

## Specimen for Class 09: Downloadable computer software for the scientific analysis and management of protein and genetic sequences.

It is common for software to access data remotely via either native APIs or generically via ODBC. Below example is a Microsoft Access data accessing data hosted on a remote SQL Server database. Here Microsoft Access is used as a “front-end” tool, “attaching” to remote tables. This Microsoft Access software database file is stored on a cloud drive, and may be downloaded by anyone with a connection to the drive. Editing data here will update the data in the “back-end” database because of the live connection.

Tools such as R likewise have database connection software libraries that similarly connect to a remote database server. So, for example *machine learning* libraries can easily access and analyze scientific data.

PDBID	Title	ChainLabel	ChainIndex	ResidueSequence	numResidue	ResidueNames
168L	PROTEIN FLEXIBILITY AND ADAPTABILITY SEEN IN 25 CRYSTAL FORMS OF T4 LYSOZYME	A	1	MNIFEMLRIDEGLRLKIYKDEGYTIGIHLTKSPSLNAAKSELDKAIGRNCNGVITKDEAEKLFNQDVAAVRGLIRN AKLKPYVDSLDAVRRCALINMVFQMGETGVAGFTNSLRMLQQRWDAAAAALAAAWYNGTPNRAKRVIITFRGTWDAYKNL	164	Met,Asn,Ile,Phe,Glu,Met,Leu,Arg,Ile,Asp,Gly,Leu,Arg,Leu,Lys,Ile,Tyr,Lys,Asp,Thr,Glu,Tyr,Thr,Thr,Ile,Gly,Ile,Gly,His,Leu,Leu,Thr,Lys,Ser,Pro,Ser,Leu,Asn,Ala,Ala,Lys,Ser,Glu,Leu,Asp,Lys,Ala,Ile,Gly,Arg,Asn,Cys,Asn,Gly,Val,Ile,Thr,Lys,Asp,Glu,Ala,Glu,Lys,Leu,
168L	PROTEIN FLEXIBILITY AND ADAPTABILITY SEEN IN 25 CRYSTAL FORMS OF T4 LYSOZYME	B	2	MNIFEMLRIDEGLRLKIYKDEGYTIGIHLTKSPSLNAAKSELDKAIGRNCNGVITKDEAEKLFNQDVAAVRGLIRN AKLKPYVDSLDAVRRCALINMVFQMGETGVAGFTNSLRMLQQRWDAAAAALAAAWYNGTPNRAKRVIITFRGTWDAYKNL	164	Met,Asn,Ile,Phe,Glu,Met,Leu,Arg,Ile,Asp,Gly,Leu,Arg,Leu,Lys,Ile,Tyr,Lys,Asp,Thr,Glu,Tyr,Thr,Thr,Ile,Gly,Ile,Gly,His,Leu,Leu,Thr,Lys,Ser,Pro,Ser,Leu,Asn,Ala,Ala,Lys,Ser,Glu,Leu,Asp,Lys,Ala,Ile,Gly,Arg,Asn,Cys,Asn,Gly,Val,Ile,Thr,Lys,Asp,Glu,Ala,Glu,Lys,Leu,
