149174 Biological
Macromolecular Structures
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Refinements

ORGANISM

Homo sapiens (1266)
Mus musculus (310)
Arabidopsis thaliana (30)
Escherichia coli (26)
Plasmodium falciparum (16)
Rattus norvegicus (15)
Thermotoga maritima (14)
Other (278)

UNIPROT MOLECULE NAME

Uncharacterized protein (61)
Zinc finger protein ZFAT (30)
Zinc finger protein 268 (23)
Major prion protein (23)
Filamin-B (17)
Zinc finger protein 347 (16)
Zinc finger protein 224 (16)
Refine Query

TAXONOMY

Eukaryota (1714)
Bacteria (168)
Viruses (51)
Archaea (14)
Other (13)
Unassigned (1)

EXPERIMENTAL METHOD

Solution NMR (1633)
X-ray (292)
Electron Microscopy (9)
Solid-State NMR (5)
Hybrid (1)

X-RAY RESOLUTION

less than 1.5 Å (12)
1.5 - 2.0 Å (83)
2.0 - 2.5 Å (117)
2.5 - 3.0 Å (60)
3.0 and more Å (20)
Refine Query

RELEASE DATE

before 2000 (7)
2000 - 2005 (270)
2005 - 2010 (1175)
2010 - 2015 (263)
2015 - today (225)
this year (4)
this month (2)
Refine Query

Currently showing1 - 25 of 1940 Page: 1 of 78 ← Previous Next → Displaying 25 R

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3D View

6G99

Solution structure of FUS-ZnF bound to UGGUG

Loughlin, F.E., Lukavsky, P.J., Kazeeva, T., Reber, S., Hock, E.M., Colombo, M., Vo
O., Polymenidou, M., Ruepp, M.D., Allain, F.H.-T.

(2019) Mol Cell **73** 490-504.e6

Released: 2/20/2019
Method: Solution NMR
Residue Count: 46

Macromo
RNA-binc
Unique L

3D View

6GBM

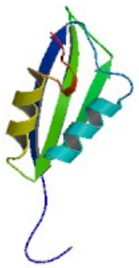
Solution structure of FUS-RRM bound to stem-loop RNA

Loughlin, F.E., Lukavsky, P.J., Kazeeva, T., Reber, S., Hock, E.M., Colombo, M., Vo
O., Polymenidou, M., Ruepp, M.D., Allain, F.H.-T.

(2019) Mol Cell **73** 490-504.e6

Released: 2/20/2019
Method: Solution NMR
Residue Count: 125

Macromo
RNA-binc
Unique L



3D View

6FBL

NMR Solution Structure of MINA-1(254-334)

Sendoel, A., Subasic, D., Ducoli, L., Keller, M., Michel, E., Kohler, I., Singh, K.D., Z
Y., Kanitz, A., Kaech, A., Mittal, N., Matia-Gonzalez, A.M., Gerber, A.P., Zavolan, M.
M.O.

(2019) Cell Death Differ

Released: 1/30/2019
Method: Solution NMR
Residue Count: 86

Macromo
MINA-1 (
Unique L

POLYMER TYPE

Protein (1917)
Mixed (23)

ENZYME CLASSIFICATION

2: Transferases (229)
3: Hydrolases (143)
1: Oxidoreductases (46)
5: Isomerases (20)
6: Ligases (10)
4: Lyases (4)
7: Translocases (2)

SCOP CLASSIFICATION

All beta proteins (182)
Alpha and beta proteins (... (176)
All alpha proteins (126)
Small proteins (103)
Designed proteins (100)
Alpha and beta proteins (... (30)
Multi-domain proteins (al ... (6)
Other (1)

PROTEIN SYMMETRY

Asymmetric (1827)
Cyclic (91)
Dihedral (12)
Icosahedral (2)
Refine Query

PROTEIN STOICHIOMETRY

Monomer (1756)
Homomer (92)
Heteromer (84)
Refine Query

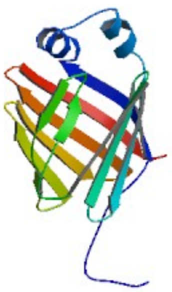
MEMBRANE PROTEINS

MONOTOPIC MEMBRANE PROTEINS (6)
ALPHA-HELICAL (3)

REPRESENTATIVE STRUCTURES

100%
95%
90%
70%
50%
40%
30%

Query Details



3D View

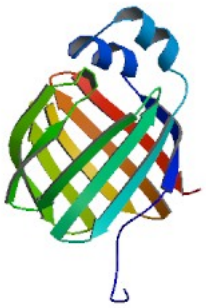
6DO7

NMR solution structure of wild type hFABP1 with GW7647

Patil, R., Mohanty, B., Liu, B., Chandrashekaran, I.R., Headey, S.J., Williams, M.L., Genissel, P., Weaver, R.J., Vuillard, L., Halls, M.L., Porter, C.J.H., Scanlon, M.J.

