

Journal articles with JD as (co-)author

2011

The structure of the NPC1L1 N-terminal domain in a closed conformation.
Kwon HJ, Palnitkar M, Deisenhofer J, *PLoS One* 2011 6 4 e18722

2010

Crystal structure of Spot 14, a modulator of fatty acid synthesis.
Colbert CL, Kim CW, Moon YA, Henry L, Palnitkar M, Mckean WB, Fitzgerald K, Deisenhofer J, Horton JD, Kwon HJ, *Proc. Natl. Acad. Sci. U.S.A.* 2010 107 44 18820-25

A heterodimeric complex of the LRR proteins LRIM1 and APL1C regulates complement-like immunity in *Anopheles gambiae*.
Baxter RH, Steinert S, Chelliah Y, Volohonsky G, Levashina EA, Deisenhofer J, *Proc. Natl. Acad. Sci. U.S.A.* 2010 107 39 16817-22

Model of human low-density lipoprotein and bound receptor based on CryoEM.
Ren G, Rudenko G, Ludtke SJ, Deisenhofer J, Chiu W, Pownall HJ, *Proc. Natl. Acad. Sci. U.S.A.* 2010 107 3 1059-64

2009

Structure of N-terminal domain of NPC1 reveals distinct subdomains for binding and transfer of cholesterol.
Kwon HJ, Abi-Mosleh L, Wang ML, Deisenhofer J, Goldstein JL, Brown MS, Infante RE, *Cell* 2009 137 7 1213-24

Insights into pilus assembly and secretion from the structure and functional characterization of usher PapC.
Huang Y, Smith BS, Chen LX, Baxter RH, Deisenhofer J, *Proc. Natl. Acad. Sci. U.S.A.* 2009 106 18 7403-07

2008

Molecular basis for LDL receptor recognition by PCSK9.
Kwon HJ, Lagace TA, Mcnutt MC, Horton JD, Deisenhofer J, *Proc. Natl. Acad. Sci. U.S.A.* 2008 105 6 1820-25

2007

Signal transduction pathway of TonB-dependent transporters.
Ferguson AD, Amezcua CA, Halabi NM, Chelliah Y, Rosen MK, Ranganathan R, Deisenhofer J, *Proc. Natl. Acad. Sci. U.S.A.* 2007 104 2 513-18

The peptidoglycan recognition proteins LCa and LCx.
Chang CI, Deisenhofer J, *Cellular and Molecular Life Sciences* 2007 64 11 1395-402

Structural basis for conserved complement factor-like function in the antimalarial protein TEP1.

Baxter RH, Chang CI, Chelliah Y, Blandin S, Levashina EA, Deisenhofer J, *Proc. Natl. Acad. Sci. U.S.A.* 2007 104 28 11615-20

2006

NMR structures of the selenoproteins Sep15 and SelM reveal redox activity of new thioredoxin-like family.

Ferguson AD, Labunskyy VM, Fomenko DE, Arac D, Chelliah Y, Amezcua CA, Rizo J, Gladyshev VN, Deisenhofer J, *J. Biol. Chem.* 2006 281 6 3536-43

Structure of tracheal cytotoxin in complex with a heterodimeric pattern-recognition receptor.

Chang CI, Chelliah Y, Borek D, Mengin-Lecreulx D, Deisenhofer J, *Science* 2006 311 5768 1761-64

Mechanism of substrate specificity in *Bacillus subtilis* ResA, a thioredoxin-like protein involved in cytochrome c maturation.

Colbert CL, Wu Q, Erbel PJ, Gardner KH, Deisenhofer J, *Proc. Natl. Acad. Sci. U.S.A.* 2006 103 12 4410-15

Crystal structure of cryptochrome 3 from *Arabidopsis thaliana* and its implications for photolyase activity.

Huang Y, Baxter R, Smith BS, Partch CL, Colbert CL, Deisenhofer J, *Proc. Natl. Acad. Sci. U.S.A.* 2006 103 47 17701-06

2005

Structure of the ectodomain of *Drosophila* peptidoglycan-recognition protein LCa suggests a molecular mechanism for pattern recognition.

