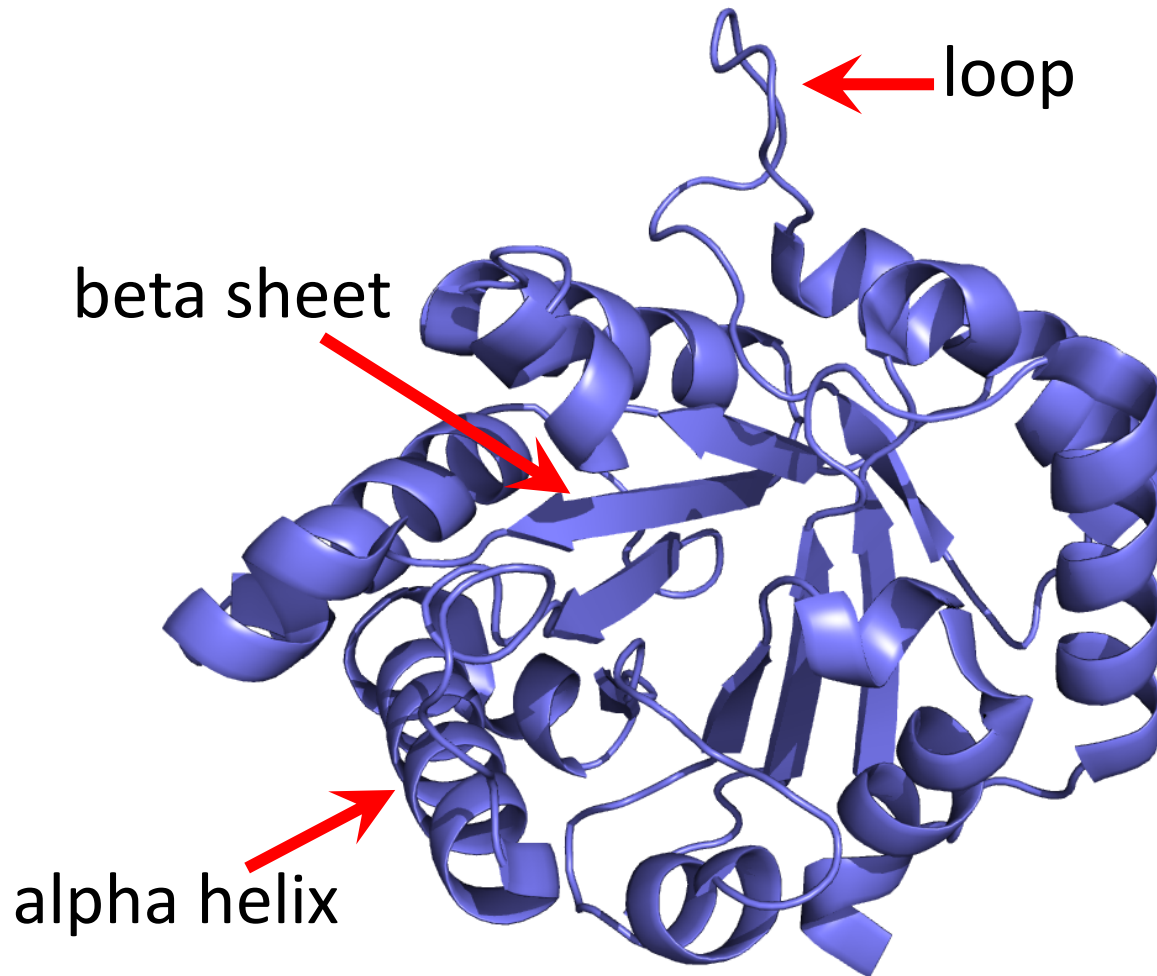


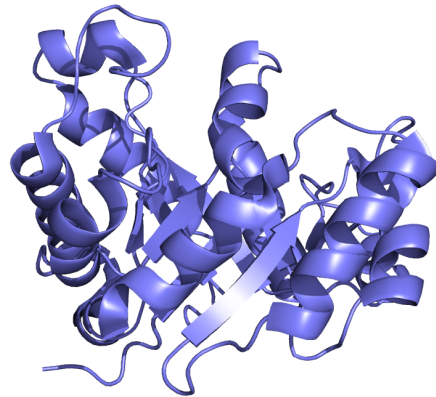
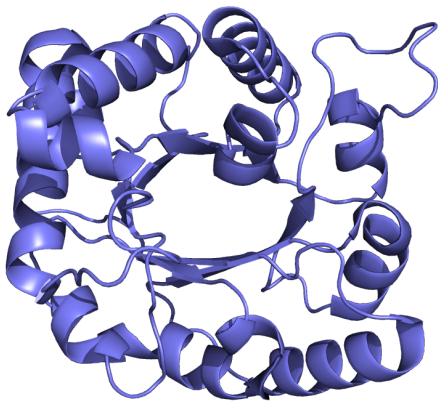
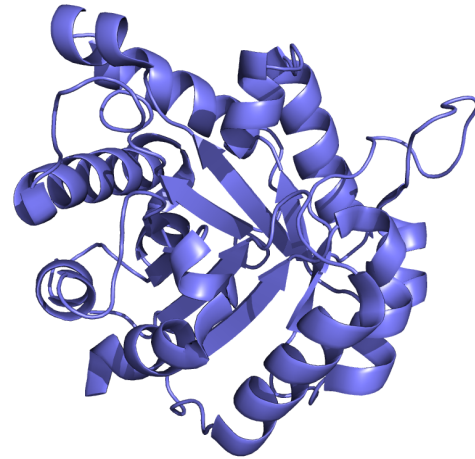
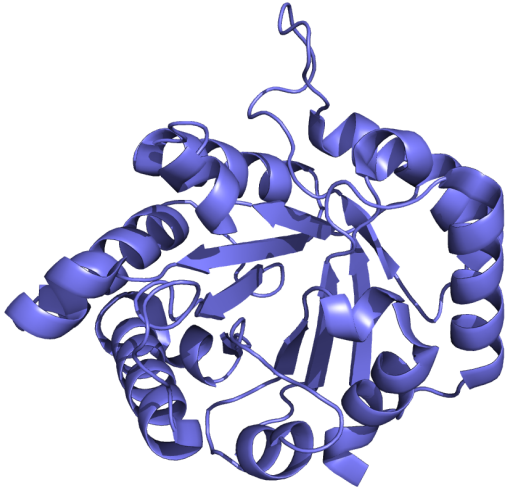
Working with protein structures / PDB files