168L	PROTEIN FLEXIBILITY AND ADAPTABILITY SEEN IN 25 CRYSTAL FORMS OF T4 LYSOZYME	C	3	MNIFEMLRIDEGLRLKIYKDEGYTIGIHLTKSPSLNAAKSELDKAIGRNCNGVITKDEAEKLFNQDVAAVRGLIRN AKLKPYVDSLDAVRRCALINMVFQMGETGVAGFTNSLRMLQQRWDAAAAALAAAWYNGTPNRAKRVIITFRGTWDAYKNL	164	Met,Asn,Ile,Phe,Glu,Met,Leu,Arg,Ile,Asp,Gly,Leu,Arg,Leu,Lys,Ile,Tyr,Lys,Asp,Thr,Glu,Tyr,Thr,Thr,Ile,Gly,Ile,Gly,His,Leu,Leu,Thr,Lys,Ser,Pro,Ser,Leu,Asn,Ala,Ala,Lys,Ser,Glu,Leu,Asp,Lys,Ala,Ile,Gly,Arg,Asn,Cys,Asn,Gly,Val,Ile,Thr,Lys,Asp,Glu,Ala,Glu,Lys,Leu,
168L	PROTEIN FLEXIBILITY AND ADAPTABILITY SEEN IN 25 CRYSTAL FORMS OF T4 LYSOZYME	D	4	MNIFEMLRIDEGLRLKIYKDEGYTIGIHLTKSPSLNAAKSELDKAIGRNCNGVITKDEAEKLFNQDVAAVRGLIRN AKLKPYVDSLDAVRRCALINMVFQMGETGVAGFTNSLRMLQQRWDAAAAALAAAWYNGTPNRAKRVIITFRGTWDAYKNL	164	Met,Asn,Ile,Phe,Glu,Met,Leu,Arg,Ile,Asp,Gly,Leu,Arg,Leu,Lys,Ile,Tyr,Lys,Asp,Thr,Glu,Tyr,Thr,Thr,Ile,Gly,Ile,Gly,His,Leu,Leu,Thr,Lys,Ser,Pro,Ser,Leu,Asn,Ala,Ala,Lys,Ser,Glu,Leu,Asp,Lys,Ala,Ile,Gly,Arg,Asn,Cys,Asn,Gly,Val,Ile,Thr,Lys,Asp,Glu,Ala,Glu,Lys,Leu,
168L	PROTEIN FLEXIBILITY AND ADAPTABILITY SEEN IN 25 CRYSTAL FORMS OF T4 LYSOZYME	E	5	MNIFEMLRIDEGLRLKIYKDEGYTIGIHLTKSPSLNAAKSELDKAIGRNCNGVITKDEAEKLFNQDVAAVRGLIRN AKLKPYVDSLDAVRRCALINMVFQMGETGVAGFTNSLRMLQQRWDAAAAALAAAWYNGTPNRAKRVIITFRGTWDAYKNL	164	Met,Asn,Ile,Phe,Glu,Met,Leu,Arg,Ile,Asp,Gly,Leu,Arg,Leu,Lys,Ile,Tyr,Lys,Asp,Thr,Glu,Tyr,Thr,Thr,Ile,Gly,Ile,Gly,His,Leu,Leu,Thr,Lys,Ser,Pro,Ser,Leu,Asn,Ala,Ala,Lys,Ser,Glu,Leu,Asp,Lys,Ala,Ile,Gly,Arg,Asn,Cys,Asn,Gly,Val,Ile,Thr,Lys,Asp,Glu,Ala,Glu,Lys,Leu,
1A81	SI FORM CRAMBIN	A	1	TTCCPSIVARSNFVCRLPGTSEICATYTGCIIPGATCPGDYAN	46	Thr,Thr,Cys,Cys,Pro,Ser,Ile,Val,Ala,Arg,Ser,Asn,Phe,Asn,Val,Cys,Arg,Leu,Pro,Gly,Thr,Ser,Glu,Ala,Ile,Cys,Ala,Thr,Tyr,Thr,Gly,Cys,Ile,Ile,Pro,Gly,Ala,Thr,Cys,Pro,Gly,Asp,Tyr,Ala,Asn
1A81	SI FORM CRAMBIN	A	2	X	1	Eoh