Chang CI, Ihara K, Chelliah Y, Mengin-Lecreulx D, Wakatsuki S, Deisenhofer J, *Proc Natl Acad Sci U S A* 2005 102 29 10279-84

Mechanistic insight into the allosteric activation of a ubiquitin-conjugating enzyme by RING-type ubiquitin ligases.

Ozkan E, Yu H, Deisenhofer J, *Proc. Natl. Acad. Sci. U.S.A.* 2005 102 52 18890-95

2004

Tetramerization and ATP binding by a protein comprising the A, B, and C domains of rat synapsin I.

Brautigam CA, Chelliah Y, Deisenhofer J, *J. Biol. Chem.* 2004 279 12 11948-56

Metal Import through Microbial Membranes.

Ferguson AD, Deisenhofer J, *Cell* 2004 116 1 15-24

A Drosophila Pattern Recognition Receptor Contains a Peptidoglycan Docking Groove and Unusual L,D-Carboxypeptidase Activity.

Chang CI, Pili-Floury SS, Herve M, Parquet C, Chelliah Y, Lemaitre B, Mengin-Lecreulx D, Deisenhofer J, *PLoS Biology* 2004 2 9 1293-302

Structure of the photolyase-like domain of cryptochrome 1 from *Arabidopsis thaliana*.

Brautigam CA, Smith BS, Ma Z, Palnitkar M, Tomchick DR, Machius M, Deisenhofer J, *Proc. Natl. Acad. Sci. U.S.A.* 2004 101 33 12142-47

2003

Ping-pong cross-validation in real space: a method for increasing the phasing power of a partial model without risk of model bias.

Hunt JF, Deisenhofer J, *Acta Cryst.* 2003 D59(3) 214-24

The low-density lipoprotein receptor: ligands, debates and lore.

Rudenko G, Deisenhofer J, *Current Opinion in Structural Biology* 2003 13 6 683-89

'MAD'ly phasing the extracellular domain of the LDL receptor: a medium-sized protein, large tungsten clusters and multiple non-isomorphous crystals.

Rudenko G, Henry L, Vornrhein C, Bricogne G, Deisenhofer J, *Acta Cryst.* 2003 D59(11) 1978-86

2002

TonB-dependent receptors-structural perspectives.

Ferguson AD, Deisenhofer J, *Biochimica et Biophysica Acta* 2002 1565 2 318-32

Structure of the LDL Receptor Extracellular Domain at Endosomal pH.

Rudenko G, Henry L, Henderson K, Ichtchenko K, Brown MS, Goldstein JL, Deisenhofer J, *Science* 2002 298 5602 2353-58

Structure of factor-inhibiting hypoxia-inducible factor 1: An asparaginyl hydroxylase involved in the hypoxic response pathway.

Dann CE, 3rd, Bruick RK, Deisenhofer J, *Proc. Natl. Acad. Sci. U.S.A.* 2002 99 24 15351-56

Nucleotide control of interdomain interactions in the conformational reaction cycle of SecA.

Hunt JF, Weinkauff S, Henry L, Fak JJ, McNicholas P, Oliver DB, Deisenhofer J, *Science* 2002 297 5589 2018-26

Bipartite gating in the outer membrane protein FecA.

Van Der Helm D, Chakraborty R, Ferguson AD, Smith BS, Esser L, Deisenhofer J, *Biochemical Society Transactions* 2002 30 4 708-10

Structural basis of gating by the outer membrane transporter FecA.

Ferguson AD, Chakraborty R, Smith BS, Esser L, Van Der Helm D, Deisenhofer J, *Science* 2002 295 5560 1715-19.

2001

APC2 Cullin Protein and APC11 RING Protein Comprise the Minimal Ubiquitin Ligase Module of the Anaphase-promoting Complex.

Tang Z, Li B, Bharadwaj R, Zhu H, Ozkan E, Hakala K, Deisenhofer J, Yu H, *Molecular Biology of the Cell* 2001 12 12 3839-51.