(2018) J Biol Chem

Released: 1/2/2019 **Macromc**
Method: Solution NMR Fatty acic
Residue Count: 135 **Unique L**



3D View

6DO6

NMR solution structure of wild type apo hFABP1 at 308 K

Patil, R., Mohanty, B., Liu, B., Chandrashekaran, I.R., Headey, S.J., Williams, M.L., Genissel, P., Weaver, R.J., Vuillard, L., Halls, M.L., Porter, C.J.H., Scanlon, M.J.

(2018) J Biol Chem

Released: 12/26/2018 **Macromc**
Method: Solution NMR Fatty acic
Residue Count: 135 **Unique L**

3D View

6GT7

NMR structure of the free helix bundle domain from the functiona

Boudet, J., Devillier, J.C., Wiegand, T., Salmon, L., Meier, B.H., Lipps, G., Allain, F.H

Released: 12/26/2018 **Macromc**
Method: Solution NMR functional
Residue Count: 115 **Unique L**

3D View

6GVQ

DNA-bound pRN1 helix bundle domain with ATP and magnesium

Boudet, J., Devillier, J.C., Wiegand, T., Salmon, L., Meier, B.H., Lipps, G., Allain, F.H

Released: 12/26/2018 **Macromc**
Method: Solution NMR functional
Residue Count: 124 **Unique L**

3D View

6GVT

Hybrid structure of the pRN1 helix bundle domain in complex witl

Boudet, J., Devillier, J.C., Wiegand, T., Salmon, L., Meier, B.H., Lipps, G., Allain, F.H

Released: 12/26/2018 **Macromc**
Method: Solid-State NMR,Solution NMR functional
Residue Count: 124 **Unique L**

3D View

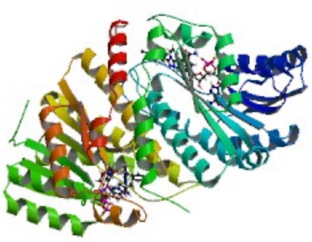
6GVU

NMR structure of the DNA-bound helix bundle domain from the fu

Boudet, J., **Devillier, J.C.**, **Wiegand, T.**, **Salmon, L.**, **Meier, B.H.**, **Lipps, G.**, **Allain, F.H**

Released: 12/26/2018
Method: Solution NMR
Residue Count: 124

Macromo
functional
Unique L



3D View

5QII

CRYSTAL STRUCTURE OF 11BETA-HSD1 DOUBLE MUTANT (L26 (1-(4-CHLOROPHENYL)CYCLOPROPYL) -[1,2,4]TRIAZOLO[4,3-A]

Li, J., **Kennedy, L.J.**, **Walker, S.J.**, **Wang, H.**, **Li, J.J.**, **Hong, Z.**, **O'Connor, S.P.**, **Ye, X.** **Camac, D.M.**, **Ramamurthy, V.**, **Morin, P.E.**, **Sheriff, S.**, **Wang, M.**, **Harper, T.W.**, **Goll** **Morgan, N.N.**, **Taylor, J.R.**, **Zebo, R.**, **Maxwell, B.**, **Moulin, F.**, **Gordon, D.A.**, **Robl, J.**

(2018) ACS Med Chem Lett **9** 1170-1174

Released: 12/19/2018
Method: X-ray Diffraction
Resolution: 2.45 Å
Residue Count: 1144

Macromo
Corticoste
Unique L

3D View

5QIJ

CRYSTAL STRUCTURE OF MURINE 11B- HYDROXYSTEROIDDE (3-(1-(4- CHLOROPHENYL)CYCLOPROPYL)-[1,2,4]TRIAZOLO[4,3

Li, J., **Kennedy, L.J.**, **Walker, S.J.**, **Wang, H.**, **Li, J.J.**, **Hong, Z.**, **O'Connor, S.P.**, **Ye, X.** **Camac, D.M.**, **Ramamurthy, V.**, **Morin, P.E.**, **Sheriff, S.**, **Wang, M.**, **Harper, T.W.**, **Goll** **Morgan, N.N.**, **Taylor, J.R.**, **Zebo, R.**, **Maxwell, B.**, **Moulin, F.**, **Gordon, D.A.**, **Robl, J.**