1AHO	THE AB INITIO STRUCTURE DETERMINATION AND REFINEMENT OF A SC PROTEIN TOXIN	A	1	VKGDYIVDDVNCYFCGRNAYCNEECKLKGESGYCQWASPYGNACYKLPDHRVTKGPGRCH	64	Val,Lys,Asp,Gly,Tyr,Ile,Val,Asp,Asp,Val,Asn,Cys,Thr,Tyr,Phe,Cys,Gly,Arg,Asn,Ala,Tyr,Cys,Asn,Glu,Gly,Cys,Thr,Lys,Leu,Lys,Gly,Ser,Gly,Tyr,Cys,Gln,Trp,Ala,Ser,Pro,Tyr,Gly,Asn,Ala,Cys,Tyr,Cys,Tyr,Lys,Leu,Pro,Asp,His,Val,Arg,Thr,Lys,Gly,Pro,Gly,Arg,Cys,His
1B0Y	MUTANT H42Q OF HIPIP FROM CHROMATIUM VINOSUM AT 0.93A	A	1	SAPANAVAADNATAIALKYNQDATKSERVAAARPLPEEQQCANCQFMQADAAGATDEWKGQCLFPGLINLVNGWCASWTLKAG	85	Ser,Ala,Pro,Ala,Asn,Ala,Val,Ala,Ala,Asp,Asn,Ala,Thr,Ala,Ile,Ala,Leu,Lys,Tyr,Asn,Gln,Asp,Ala,Thr,Lys,Ser,Glu,Arg,Val,Ala,Ala,Arg,Pro,Gly,Leu,Pro,Pro,Glu,Gln,Gln,Cys,Ala,Asn,Cys,Gln,Phe,Met,Gln,Ala,Asp,Ala,Ala,Gly,Ala,Thr,Asp,Glu,Trp,Lys,Gly,Cys,Gln,Leu,P
1B0Y	MUTANT H42Q OF HIPIP FROM CHROMATIUM VINOSUM AT 0.93A	A	2	X	1	Sf4
1BEN	INSULIN COMPLEXED WITH 4-HYDROXYBENZAMIDE	A	1	GIVEQCCTSICSLYQLENYCN	21	Gly,Ile,Val,Glu,Gln,Cys,Cys,Thr,Ser,Ile,Cys,Ser,Leu,Tyr,Gln,Leu,Glu,Asn,Tyr,Cys,Asn
1BEN	INSULIN COMPLEXED WITH 4-HYDROXYBENZAMIDE	B	2	FVNQHLGSHLVEALYLVCGERGFYPTKTX	31	Phe,Val,Asn,Gln,His,Leu,Cys,Gly,Ser,His,Leu,Val,Glu,Ala,Leu,Tyr,Leu,Val,Cys,Gly,Glu,Arg,Gly,Phe,Phe,Tyr,Thr,Pro,Lys,Thr,ZN
1BEN	INSULIN COMPLEXED WITH 4-HYDROXYBENZAMIDE	C	3	GIVEQCCTSICSLYQLENYCN	21	Gly,Ile,Val,Glu,Gln,Cys,Cys,Thr,Ser,Ile,Cys,Ser,Leu,Tyr,Gln,Leu,Glu,Asn,Tyr,Cys,Asn
1BEN	INSULIN COMPLEXED WITH 4-HYDROXYBENZAMIDE	C	4	X	1	Hbd
1BEN	INSULIN COMPLEXED WITH 4-HYDROXYBENZAMIDE	D	5	FVNQHLGSHLVEALYLVCGERGFYTP	28	Phe,Val,Asn,Gln,His,Leu,Cys,Gly,Ser,His,Leu,Val,Glu,Ala,Leu,Tyr,Leu,Val,Cys,Gly,Glu,Arg,Gly,Phe,Phe,Tyr,Thr,Pro
1BEN	INSULIN COMPLEXED WITH 4-HYDROXYBENZAMIDE	D	6	XX	2	ZN,CL

**Specimen for Class 42.** This is a query from our database running in SQL Server 2016 on a Windows Server 2016 server. Data is accessible remotely via a VPN. Microsoft provides tools to “upsized” from on-premise server to the Microsoft Azure cloud version of SQL Server. Remote access from the cloud would use similar connectivity to access data.