The plug domain of FepA, a TonB-dependent transport protein from *Escherichia coli*, binds its siderophore in the absence of the transmembrane barrel domain.

Usher KC, Ozkan E, Gardner KH, Deisenhofer J, *Proc. Natl. Acad. Sci. U.S.A.* 2001 98 19 10676-81.

Crystal structures of mitochondrial processing peptidase reveal the mode for specific cleavage of import signal sequences.

Taylor AB, Smith BS, Kitada S, Kojima K, Miyaura H, Otwinowski Z, Ito A, Deisenhofer J, *Structure* 2001 9 615-25

Crystal structure of a T cell receptor valpha11 (av11s5) domain: new canonical forms for the first and second complementarity determining regions.

Machius M, Cianga P, Deisenhofer J, Ward ES, *J. Mol. Biol.* 2001 310 4 689-98.

Structural mechanism for statin inhibition of HMG-CoA reductase.

Istvan ES, Deisenhofer J, *Science* 2001 292 5519 1160-64.

Conformational stabilization and crystallization of the SecA translocation ATPase from *Bacillus subtilis*.

Weinkauff S, Hunt JF, Scheuring J, Henry L, Fak J, Oliver DB, Deisenhofer J, *Acta Cryst.* 2001 D57(4) 559-65.

2000

The structure of the catalytic portion of human HMG-CoA reductase.

Istvan ES, Deisenhofer J, *Biochimica et Biophysica Acta* 2000 1529 1-3 9-18.

DNA photolyases and cryptochromes.

Deisenhofer J, *Mutation Research* 2000 460 3-4 143-49

Crystal structure of the catalytic portion of human HMG-CoA reductase: insights into regulation of activity and catalysis.

Istvan ES, Palnitkar M, Buchanan SK, Deisenhofer J, *EMBO Journal* 2000 19 5 819-30

Crystal structure of Rab geranylgeranyltransferase at 2.0 Å resolution.

Zhang H, Seabra MC, Deisenhofer J, *Structure with Folding & Design* 2000 8 241-51

1999

Crystal structure of the DNA nucleotide excision repair enzyme UvrB from *thermus thermophilus*.

Machius M, Henry L, Palnitkar M, Deisenhofer J, *Proc. Natl. Acad. Sci. U.S.A.* 1999 96 21 11717-22

The structure of the ligand-binding domain of neurexin 1β: Regulation of LNS domain function by alternative splicing.

Rudenko G, Nguyen T, Chelliah Y, Südhof TC, Deisenhofer J, *Cell* 1999 99 93-101

Structure of antimycin A1, a specific electron transfer inhibitor of ubiquinol-cytochrome c oxidoreductase.

Kim H, Esser L, Hossain MB, Xia D, Yu CA, Rizo J, Van Der Helm D, Deisenhofer J, *J. Amer. Chem. Soc.* 1999 121 4902-03

Crystal structure of the outer membrane active transporter FepA from *Escherichia coli*.

Buchanan SK, Smith BS, Venkatramani L, Xia D, Esser L, Palnitkar M, Chakraborty R, Van Der Helm D, Deisenhofer J, *Nature Structural Biology* 1999 6 56-63

Structural basis of multifunctional bovine mitochondrial cytochrome bc1 complex.

Yu CA, Tian H, Zhang L, Deng KP, Shenoy SK, Yu L, Xia D, Kim H, Deisenhofer J, *Journal of Bioenergetics and Biomembranes* 1999 31 3 191-99

1998

A novel electron transfer mechanism suggested by crystallographic studies of mitochondrial cytochrome *bc1* complex.

Xia D, Kim H, Yu CA, Yu L, Kachurin A, Zhang L, Deisenhofer J, *Biochemistry and Cell Biology* 1998 76 673-79

Mechanism of Rab geranylgeranylation: Formation of the catalytic ternary complex.
Anant JS, Desnoyers L, Machius M, Demeler B, Hansen JC, Westover KD, Deisenhofer J, Seabra MC, *Biochemistry* 1998 37 12559-68

Activation of a matrix processing peptidase from the crystalline cytochrome *bc₁* complex of bovine heart mitochondria.