Structure of Triosephosphate Isomerase

PDB ID: 1HTI

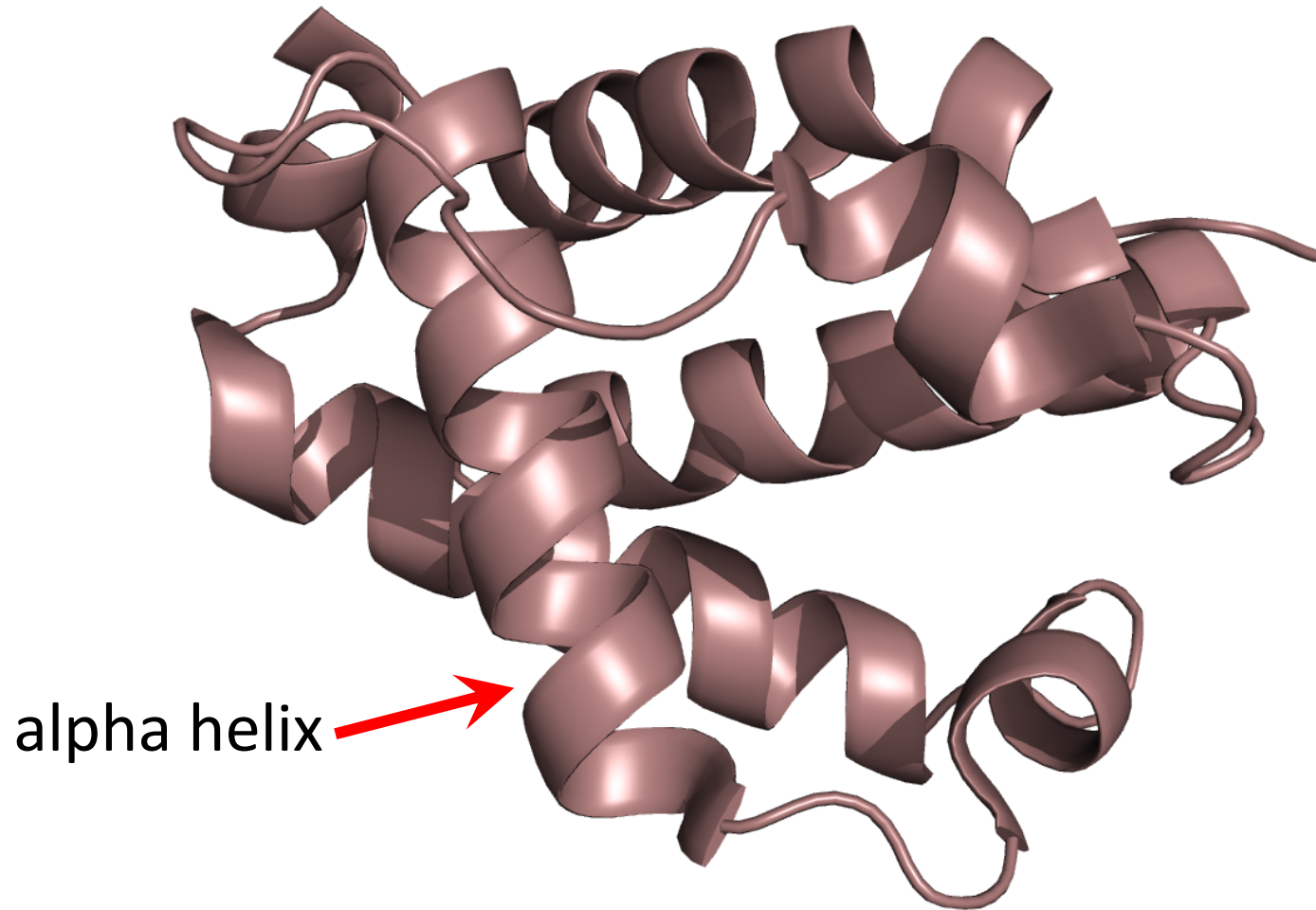


Different perspectives of the same structure



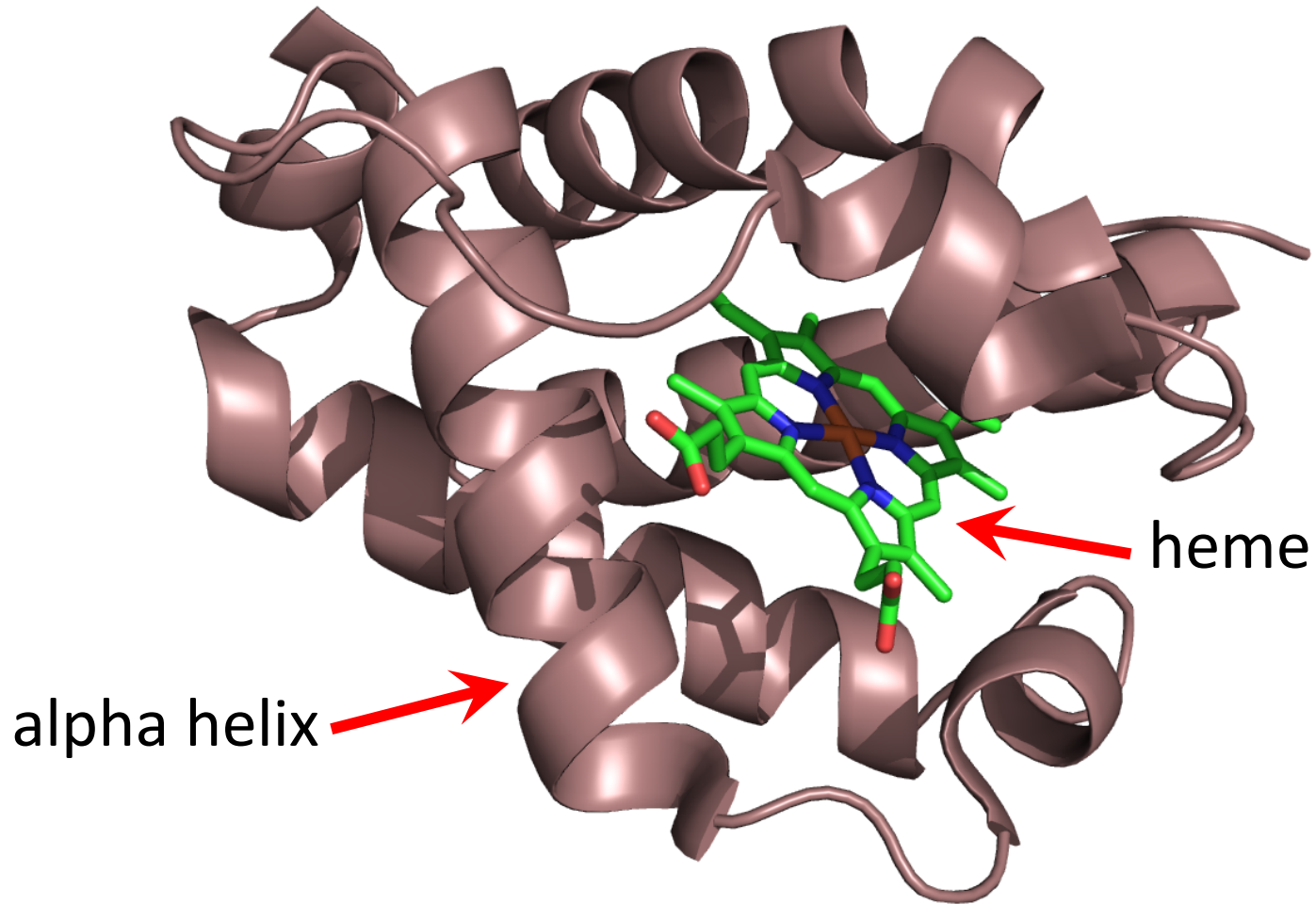
Structure of Truncated Hemoglobin

PDB ID: 1DLW



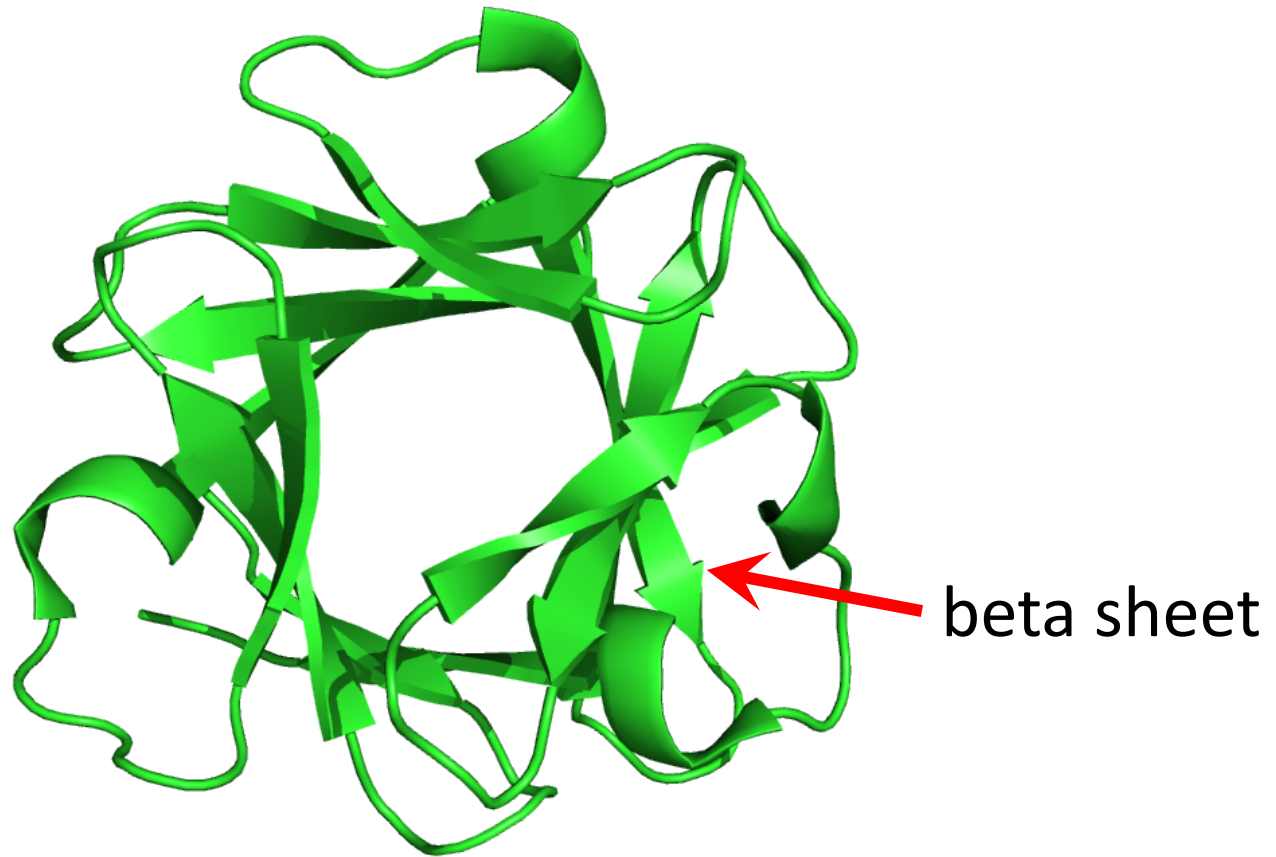
Structure of Truncated Hemoglobin

PDB ID: 1DLW



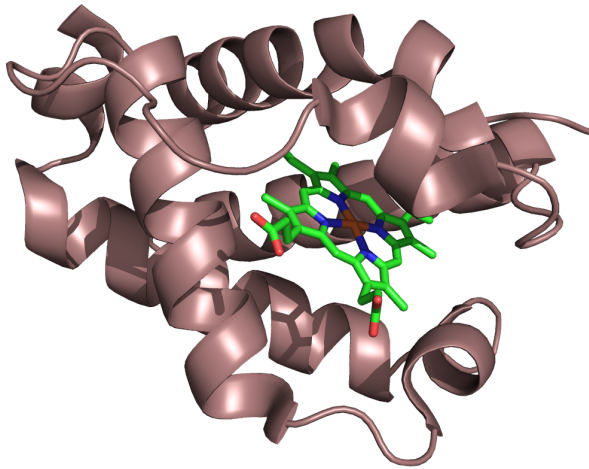
Structure of Basic Fibroblast Growth Factor