(2018) ACS Med Chem Lett **9** 1170-1174

Released: 12/19/2018
Method: X-ray Diffraction
Resolution: 2.65 Å
Residue Count: 552

Macromo
Corticoste
Unique L

3D View

6E0B

Plasmodium falciparum dihydroorotate dehydrogenase C276F mu based inhibitor DSM1

White, J., **Dhingra, S.**, **Deng, X.**, **El Mazouni, F.**, **Lee, M.**, **Afanador, G.**, **Lawong, A.**, **Fidock, D.A.**, **Phillips, M.A.**

(2018) ACS Infect Dis

Released: 11/14/2018
Method: X-ray Diffraction
Resolution: 2.1 Å
Residue Count: 401

Macromo
Dihydroor
Unique L

3D View

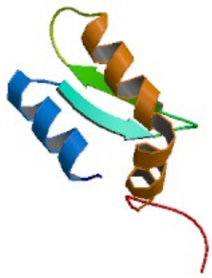
6CE5

NMR structure of the Rous sarcoma virus matrix protein (M-doma hexakisphosphate

Vlach, J., **Eastep, G.N.**, **Ghanam, R.H.**, **Watanabe, S.M.**, **Carter, C.A.**, **Saad, J.S.**(201

Released: 11/7/2018
Method: Solution NMR
Residue Count: 87

Macromo
virus matr
Unique L



3D View

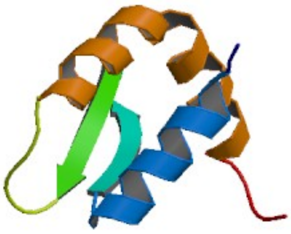
6EWS

Solution Structure of Rhabdopeptide NRPS Docking Domain Kj12

Hacker, C., **Cai, X.**, **Kegler, C.**, **Zhao, L.**, **Weickhmann, A.K.**, **Wurm, J.P.**, **Bode, H.B.**

Released: 10/31/2018
Method: Solution NMR
Residue Count: 63

Macromo
NRPS Kj1
Unique L



3D View

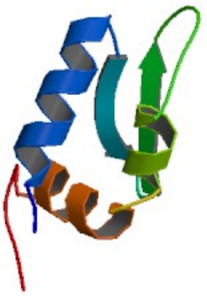
6EWT

Solution Structure of Rhabdopeptide NRPS Docking Domain Kj12

Hacker, C., **Cai, X.**, **Kegler, C.**, **Zhao, L.**, **Weickhmann, A.K.**, **Wurm, J.P.**, **Bode, H.B.**

Released: 10/31/2018
Method: Solution NMR
Residue Count: 62

Macromo
NRPS Kj1
Unique L



3D View

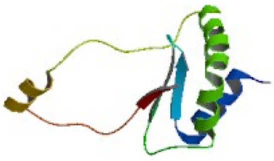
6EWU

Solution Structure of Rhabdopeptide NRPS Docking Domain Kj12

Hacker, C., **Cai, X.**, **Kegler, C.**, **Zhao, L.**, **Weickhmann, A.K.**, **Wurm, J.P.**, **Bode, H.B.**

Released: 10/31/2018
Method: Solid-State NMR
Residue Count: 63

Macromo
NRPS Kj1
Unique L



3D View

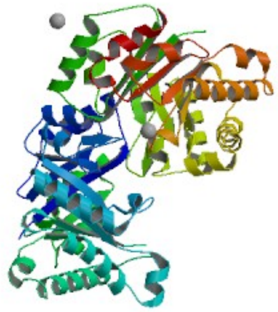
6EWV

Solution Structure of Docking Domain Complex of RXP NRPS: Kj

Hacker, C., **Cai, X.**, **Kegler, C.**, **Zhao, L.**, **Weickhmann, A.K.**, **Wurm, J.P.**, **Bode, H.B.**

Released: 10/31/2018
Method: Solution NMR
Residue Count: 99

Macromo
NRPS Kj1
Unique L



3D View

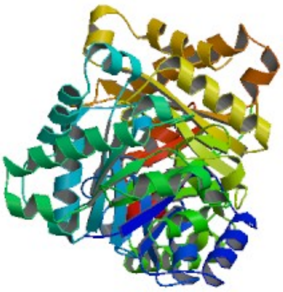
5ZFX

Crystal Structure of Triosephosphate isomerase from Opisthorchi

Son, J., Kim, S., Kim, S.E., Lee, H., Lee, M.R., Hwang, K.Y.(2018) Sci Rep **8** 15075-1