Deng KP, Zhang L, Kachurin AM, Yu L, Xia D, Kim H, Deisenhofer J, Yu CA, *J. Biol. Chem.* 1998 273 20752-57

Crystallization and preliminary X-ray analysis of ferric enterobactin receptor FepA, an integral membrane protein from *Escherichia coli*.

Smith BS, Kobe B, Kurumbail R, Buchanan SK, Venkatramani L, Van Der Helm D, Deisenhofer J, *Acta Cryst* 1998 D54 697-99

Structural basis of functions of the mitochondrial cytochrome *bc₁* complex.

Yu CA, Xia D, Kim H, Deisenhofer J, Zhang L, Kachurin AM, Yu L, *Biochimica et Biophysica Acta: Bio-Energetics* 1998 1365 151-58

Inhibitor binding changes domain mobility in the iron-sulfur protein of the mitochondrial *bc₁* complex from bovine heart.

Kim H, Xia D, Yu CA, Xia J-Z, Kachurin AM, Zhang L, Yu L, Deisenhofer J, *Proc. Natl. Acad. Sci. U.S.A.* 1998 95 8026-33

Synapsin I is structurally similar to ATP-utilizing enzymes.

Esser L, Wang C-R, Hosaka M, Smagula CS, Südhof TC, Deisenhofer J, *EMBO Journal* 1998 17 977-84

1997

Identification, expression, and crystallization of the protease-resistant conserved domain of synapsin I.

Wang C-R, Esser L, Smagula CS, Südhof TC, Deisenhofer J, *Protein Science* 1997 6 2264-67

Photophysics of photosynthesis. Structure and spectroscopy of reaction centers of purple bacteria.

Hoff AJ, Deisenhofer J, *Physics Reports* 1997 287 1-247

Structural adaptations in the specialized bacteriophage T4 co-chaperonin Gp31 expand the size of the Anfinsen cage.

Hunt JF, Van Der Vies SM, Henry L, Deisenhofer J, *Cell* 1997 90 361-71

Crystal structure of the cytochrome *bc₁* complex from bovine heart mitochondria.

Xia D, Yu CA, Kim H, Xian JZ, Kachurin AM, Zhang L, Yu L, Deisenhofer J, *Science* 1997 277 60-66

A connected set algorithm for the identification of spatially contiguous regions in crystallographic envelopes.

Hunt JF, Vellieux FMD, Deisenhofer J, *Acta Cryst* 1997 D53 434-37

1996

Mechanism of ribonuclease inhibition by ribonuclease inhibitor protein based on the crystal structure of its complex with ribonuclease A.

Kobe B, Deisenhofer J, *J. Mol. Biol.* 1996 264 1028-43

The crystal structure of the bifunctional enzyme 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase reveals distinct domain homologies.

Hasemann CA, Istvan ES, Uyeda K, Deisenhofer J, *Structure* 1996 4 1017-29

Crystallization and preliminary structure of beef heart mitochondrial cytochrome-*bc₁* complex.

Yu CA, Xia J-Z, Kachurin AM, Yu L, Xia D, Kim H, Deisenhofer J, *Biochimica et Biophysica Acta* 1996 1275 47-53

Crystal structure of the MHC class Ib molecule H2-M3.

Wang CR, Fischer Lindahl K, Deisenhofer J, *Research in Immunology* 1996 147 313-21

The crystal structure of the GroES co-chaperonin at 2.8 Å resolution.

Hunt JF, Weaver AJ, Landry SJ, Gierasch LM, Deisenhofer J, *Nature* 1996 379 37-45

1995

Crystallization and preliminary X-ray analysis of fructose 6-phosphate, 2-kinase:fructose 2,6-bisphosphatase.

Istvan ES, Hasemann CA, Kurumbail RG, Uyeda K, Deisenhofer J, *Protein Science* 1995 4 2439-41

Nonclassical binding of formylated peptide in crystal structure of the MHC Class Ib molecule H2-M3.