The screenshot displays the Microsoft SQL Server Management Studio interface. The top menu bar includes File, Edit, View, Query, Project, Debug, Tools, Window, and Help. The Object Explorer on the left shows the server hierarchy for 'BLADERUNNER\VRIRON (SQL Server 13.0.4259.0 - BLADERUNNER.dev)'. The main window shows a SQL query titled 'SQLQuery1.sql - B...DERUNNER.dev (63)' with the following code:

```

/***** Script for SelectTopRows command from SSIS *****/
SELECT TOP (1000) [PDBID]
, [Title]
, [ChainLabel]
, [ChainIndex]
, [ResidueSequence]
, [numResidues]
, [ResidueNames]
, [pdbFilename]
FROM [small].[dbo].[qryProteinChains]

```

The Results pane shows the following data:

PDBID	Title	ChainLabel	ChainIndex	ResidueSequence	numResidues	Residue Names
1	168L	PROTEIN FLEXIBILITY AND ADAPTABILITY SEEN IN 25 CRYSTA...	A	1	1	Met, Ala, Ile, Phe, Glu, Met, Leu, Arg, Ile, Asp, Glu, Gly, Leu, Arg, Leu, Lys, Ile, Tyr, Lys, Asp, Thr, Glu, Gly, Tyr, Tyr, Thr, Ile, Gly, Ile, Gly, His, Le
2	168L	PROTEIN FLEXIBILITY AND ADAPTABILITY SEEN IN 25 CRYSTA...	B	2	1	Met, Ala, Ile, Phe, Glu, Met, Leu, Arg, Ile, Asp, Glu, Gly, Leu, Arg, Leu, Lys, Ile, Tyr, Lys, Asp, Thr, Glu, Gly, Tyr, Tyr, Thr, Ile, Gly, Ile, Gly, His, Le
3	168L	PROTEIN FLEXIBILITY AND ADAPTABILITY SEEN IN 25 CRYSTA...	C	3	1	Met, Ala, Ile, Phe, Glu, Met, Leu, Arg, Ile, Asp, Glu, Gly, Leu, Arg, Leu, Lys, Ile, Tyr, Lys, Asp, Thr, Glu, Gly, Tyr, Thr, Thr, Ile, Gly, Ile, Gly, His, Le
4	168L	PROTEIN FLEXIBILITY AND ADAPTABILITY SEEN IN 25 CRYSTA...	D	4	1	Met, Ala, Ile, Phe, Glu, Met, Leu, Arg, Ile, Asp, Glu, Gly, Leu, Arg, Leu, Lys, Ile, Tyr, Lys, Asp, Thr, Glu, Gly, Tyr, Thr, Thr, Ile, Gly, Ile, Gly, His, Le
5	168L	PROTEIN FLEXIBILITY AND ADAPTABILITY SEEN IN 25 CRYSTA...	E	5	1	Met, Ala, Ile, Phe, Glu, Met, Leu, Arg, Ile, Asp, Glu, Gly, Leu, Arg, Leu, Lys, Ile, Tyr, Lys, Asp, Thr, Glu, Gly, Tyr, Thr, Thr, Ile, Gly, Ile, Gly, His, Le
6	1AB1	SI FORM CRAMBIN	A	1	46	Thr, Thr, Cys, Cys, Pro, Ser, Ile, Val, Ala, Arg, Ser, Asn, Phe, Asn, Val, Cys, Arg, Leu, Pro, Gly, Thr, Ser, Glu, Ala, Ile, Cys, Ala, Thr, Tyr, Thr, Gly, I
7	1AB1	SI FORM CRAMBIN	A	2	1	Esh
8	1AHO	THE AB INITIO STRUCTURE DETERMINATION AND REFINEME...	A	1	64	Val, Lys, Asp, Gly, Tyr, Ile, Val, Asp, Asp, Val, Asn, Cys, Thr, Tyr, Phe, Cys, Gly, Arg, Asn, Ala, Tyr, Cys, Asn, Glu, Glu, Cys, Thr, Lys, Leu, Lys, Gl
9	1BOY	MUTANT H42Q OF HIPIP FROM CHROMATIUM VINOSUM AT 0.9...	A	1	85	Ser, Ala, Pro, Ala, Asn, Ala, Val, Ala, Ala, Asp, Asn, Ala, Thr, Ala, Ile, Ala, Leu, Lys, Tyr, Asn, Gln, Asp, Ala, Thr, Lys, Ser, Glu, Arg, Val, Ala, Ala, F