Released: 10/24/2018
Method: X-ray Diffraction
Resolution: 1.75 Å
Residue Count: 1088

Macromo
Triosepho
Unique L



3D View

5ZG4

Crystal Structure of Triosephosphate isomerase SAD deletion mu

Son, J., Kim, S., Kim, S.E., Lee, H., Lee, M.R., Hwang, K.Y.(2018) Sci Rep **8** 15075-1

Released: 10/24/2018
Method: X-ray Diffraction
Resolution: 1.75 Å
Residue Count: 1076

Macromo
Triosepho
Unique L

3D View

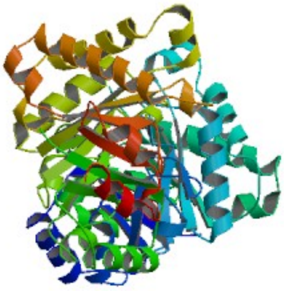
5ZG5

Crystal Structure of Triosephosphate isomerase SADsubAAA mut

Son, J., Kim, S., Kim, S.E., Lee, H., Lee, M.R., Hwang, K.Y.(2018) Sci Rep **8** 15075-1

Released: 10/24/2018
Method: X-ray Diffraction
Resolution: 1.6 Å
Residue Count: 544

Macromo
Triosepho
Unique L



3D View

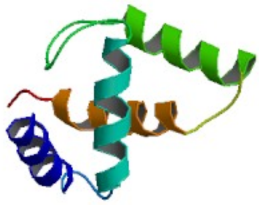
5ZGA

Crystal Structure of Triosephosphate isomerase SAD deletion anc viverrini

Son, J., Kim, S., Kim, S.E., Lee, H., Lee, M.R., Hwang, K.Y.(2018) Sci Rep **8** 15075-1

Released: 10/24/2018
Method: X-ray Diffraction
Resolution: 1.79 Å
Residue Count: 1076

Macromo
Triosepho
Unique L



6CCJ

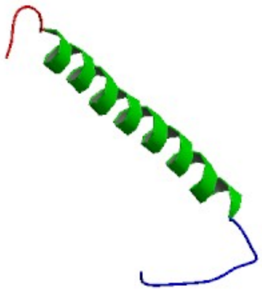
NMR structure of the Rous sarcoma virus matrix protein (M doma

Vlach, J., Eastep, G.N., Ghanam, R.H., Watanabe, S.M., Carter, C.A., Saad, J.S.(201

Released: 10/24/2018
Method: Solution NMR
Residue Count: 87

Macromo
virus matı
Unique L

3D View



3D View

5ZAZ

Solution structure of integrin b2 monomer tranmembrane domain

Guo, J., **Zhang, Y.**, **Li, H.**, **Chu, H.**, **Wang, Q.**, **Jiang, S.**, **Li, Y.**, **Shen, H.**, **Li, G.**, **Chen,**

Released: 10/17/2018
Method: Solution NMR
Residue Count: 52

Macrom
Integrin b
Unique L

3D View

6H5N

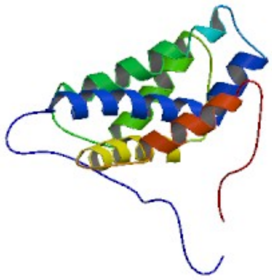
Plasmodium falciparum Pfs48/45 C-terminal domain bound to m

Lennartz, F., **Brod, F.**, **Dabbs, R.**, **Miura, K.**, **Mekhaiel, D.**, **Marini, A.**, **Jore, M.M.**, **So**
Sauerwein, R.W., **Long, C.A.**, **Biswas, S.**, **Higgins, M.K.**

(2018) Nat Commun **9** 3822-3822

Released: 9/26/2018
Method: X-ray Diffraction
Resolution: 3.23 Å
Residue Count: 1136

Macrom
Gametoc
Unique L



3D View

6G03

NMR Solution Structure of yeast TSR2(1-152)

Schuetz, S., **Michel, E.**, **Damberger, F.F.**, **Oplova, M.**, **Pena, C.**, **Leitner, A.**, **Aebersol**

(2018) Nat Commun **9** 3669-3669

Released: 9/19/2018
Method: Solution NMR
Residue Count: 156

Macrom
Pre-rRNA
Unique L

← Previous Next →

The RCSB PDB is funded by a grant (DBI-1338415) from the National Science Foundation, the National Institutes of Health, and the US Department of Energy.