Wang CR, Castaño AR, Peterson PA, Slaughter CA, Fischer Lindahl K, Deisenhofer J, *Cell* 1995 82 655-64

Proteins with leucine-rich repeats.

Kobe B, Deisenhofer J, *Current Opinion in Structural Biology* 1995 5 409-16

Crystal structure of DNA photolyase from *Escherichia coli*.

Park HW, Kim ST, Sancar A, Deisenhofer J, *Science* 1995 268 1866-72

A structural basis of the interactions between leucine-rich repeats and protein ligands.

Kobe B, Deisenhofer J, *Nature* 1995 374 183-86

Crystallographic refinement at 2.3 Å resolution and refined model of the photosynthetic reaction centre from *Rhodospseudomonas viridis*.

Deisenhofer J, Epp O, Sinning I, Michel H, *J. Mol. Biol.* 1995 246 3 429-57

Structure and function of cytochromes P450: a comparative analysis of three crystal structures.

Hasemann CA, Kurumbail RG, Boddupalli SS, Peterson JA, Deisenhofer J, *Structure* 1995 3 41-62

1994

Crystal structure of the receptor-binding domain of adenovirus type 5 fiber protein at 1.7 Å resolution.

Xia D, Henry LJ, Gerard RD, Deisenhofer J, *Structure* 1994 2 1259-70

Crystallization of mitochondrial cytochrome *b-c1* complex from gel with or without reduced pressure.

Yu CA, Xia D, Deisenhofer J, Yu L, *J. Mol. Biol.* 1994 243 802-05

The leucine-rich repeat: a versatile binding motif.

Kobe B, Deisenhofer J, *Trends in Biochemical Sciences* 1994 19 415-21

Characterization of the knob domain of the adenovirus type 5 fiber protein expressed in *Escherichia coli*.

Henry LJ, Xia D, Wilke ME, Deisenhofer J, Gerard RD, *Journal of Virology* 1994 68 5239-46

Complex between bovine ribonuclease A and porcine ribonuclease inhibitor crystallizes in a similar unit cell as free ribonuclease inhibitor.

Kobe B, Ma Z, Deisenhofer J, *J. Mol. Biol.* 1994 241 288-91

Crystal structure and refinement of cytochrome P450_{terp} at 2.3 Å resolution.

Hasemann CA, Ravichandran KG, Peterson JA, Deisenhofer J, *J. Mol. Biol.* 1994 236 1169-85

1993

Crystal structure of porcine ribonuclease inhibitor, a protein with leucine-rich repeats.

Kobe B, Deisenhofer J, *Nature* 1993 366 751-56

Expression, purification, and characterization of recombinant *Drosophila* choline acetyltransferase.

Wu D, Schormann N, Lian W, Deisenhofer J, Hersh LB, *Journal of Neurochemistry* 1993 61 1416-22

Crystal structure of hemoprotein domain of P450_{BM-3}, a prototype for microsomal P450's.

Ravichandran KG, Boddupalli SS, Hasemann CA, Peterson JA, Deisenhofer J, *Science* 1993 261 731-36

Crystallization and preliminary crystallographic analysis of *Escherichia coli* DNA photolyase.

Park HW, Sancar A, Deisenhofer J, *J. Mol. Biol.* 1993 231 1122-25

Crystallization and preliminary X-ray analysis of porcine ribonuclease inhibitor, a protein with leucine-rich repeats.

Kobe B, Deisenhofer J, *J. Mol. Biol.* 1993 231 137-40

1992

Electron microscopy of thin-sectioned three-dimensional crystals of SecA protein from *Escherichia coli*: Structure in projection at 40 Å resolution.

Weaver AJ, McDowell AW, Oliver DB, Deisenhofer J, *Journal of Structural Biology* 1992 109 87-96

Crystallization and preliminary x-ray diffraction analysis of P450_{terp} and the hemoprotein domain of P450_{BM-3}, enzymes belonging to two distinct classes of the cytochrome P450 superfamily.