PDB ID: 1BFG

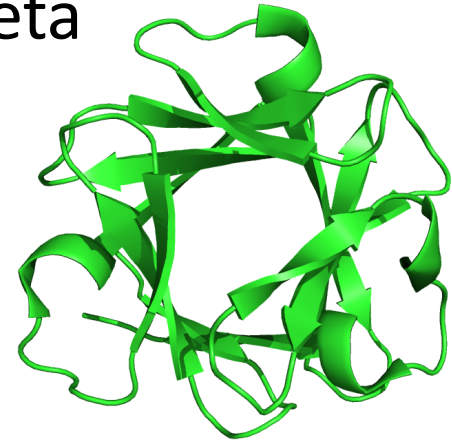


We classify structures by their alpha and beta content

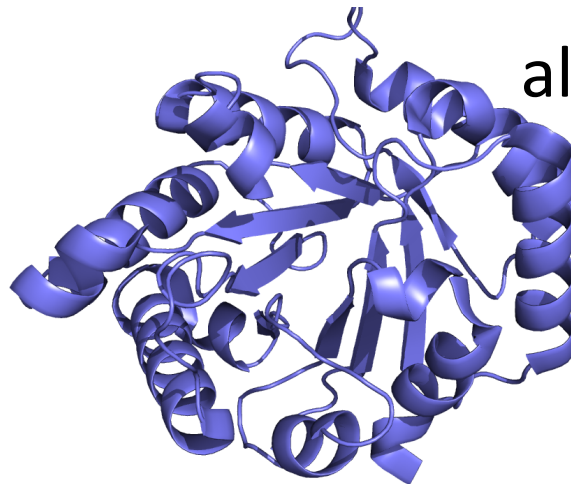
all alpha



all beta

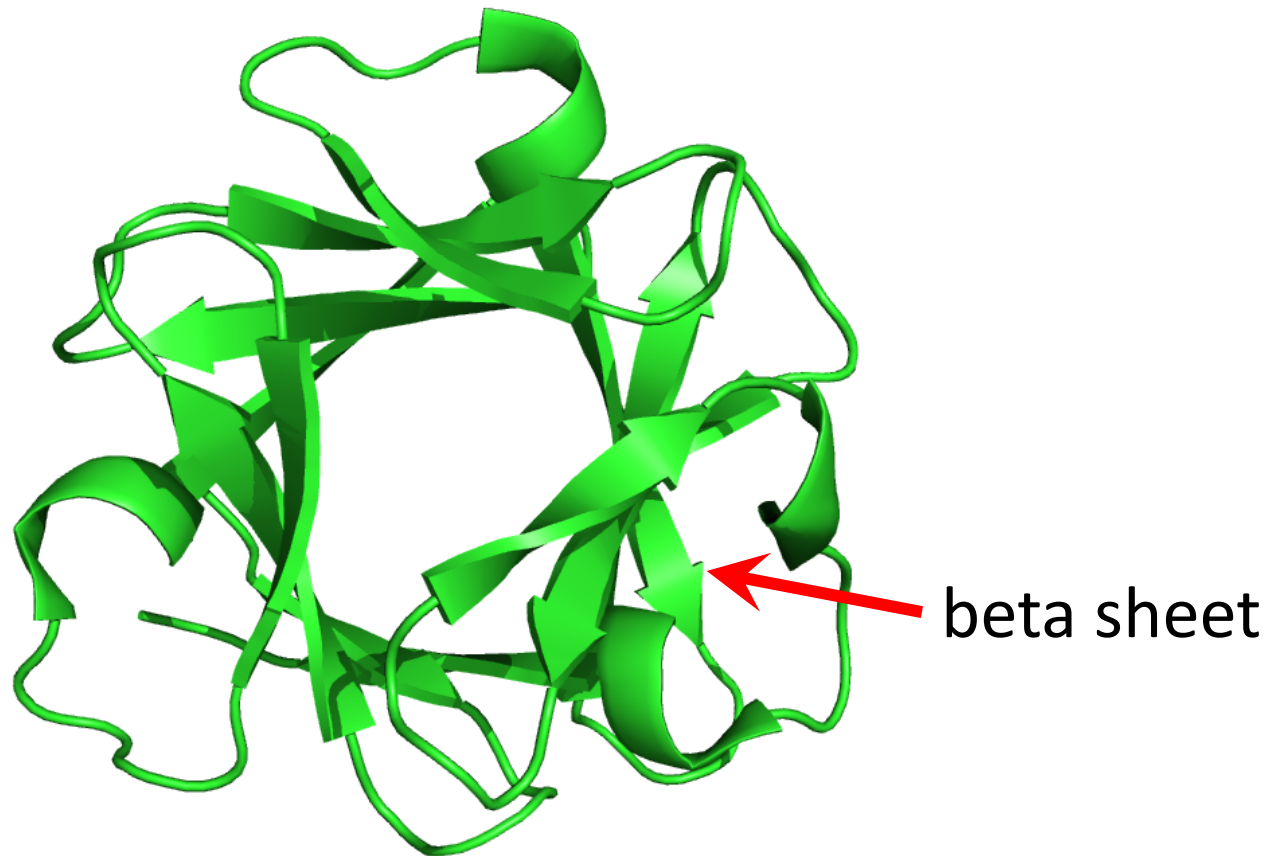


alpha and beta

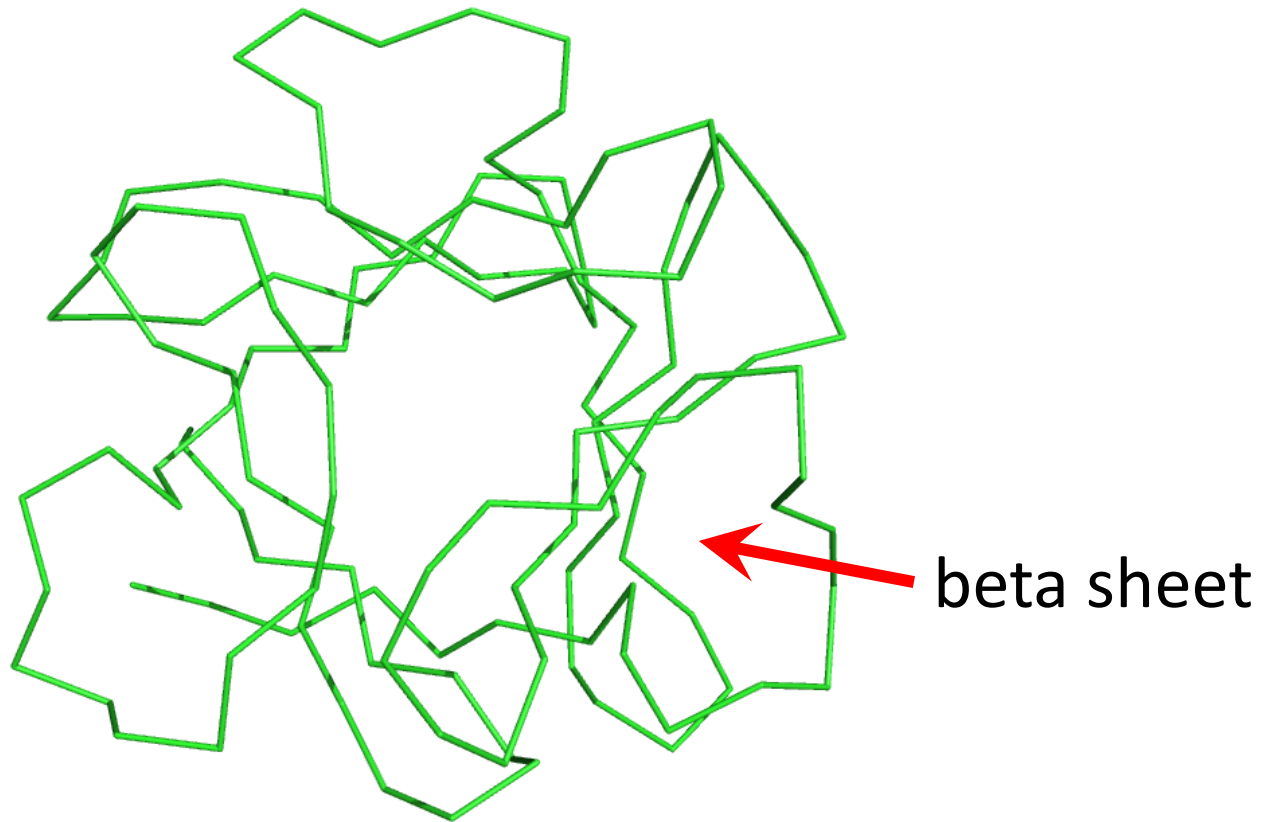


Different visualizations of a structure:

Cartoon

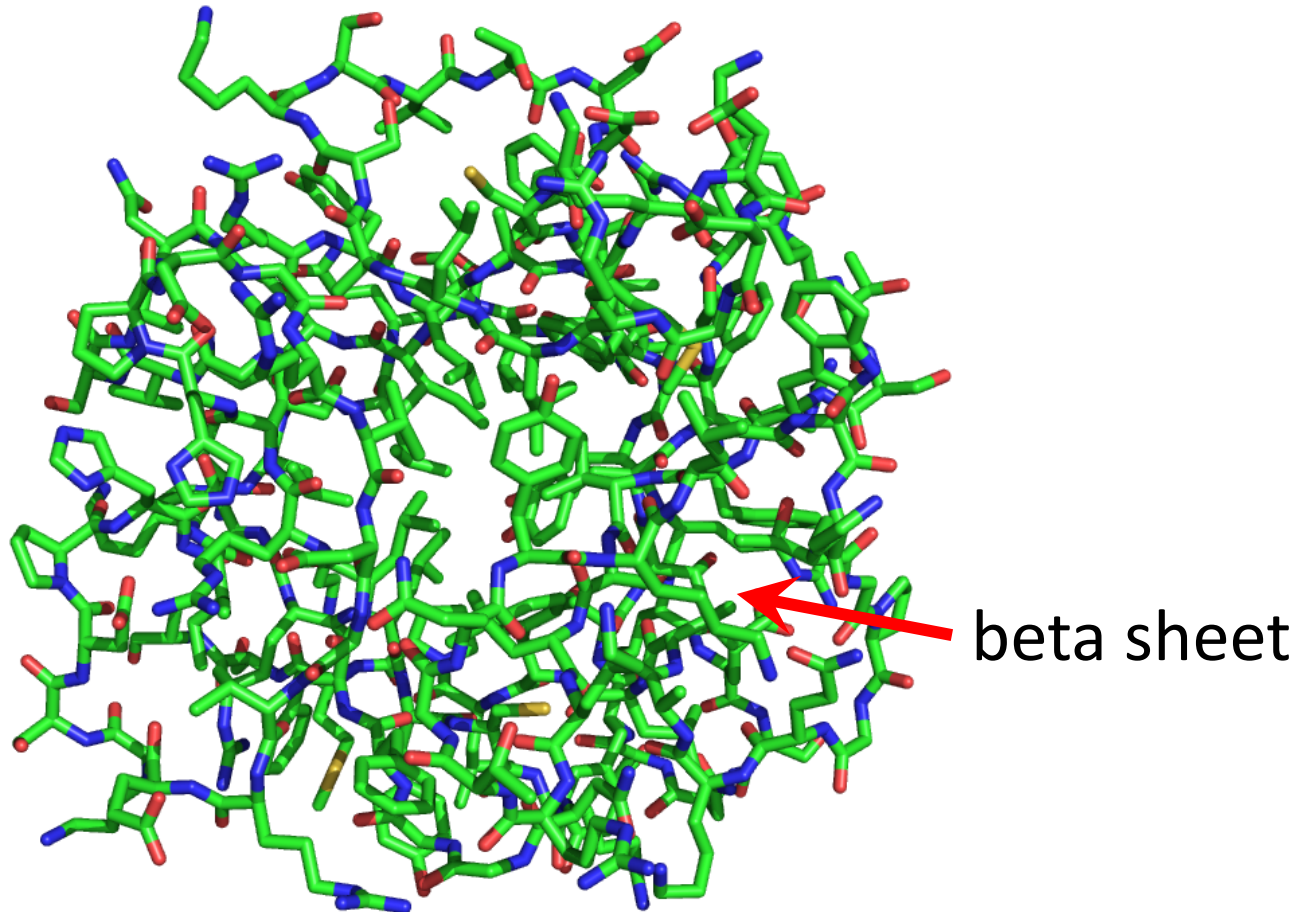


Different visualizations of a structure: Ribbon



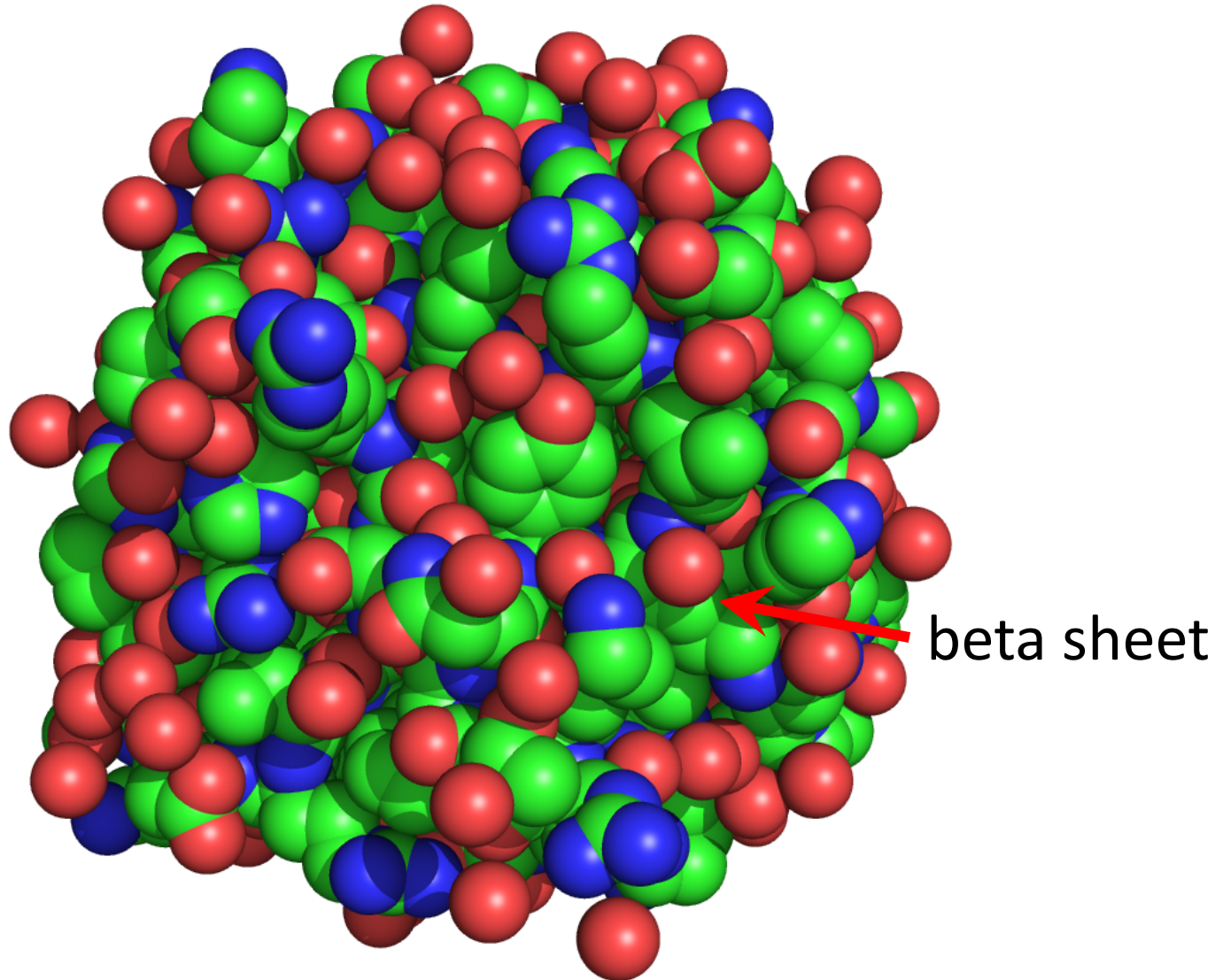
Different visualizations of a structure:

Sticks

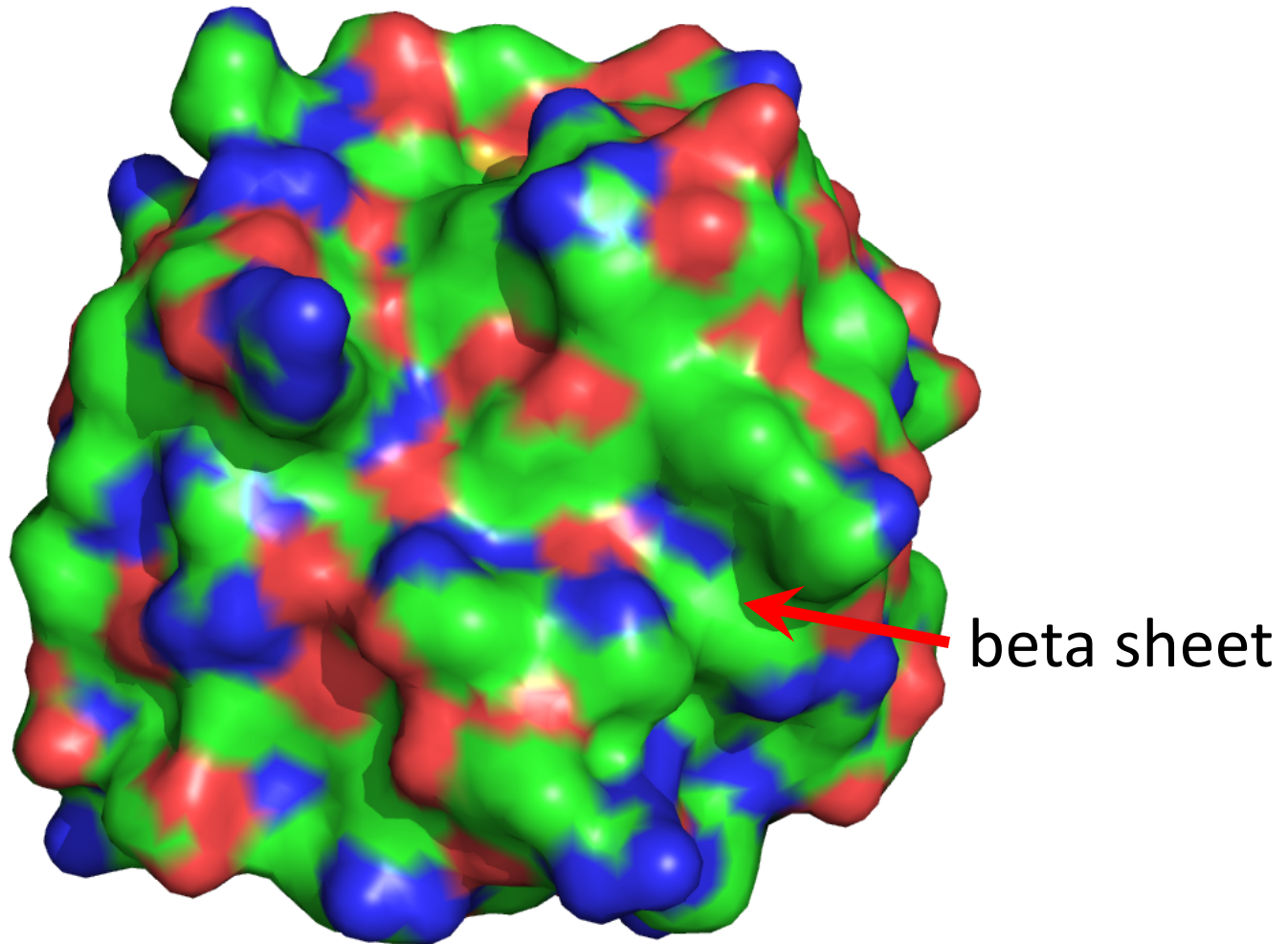


Different visualizations of a structure:

Spheres

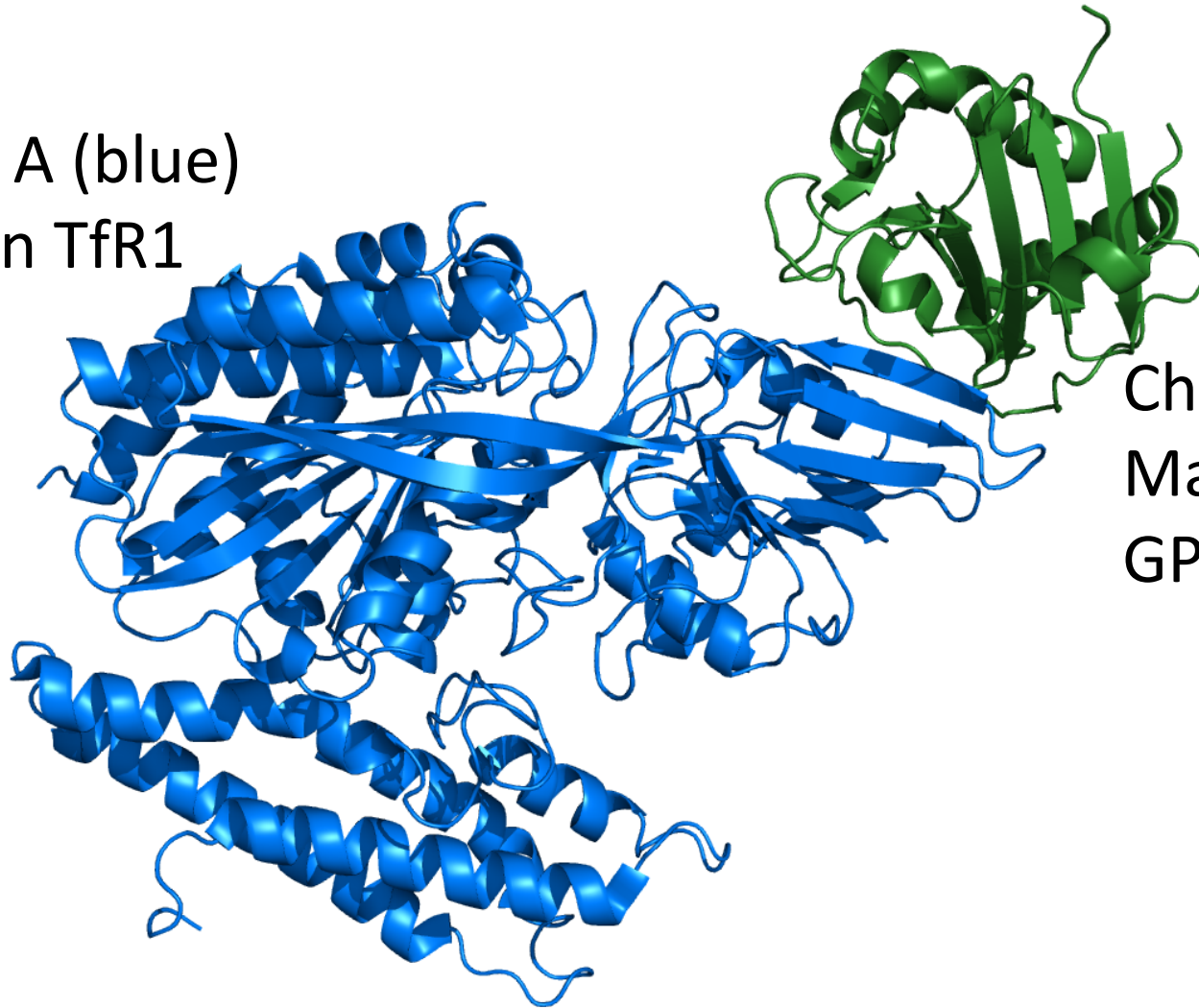


Different visualizations of a structure: Surface



PDB files can contain multiple chains

Chain A (blue)
human TfR1



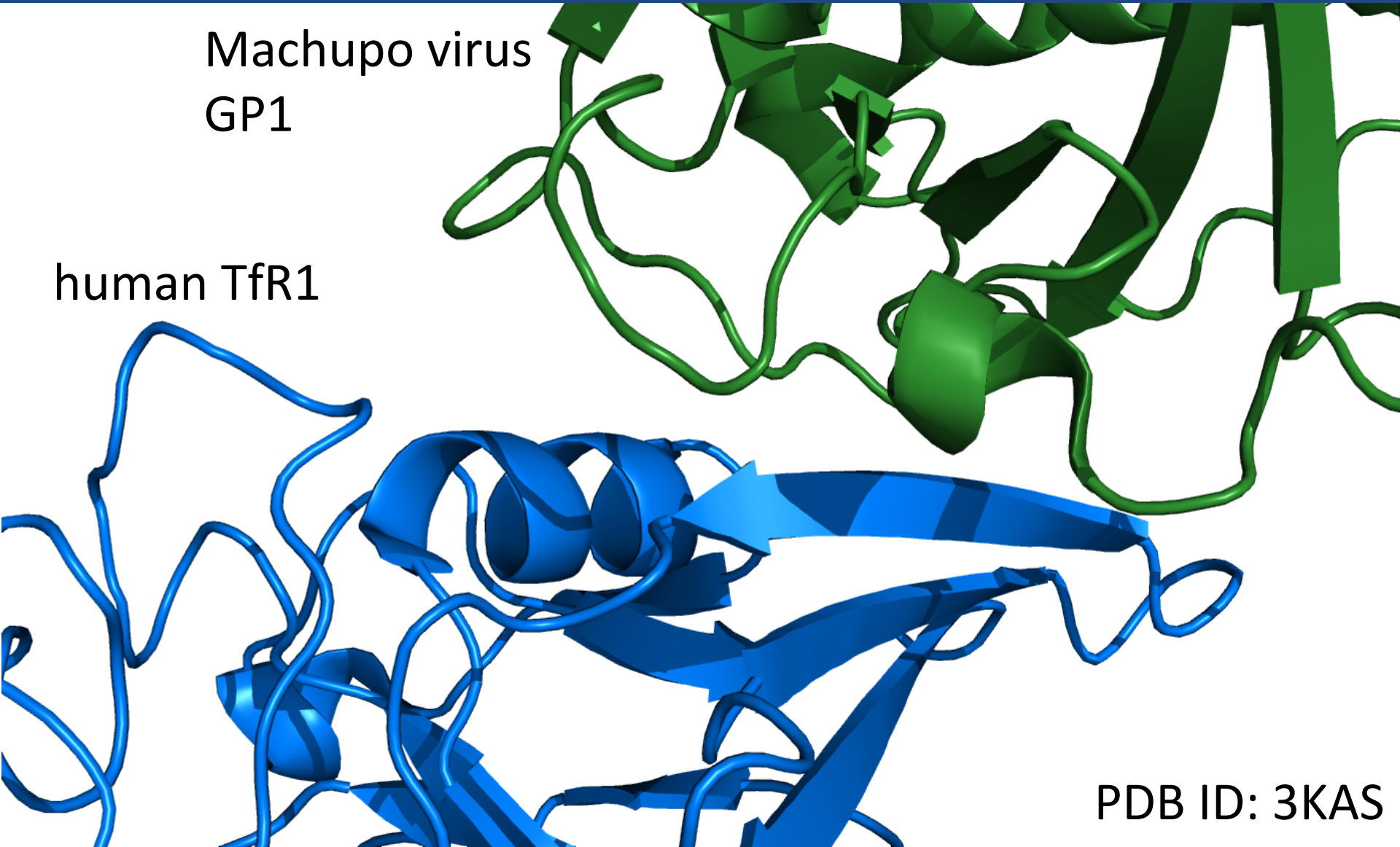
Chain B (green)
Machupo virus
GP1

PDB ID: 3KAS

PDB files can contain multiple chains

Machupo virus
GP1

human TfR1



PDB ID: 3KAS

Anatomy of a PDB file

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HEADER      GROWTH FACTOR                      15-APR-93    1BFG
TITLE       CRYSTAL STRUCTURE OF BASIC FIBROBLAST GROWTH FACTOR AT 1.6
TITLE       2  ANGSTROMS RESOLUTION
COMPND      MOL_ID: 1;
COMPND      2  MOLECULE: BASIC FIBROBLAST GROWTH FACTOR;
COMPND      3  CHAIN: A;
COMPND      4  ENGINEERED: YES
SOURCE      MOL_ID: 1;
SOURCE      2  ORGANISM_SCIENTIFIC: HOMO SAPIENS;
SOURCE      3  ORGANISM_COMMON: HUMAN;
SOURCE      4  ORGANISM_TAXID: 9606
KEYWDS      GROWTH FACTOR
EXPDTA      X-RAY DIFFRACTION
AUTHOR      Y.KITAGAWA,H.AGO,Y.KATSUBE,A.FUJISHIMA,Y.MATSUURA
REVDAT      3    24-FEB-09 1BFG      1          VERSN
REVDAT      2    01-APR-03 1BFG      1          JRNL
REVDAT      1    31-JAN-94 1BFG      0
JRNL        AUTH    H.AGO,Y.KITAGAWA,A.FUJISHIMA,Y.MATSUURA,Y.KATSUBE
JRNL        TITL    CRYSTAL STRUCTURE OF BASIC FIBROBLAST GROWTH
JRNL        TITL    2  FACTOR AT 1.6 A RESOLUTION.
JRNL        REF     J.BIOCHEM.(TOKYO)                      V. 110    360 1991
JRNL        REFN                                ISSN 0021-924X
JRNL        PMID    1769963
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Anatomy of a PDB file

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HEADER      GROWTH FACTOR                      15-APR-93      1BFG
TITLE       CRYSTAL STRUCTURE OF BASIC FIBROBLAST GROWTH FACTOR AT 1.6
TITLE       2  ANGSTROMS RESOLUTION
COMPND      MOL_ID: 1;
COMPND      2  MOLECULE: BASIC FIBROBLAST GROWTH FACTOR;