10	1BOY	MUTANT H42Q OF HIPIP FROM CHROMATIUM VINOSUM AT 0.9...	A	2	1	SH4
11	1BEN	INSULIN COMPLEXED WITH 4-HYDROXYBENZAMIDE	A	1	21	Gly, Ile, Val, Glu, Gln, Cys, Cys, Thr, Ser, Ile, Cys, Ser, Leu, Tyr, Gln, Leu, Glu, Asn, Tyr, Cys, Asn
12	1BEN	INSULIN COMPLEXED WITH 4-HYDROXYBENZAMIDE	B	2	31	Phe, Val, Asn, Gln, His, Leu, Cys, Gly, Ser, His, Leu, Val, Glu, Ala, Leu, Tyr, Leu, Val, Cys, Gly, Glu, Arg, Gly, Phe, Phe, Tyr, Thr, Pro, Lys, Thr, Z
13	1BEN	INSULIN COMPLEXED WITH 4-HYDROXYBENZAMIDE	C	3	21	Gly, Ile, Val, Glu, Gln, Cys, Cys, Thr, Ser, Ile, Cys, Ser, Leu, Tyr, Gln, Leu, Glu, Asn, Tyr, Cys, Asn
14	1BEN	INSULIN COMPLEXED WITH 4-HYDROXYBENZAMIDE	C	4	1	Hbd
15	1BEN	INSULIN COMPLEXED WITH 4-HYDROXYBENZAMIDE	D	5	28	Phe, Val, Asn, Gln, His, Leu, Cys, Gly, Ser, His, Leu, Val, Glu, Ala, Leu, Tyr, Leu, Val, Cys, Gly, Glu, Arg, Gly, Phe, Phe, Tyr, Thr, Pro
16	1BEN	INSULIN COMPLEXED WITH 4-HYDROXYBENZAMIDE	D	6	2	ZN, CL
17	1BEN	INSULIN COMPLEXED WITH 4-HYDROXYBENZAMIDE	D	7	1	Hbd
18	1BPI	THE STRUCTURE OF BOVINE PANCREATIC TRYPSIN INHIBIT...	A	1	59	Arg, Pro, Asp, Phe, Cys, Leu, Glu, Pro, Pro, Tyr, Thr, Gly, Pro, Cys, Lys, Ala, Arg, Ile, Ile, Arg, Tyr, Phe, Tyr, Asn, Ala, Lys, Ala, Gly, Leu, Cys, Gln
19	1BO8	RUBREDOXIN (METHIONINE MUTANT) FROM PYROCOCCUS FU...	A	1	55	Met, Ala, Lys, Trp, Val, Cys, Lys, Ile, Cys, Gly, Tyr, Ile, Tyr, Asp, Glu, Asp, Ala, Gly, Asp, Pro, Asp, Asn, Gly, Ile, Ser, Pro, Gly, Thr, Lys, Phe, Glu, C
20	1BO9	RUBREDOXIN (FORMYL METHIONINE MUTANT) FROM PYROC...	A	1	55	Fme, Ala, Lys, Trp, Val, Cys, Lys, Ile, Cys, Gly, Tyr, Ile, Tyr, Asp, Glu, Asp, Ala, Gly, Asp, Pro, Asp, Asn, Gly, Ile, Ser, Pro, Gly, Thr, Lys, Phe, Glu, I
21	1BFR	RUBREDOXIN (WILD TYPE) FROM PYROCOCCUS FURIOSUS	A	1	54	Ala, Lys, Trp, Val, Cys, Lys, Ile, Cys, Gly, Tyr, Ile, Tyr, Asp, Glu, Asp, Ala, Gly, Asp, Pro, Asp, Asn, Gly, Ile, Ser, Pro, Gly, Thr, Lys, Phe, Glu, Glu, L
22	1BX7	HIRUSTASIN FROM HIRUDO MEDICINALIS AT 1.2 ANGSTROMS	A	1	51	Gly, Asn, Thr, Cys, Gly, Gly, Glu, Thr, Cys, Ser, Ala, Ala, Gln, Val, Cys, Leu, Lys, Gly, Lys, Cys, Val, Cys, Asn, Glu, Val, His, Cys, Arg, Ile, Arg, Cys,
23	1BX7	HIRUSTASIN FROM HIRUDO MEDICINALIS AT 1.2 ANGSTROMS	A	2	2	So4, So4
24	1BX8	HIRUSTASIN FROM HIRUDO MEDICINALIS AT 1.4 ANGSTROMS	A	1	49	Thr, Cys, Gly, Gly, Glu, Thr, Cys, Ser, Ala, Ala, Gln, Val, Cys, Leu, Lys, Gly, Lys, Cys, Val, Cys, Asn, Glu, Val, His, Cys, Arg, Ile, Arg, Cys, Lys, Tyr, I
