RNACentral, ENA, Malacards, and GeneCards, ensuring broad data accessibility.

3. Data Source

This section documents detailed bibliographic information of the source publications, including the title, journal, publication year, DOI, PubMed ID, and the precise location of the data within the publication, ensuring traceability and reproducibility.

4. Kinetics Information

The kinetics section provides binding parameters such as K_d , K_a , k_{on} , k_{off} . Experimental conditions, including pH, temperature, buffer composition, measurement methods, and additional notes, are also recorded, allowing users to contextualize and evaluate the reliability of the data.

Protein Information

Protein Name	Uncharacterized protein
Protein Source	Pyrococcus horikoshii
Uniprot	O59282
Sequence	MGEEFEKLMKKFENVNKDGE... Show Full
Mutation	wild
Region	
PDB	2E3U

Nucleic Acid Sequence and Gene Databases ▼

Domain and Functional Classification Databases ▼

Protein-Protein Interaction Databases ▼

Gene Ontology and Pathway Databases ▼

Disease and Drug Databases ▼

Reference Information

Title	An archaeal Dim2-like protein, aDim2p, forms a ternary complex with a/eIF2 alpha and the 3' end fragment of 16S rRNA.
Journal	Journal of molecular biology (2010)
DOI	10.1016/j.jmb.2010.03.055
PubMed	20363226
Location	Table 1; Page No:775

RNA Information

RNA Name	rRNA fragment
RNA Source	Synthetic nucleic acid
Type of RNA	rRNA
Sequence of chain 1	GGAUACACCUCC
Sequence of chain 2	
Mutation	wild

RNA Databases ▼

Kinetic Information

K_d (Wild)	9.80E-10
K_d (Mutation)	4.40E-08
K_a (Wild)	1.02E+09
K_a (Mutation)	2.27E+07
K_{on}	4.80E+04
K_{off}	2.10E-03
pH	8.5
Temperature	298
Buffer	10 mM Tris-HCl 2mM EDTA, and 0.005% Surfactant P20
Method	Surface plasmon resonance (SPR)
Addition	

5. Structural Information

The structural information section offers three-dimensional structural data for both proteins and complexes. For structures available in PDB, the best monomer structure is selected based on the following criteria: highest resolution, lowest R-factor, and most recent release date. The provided details include PDB ID, molecule name, chain count, method, resolution (Å), PubMed link, and release date. Additional structural resources include: Links to AlphaFold Protein Structure Database and SWISS-MODEL Repository for protein structures. Links to the NAKB database for complex structures.

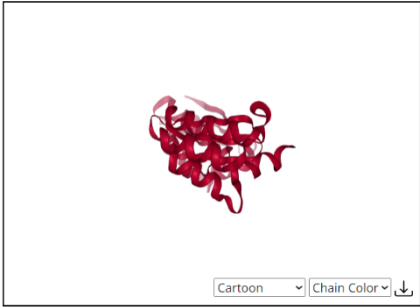
Predicted RNA secondary and tertiary structures generated using RNAFold and RhoFold+. All 3D structures are visualized using ngl.js, with options for customizable coloring schemes, display modes, and download functionality. Secondary structures are provided with zoom and download options.

Structure Information

Protein Structure

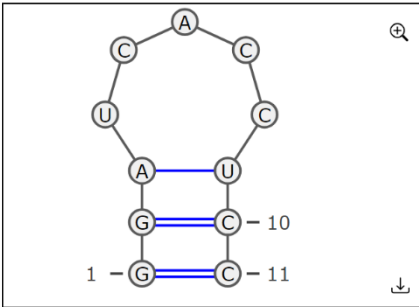
PDB ID	2E3U
Molecule Name	Crystal structure analysis of Dim2p from <i>Pyrococcus horikoshii</i> OT3
Chain Count	2
Method	X-RAY DIFFRACTION
Resolution(Å)	2.3
PubMed	17654551
Release Date	2007-10-23
Other Database	AlphaFold SMR

PDB Visualization with NGL

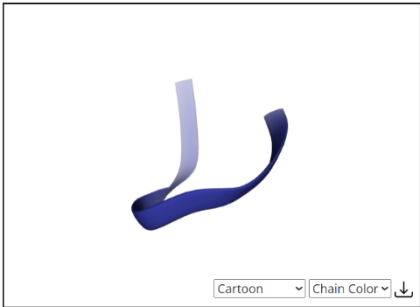


PDB Visualization with NGL

RNA Structure



Predicted RNA secondary structure

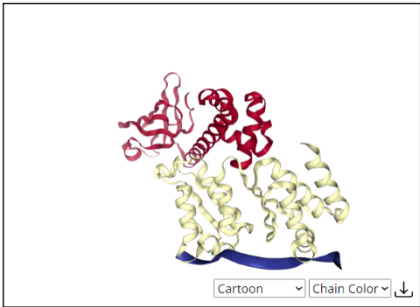


Predicted RNA tertiary structure

Complex Structure

PDB ID	3AEV
Molecule Name	Crystal structure of a/eIF2alpha-aDim2p-rRNA complex from <i>Pyrococcus horikoshii</i> OT3
Chain Count	3
Method	X-RAY DIFFRACTION
Resolution(Å)	2.8
PubMed	20363226
Release Date	2010-04-21
Other Database	NAKB

PDB Visualization with NGL



PDB Visualization with NGL

6. Related Entries

This section lists entries with identical protein or RNA sequences, enabling users to compare and analyze similar interactions efficiently.

Related Entries						
ID	Protein Name	Uniprot	RNA Name	K_{off}	K_{on}	K_d
2998	Uncharacterized protein	O59282	rRNA fragment	2.50E-04	2.20E+05	1.10E-09
2999	Uncharacterized protein	O59282	rRNA fragment	1.20E-04	1.00E+05	1.20E-09
3000	Uncharacterized protein	O59282	rRNA fragment	4.10E-04	8.80E+04	4.60E-09
3001	Uncharacterized protein	O59282	rRNA fragment	3.90E-03	1.50E+05	2.60E-09
3002	Uncharacterized protein	O59282	rRNA fragment	3.00E-04	9.10E+04	3.30E-09
3003	Uncharacterized protein	O59282	rRNA fragment	4.80E-04	1.50E+05	3.20E-09
3004	Uncharacterized protein	O59282	rRNA fragment	6.00E-04	2.00E+05	3.00E-09
3005	Uncharacterized protein	O59282	rRNA fragment	4.40E-04	1.30E+05	3.40E-09
3006	Uncharacterized protein	O59282	rRNA fragment	3.30E-04	1.30E+05	2.40E-09
3007	Uncharacterized protein	O59282	rRNA fragment	6.50E-04	1.20E+05	5.40E-09

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By integrating these modules, KDBI-RP provides a comprehensive, systematic, and user-friendly resource for protein-RNA binding kinetics, supporting a wide range of studies in this field.