COMPND      3  CHAIN: A;
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SOURCE      2  ORGANISM_SCIENTIFIC: HOMO SAPIENS;
SOURCE      3  ORGANISM_COMMON: HUMAN;
SOURCE      4  ORGANISM_TAXID: 9606
KEYWDS      GROWTH FACTOR
EXPDTA      X-RAY DIFFRACTION
AUTHOR      Y.KITAGAWA,H.AGO,Y.KATSUBE,A.FUJISHIMA,Y.MATSUURA
REVDAT      3   24-FEB-09 1BFG      1      VERSN
REVDAT      2   01-APR-03 1BFG      1      JRNL
REVDAT      1   31-JAN-94 1BFG      0
JRNL        AUTH    H.AGO,Y.KITAGAWA,A.FUJISHIMA,Y.MATSUURA,Y.KATSUBE
JRNL        TITL    CRYSTAL STRUCTURE OF BASIC FIBROBLAST GROWTH
JRNL        TITL    2  FACTOR AT 1.6 A RESOLUTION.
JRNL        REF     J.BIOCHEM.(TOKYO)                      V. 110    360 1991
JRNL        REFN                                ISSN 0021-924X
JRNL        PMID    1769963
...
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Anatomy of a PDB file

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TITLE       2 ANGSTROMS RESOLUTION
COMPND      MOL_ID: 1;
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COMPND      3 CHAIN: A;
COMPND      4 ENGINEERED: YES
SOURCE      MOL_ID: 1;
SOURCE      2 ORGANISM_SCIENTIFIC: HOMO SAPIENS;
SOURCE      3 ORGANISM_COMMON: HUMAN;
SOURCE      4 ORGANISM_TAXID: 9606
KEYWDS      GROWTH FACTOR
EXPDTA      X-RAY DIFFRACTION
AUTHOR      Y.KITAGAWA,H.AGO,Y.KATSUBE,A.FUJISHIMA,Y.MATSUURA
REVDAT      3   24-FEB-09 1BFG      1      VERSN
REVDAT      2   01-APR-03 1BFG      1      JRNL
REVDAT      1   31-JAN-94 1BFG      0
JRNL        AUTH    H.AGO,Y.KITAGAWA,A.FUJISHIMA,Y.MATSUURA,Y.KATSUBE
JRNL        TITL    CRYSTAL STRUCTURE OF BASIC FIBROBLAST GROWTH
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JRNL        REF     J.BIOCHEM.(TOKYO)                      V. 110    360 1991
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Anatomy of a PDB file