Boddupalli SS, Hasemann CA, Ravichandran KG, Lu J-Y, Goldsmith EJ, Deisenhofer J, Peterson JA, *Proc. Natl. Acad. Sci. U.S.A.* 1992 89 5567-71

Chromophore-protein interactions and the function of the photosynthetic reaction center: A molecular dynamics study.

Treutlein H, Schulten K, Brünger AT, Karplus M, Deisenhofer J, Michel H, *Proc. Natl. Acad. Sci. U.S.A.* 1992 89 75-79

1989

Detergent structure in crystals of a bacterial photosynthetic reaction centre.

Roth M, Lewit-Bentley A, Michel H, Deisenhofer J, Huber R, Oesterhelt D, *Nature* 1989 340 659-62

Three-dimensional Structure of Photosynthetic Center from Purple Bacteria.

Miki K, Deisenhofer J, Michel H, *PNE* 1989 34 726-40

The photosynthetic reaction centre from the purple bacterium *Rhodospseudomonas viridis*.

Deisenhofer J, Michel H, *Chemica Scripta* 1989 29 205-20

The photosynthetic reaction centre from the purple bacterium *Rhodopseudomonas viridis*.

Deisenhofer J, Michel H, *Bioscience Reports* 1989 9 383-420

The photosynthetic reaction center from the purple bacterium *Rhodopseudomonas viridis*.

Deisenhofer J, Michel H, *Science* 1989 245 1463-73

Das Photosynthetische Reaktionszentrum des Purpurbacteriums *Rhodopseudomonas viridis*.

Deisenhofer J, Michel H, *Angewandte Chemie* 1989 101 872-92

The photosynthetic reaction center from the purple bacterium *Rhodopseudomonas viridis*.

Deisenhofer J, Michel H, *Angewandte Chemie* 1989 28 829-47

The photosynthetic reaction centre from the purple bacterium *Rhodopseudomonas viridis*

Deisenhofer J, Michel H, *EMBO Journal* 1989 8 2149-70

1988

Unidirectionality of charge separation in reaction centers of photosynthetic bacteria.

Michel-Beyerle ME, Plato M, Deisenhofer J, Michel H, Bixon M, Jortner J, *Biochimica et Biophysica Acta* 1988 932 52-70

The Structure of the Photosynthetic Reaction Centre From *Rhodopseudomonas Viridis*.

Michel H, Deisenhofer J, *Bulletin de l'Institut Pasteur* 1988 86 37-45

Relevance of the photosynthetic reaction center from purple bacteria to the structure of photosystem II.

Michel H, Deisenhofer J, *Biochemistry* 1988 27 1-7

1987

Comparison of Two Highly Refined Structures of Bovine Pancreatic Trypsin Inhibitor.

Wlodawer A, Deisenhofer J, Huber R, *J. Mol. Biol.* 1987 193 145-56

The Photosynthetic Reaction Center from the Purple Bacterium *Rhodopseudomonas viridis*.

Michel H, Deisenhofer J, *Chemica Scripta* 1987 27B 173-80

The structure of the photosynthetic reaction center from *Rhodopseudomonas viridis*.

Deisenhofer J, Michel H, *Photobiochemistry and Photobiophysics* 1987 Suppl. 133-40

1986

Pigment-protein interactions in the photosynthetic reaction centre from *Rhodospseudomonas viridis*.

Michel H, Epp O, Deisenhofer J, *EMBO Journal* 1986 5 2445-51

Die strukturelle Grundlage der Lichtreaktionen in Bakterien.

Deisenhofer J, Huber R, Michel H, *Nachrichten aus Chemie Technik und Laboratorium* 1986 34 416-22

Structural homology of reaction centers from *Rhodospseudomonas sphaeroides* and *Rhodospseudomonas viridis* as determined by x-ray diffraction.

Allen JP, Feher G, Yeates TO, Rees DC, Deisenhofer J, Michel H, Huber R, *Proc. Natl. Acad. Sci. U.S.A.* 1986 83 8589-93

1985

Correlation of structural and spectroscopic properties of a photosynthetic reaction center.