25	1BX8	HIRUSTASIN FROM HIRUDO MEDICINALIS AT 1.4 ANGSTROMS	A	2	1	So4
26	1CBN	ATOMIC RESOLUTION (0.83 ANGSTROMS) CRYSTAL STRUCTU...	A	1	46	Thr, Thr, Cys, Cys, Pro, Ser, Ile, Val, Ala, Arg, Ser, Asn, Phe, Asn, Val, Cys, Arg, Leu, Pro, Gly, Thr, Ser, Glu, Ala, Ile, Cys, Ala, Thr, Tyr, Thr, Gly, I
27	1CBN	ATOMIC RESOLUTION (0.83 ANGSTROMS) CRYSTAL STRUCTU...	A	2	1	Esh
28	1CKU	AB INITIO SOLUTION AND REFINEMENT OF TWO HIGH POTEN...	A	1	85	Ser, Ala, Pro, Ala, Asn, Ala, Val, Ala, Ala, Asp, Asp, Ala, Thr, Ala, Ile, Ala, Leu, Lys, Tyr, Asn, Gln, Asp, Ala, Thr, Lys, Ser, Glu, Arg, Val, Ala, Ala, F
29	1CKU	AB INITIO SOLUTION AND REFINEMENT OF TWO HIGH POTEN...	A	2	1	SH4
30	1CKU	AB INITIO SOLUTION AND REFINEMENT OF TWO HIGH POTEN...	B	3	85	Ser, Ala, Pro, Ala, Asn, Ala, Val, Ala, Ala, Asp, Asp, Ala, Thr, Ala, Ile, Ala, Leu, Lys, Tyr, Asn, Gln, Asp, Ala, Thr, Lys, Ser, Glu, Arg, Val, Ala, Ala, F
31	1CKU	AB INITIO SOLUTION AND REFINEMENT OF TWO HIGH POTEN...	B	4	1	SH4
32	1CNR	CORRELATED DISORDER OF THE PURE PRO22SLASHLEU25	A	1	46	Thr, Thr, Cys, Cys, Pro, Ser, Ile, Val, Ala, Arg, Ser, Asn, Phe, Asn, Val, Cys, Arg, Leu, Pro, Gly, Thr, Pro, Glu, Ala, Leu, Cys, Ala, Thr, Tyr, Thr, Gly
33	1CNR	CORRELATED DISORDER OF THE PURE PRO22SLASHLEU25	A	2	1	Esh
34	1DJT	ATOMIC RESOLUTION STRUCTURE OF SCORPION ALPHA-LIKE...	A	1	64	Val, Arg, Asp, Ala, Tyr, Ile, Ala, Lys, Pro, His, Asn, Cys, Val, Tyr, Glu, Cys, Ala, Arg, Asn, Glu, Tyr, Cys, Asn, Asp, Leu, Cys, Thr, Lys, Asn, Gly, Ala
35	1DJT	ATOMIC RESOLUTION STRUCTURE OF SCORPION ALPHA-LIKE...	B	2	64	Val, Arg, Asp, Ala, Tyr, Ile, Ala, Lys, Pro, His, Asn, Cys, Val, Tyr, Glu, Cys, Ala, Arg, Asn, Glu, Tyr, Cys, Asn, Asp, Leu, Cys, Thr, Lys, Asn, Gly, Ala
36	1EJG	CRAMBIN AT ULTRA-HIGH RESOLUTION: VALENCE ELECTRON...	A	1	46	Thr, Thr, Cys, Cys, Pro, Ser, Ile, Val, Ala, Arg, Ser, Asn, Phe, Asn, Val, Cys, Arg, Leu, Pro, Gly, Thr, Pro, Glu, Ala, Leu, Cys, Ala, Thr, Tyr, Thr, Gly
37	1EN2	UDA TETRASACCHARIDE COMPLEX. CRYSTAL STRUCTURE O...	A	1	86	Pca, Arg, Cys, Gly, Ser, Gln, Gly, Gly, Gly, Ser, Thr, Cys, Pro, Gly, Leu, Arg, Cys, Ser, Ile, Trp, Gly, Trp, Cys, Gly, Asp, Ser, Glu, Pro, Tyr, Cys
38	1EN2	UDA TETRASACCHARIDE COMPLEX. CRYSTAL STRUCTURE O...	A	2	4	Nag, Nag, Nag, Nag
39	1F94	THE 0.97 RESOLUTION STRUCTURE OF BUCANDIN. A NOVEL ...	A	1	63	Met, Glu, Cys, Tyr, Arg, Cys, Gly, Val, Ser, Gly, Cys, His, Leu, Lys, Ile, Thr, Cys, Ser, Ala, Glu, Glu, Thr, Phe, Cys, Tyr, Lys, Trp, Leu, Asn, Lys, Ile