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TITLE       2 ANGSTROMS RESOLUTION
COMPND      MOL_ID: 1;
COMPND      2 MOLECULE: BASIC FIBROBLAST GROWTH FACTOR;
COMPND      3 CHAIN: A;
COMPND      4 ENGINEERED: YES
SOURCE      MOL_ID: 1;
SOURCE      2 ORGANISM_SCIENTIFIC: HOMO SAPIENS;
SOURCE      3 ORGANISM_COMMON: HUMAN;
SOURCE      4 ORGANISM_TAXID: 9606
KEYWDS      GROWTH FACTOR
EXPDTA      X-RAY DIFFRACTION
AUTHOR      Y.KITAGAWA,H.AGO,Y.KATSUBE,A.FUJISHIMA,Y.MATSUURA
REVDAT      3    24-FEB-09 1BFG    1    VERSN
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JRNL        TITL 2  FACTOR AT 1.6 A RESOLUTION.
JRNL        REF     J.BIOCHEM.(TOKYO)                                V. 110    360 1991
JRNL        REFN                                ISSN 0021-924X
JRNL        PMID    1769963
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Anatomy of a PDB file

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ATOM      3  C   ASP A  19      7.688  14.002 -0.016  1.00 36.01      C  
ATOM      4  O   ASP A  19      8.837  14.477  0.052  1.00 35.96      O  
ATOM      5  CB  ASP A  19      5.372  14.834 -0.851  1.00 43.28      C  
ATOM      6  CG  ASP A  19      5.264  16.239 -0.268  1.00 46.36      C  
ATOM      7  OD1 ASP A  19      5.447  16.322  0.978  1.00 48.00      O  
ATOM      8  OD2 ASP A  19      5.015  17.239 -0.970  1.00 48.45      O  
ATOM      9  N   PRO A  20      7.165  13.125  0.822  1.00 33.63      N  
ATOM     10  CA  PRO A  20      7.888  12.572  1.982  1.00 30.69      C  
ATOM     11  C   PRO A  20      9.049  11.697  1.528  1.00 27.78      C  
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Anatomy of a PDB file

atom number



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ATOM     11  C   PRO A  20      9.049   11.697   1.528   1.00  27.78      C  
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Anatomy of a PDB file

atom name



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ATOM      1  N    ASP A  19      6.864   13.397  -2.220   1.00  40.02      N  
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ATOM      4  O    ASP A  19      8.837   14.477   0.052   1.00  35.96      O  
ATOM      5  CB   ASP A  19      5.372   14.834  -0.851   1.00  43.28      C  
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Anatomy of a PDB file

residue name



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ATOM      3  C   ASP A  19      7.688   14.002  -0.016   1.00  36.01      C  
ATOM      4  O   ASP A  19      8.837   14.477   0.052   1.00  35.96      O  
ATOM      5  CB  ASP A  19      5.372   14.834  -0.851   1.00  43.28      C  
ATOM      6  CG  ASP A  19      5.264   16.239  -0.268   1.00  46.36      C  
ATOM      7  OD1 ASP A  19      5.447   16.322   0.978   1.00  48.00      O  
ATOM      8  OD2 ASP A  19      5.015   17.239  -0.970   1.00  48.45      O  
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Anatomy of a PDB file

chain



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ATOM      4  O   ASP A  19      8.837   14.477   0.052   1.00  35.96      O  
ATOM      5  CB  ASP A  19      5.372   14.834  -0.851   1.00  43.28      C  
ATOM      6  CG  ASP A  19      5.264   16.239  -0.268   1.00  46.36      C  
ATOM      7  OD1 ASP A  19      5.447   16.322   0.978   1.00  48.00      O  
ATOM      8  OD2 ASP A  19      5.015   17.239  -0.970   1.00  48.45      O  
ATOM      9  N   PRO A  20      7.165   13.125   0.822   1.00  33.63      N  
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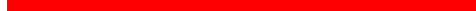

Anatomy of a PDB file

residue number



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ATOM      3  C   ASP A  19      7.688   14.002  -0.016   1.00  36.01      C  
ATOM      4  O   ASP A  19      8.837   14.477   0.052   1.00  35.96      O  
ATOM      5  CB  ASP A  19      5.372   14.834  -0.851   1.00  43.28      C  
ATOM      6  CG  ASP A  19      5.264   16.239  -0.268   1.00  46.36      C  
ATOM      7  OD1 ASP A  19      5.447   16.322   0.978   1.00  48.00      O  
ATOM      8  OD2 ASP A  19      5.015   17.239  -0.970   1.00  48.45      O  
ATOM      9  N   PRO A  20      7.165   13.125   0.822   1.00  33.63      N  
ATOM     10  CA  PRO A  20      7.888   12.572   1.982   1.00  30.69      C  
ATOM     11  C   PRO A  20      9.049   11.697   1.528   1.00  27.78      C  
...
```

x, y, z coordinates



...											...
ATOM	1	N	ASP	A	19	6.864	13.397	-2.220	1.00	40.02	N
ATOM	2	CA	ASP	A	19	6.806	14.455	-1.186	1.00	38.62	C
ATOM	3	C	ASP	A	19	7.688	14.002	-0.016	1.00	36.01	C
ATOM	4	O	ASP	A	19	8.837	14.477	0.052	1.00	35.96	O
ATOM	5	CB	ASP	A	19	5.372	14.834	-0.851	1.00	43.28	C
ATOM	6	CG	ASP	A	19	5.264	16.239	-0.268	1.00	46.36	C
ATOM	7	OD1	ASP	A	19	5.447	16.322	0.978	1.00	48.00	O
ATOM	8	OD2	ASP	A	19	5.015	17.239	-0.970	1.00	48.45	O
ATOM	9	N	PRO	A	20	7.165	13.125	0.822	1.00	33.63	N
ATOM	10	CA	PRO	A	20	7.888	12.572	1.982	1.00	30.69	C
ATOM	11	C	PRO	A	20	9.049	11.697	1.528	1.00	27.78	C
...											...

Anatomy of a PDB file

occupancy



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ATOM      4  O   ASP A  19      8.837   14.477   0.052   1.00  35.96      O  
ATOM      5  CB  ASP A  19      5.372   14.834  -0.851   1.00  43.28      C  
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ATOM      8  OD2 ASP A  19      5.015   17.239  -0.970   1.00  48.45      O  
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ATOM     11  C   PRO A  20      9.049   11.697   1.528   1.00  27.78      C  
...
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Anatomy of a PDB file

B factor



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ATOM      4  O   ASP A  19      8.837  14.477  0.052  1.00 35.96      O  
ATOM      5  CB  ASP A  19      5.372  14.834 -0.851  1.00 43.28      C  
ATOM      6  CG  ASP A  19      5.264  16.239 -0.268  1.00 46.36      C  
ATOM      7  OD1 ASP A  19      5.447  16.322  0.978  1.00 48.00      O  
ATOM      8  OD2 ASP A  19      5.015  17.239 -0.970  1.00 48.45      O  
ATOM      9  N   PRO A  20      7.165  13.125  0.822  1.00 33.63      N  
ATOM     10  CA  PRO A  20      7.888  12.572  1.982  1.00 30.69      C  
ATOM     11  C   PRO A  20      9.049  11.697  1.528  1.00 27.78      C  
...
```

PyMOL exercises

1. Download & open structure 3KAS:
`fetch 3KAS`
 - Display in various forms (cartoon, stick, spheres, ...)
 - Color different chains
 - Zoom in to display protein-protein interface
2. Download & open structure 1DLW
 - Display as cartoon
 - Show heme as sticks