Zinth W, Knapp EW, Fischer SF, Kaiser W, Deisenhofer J, Michel H, *Chemical Physics Letters* 1985 119 1-4

Analysis of optical spectra from single crystals of *Rhodospseudomonas viridis* reaction centers.

Knapp EW, Fischer SF, Zinth W, Sander M, Kaiser W, Deisenhofer J, Michel H, *Proc. Natl. Acad. Sci. U.S.A.* 1985 82 8463-67

The structural basis of photosynthetic light reactions in bacteria.

Deisenhofer J, Michel H, Huber R, *Trends in Biochemical Sciences* 1985 10 243-48

Structure of the protein subunits in the photosynthetic reaction centre of *Rhodospseudomonas viridis* at 3 Å resolution.

Deisenhofer J, Epp O, Miki K, Huber R, Michel H, *Nature* 1985 318 618-24

1984

Crystal-Structure Analysis and Molecular Model of a Complex of Citrate Synthase with Oxaloacetate and S-Acetyl Coenzyme-A.

Wiegand G, Remington SJ, Deisenhofer J, Huber R, *J. Mol. Biol.* 1984 174 205-19

Human alpha1 proteinase inhibitor. Crystal structure analysis of two crystal modifications, molecular model and preliminary analysis of the implication for function.

Löbermann H, Tokuoka R, Deisenhofer J, Huber R, *J. Mol. Biol.* 1984 177 531-56

X-Ray structure analysis of a membrane protein complex: Electron density map at 3 Å resolution and a model of the chromophores of the photosynthetic reaction center from *Rhodospseudomonas viridis*.

Deisenhofer J, Epp O, Miki K, Huber R, Michel H, *J. Mol. Biol.* 1984 180 385-98

1983

The Geometry of the Reactive Site and of the Peptide Groups in Trypsin, Trypsinogen and its Complexes with Inhibitors.

Marquart M, Walter J, Deisenhofer J, Bode W, Huber R, *Acta Cryst* 1983 B39 480-90

Structural Parameters of Ligand Binding by Lupine Leghemoglobin at 2.0 Å Resolution. Arutyunyan EG, Deisenhofer J, Teplyakov AV, Kuranova IP, Oblomova GV, Vainshtein BK, *Doklady Akademii Nauk SSSR* 1983 270 732-36

1982

The three-dimensional structure of antibodies.

Marquart M, Deisenhofer J, *Immunology Today* 1982 3 160-66

1981

Crystallographic Refinement and Atomic Models of a Human Fc Fragment and its Complex with Fragment B of Protein A From *Staphylococcus aureus* at 2.9 and 2.8 Å Resolution.

Deisenhofer J, *Biochemistry* 1981 20 2361-70

1980

Crystallographic Refinement and Atomic Models of the Intact Immunoglobulin Molecule Kol and its Antigen-binding Fragment at 3.0 Å and 1.9 Å Resolution.

Marquart M, Deisenhofer J, Huber R, Palm W, *J. Mol. Biol.* 1980 141 369-91

Crystal Structure Analysis and Molecular Model of Human C3a Anaphylatoxin.

Huber R, Scholze H, Paques EP, Deisenhofer J, *Hoppe-Seyler's Zeitschrift fuer Physiologische Chemie* 1980 361 1389-99

1978

Crystallization, Crystal Structure Analysis and Atomic Model of the Complex Formed by a Human Fc Fragment and Fragment B of Protein A from *Staphylococcus aureus*.

Deisenhofer J, Jones TA, Huber R, Sjoedahl J, Sjoquist J, *Hoppe-Seyler's Zeitschrift fuer Physiologische Chemie* 1978 359 975-85

1977

Dreidimensionale Struktur der Antikörper.

Deisenhofer J, *Die Gelben Hefte* 1977 XVII 106-15

1976

Crystallographic Structure Studies of an IgG Molecule and an Fc Fragment.

Huber R, Deisenhofer J, Colman PM, Matsushima M, Palm W, *Nature* 1976 264 415-20

Dynamics of the Aromatic Amino Acid Residues in the Globular Conformation of the Basic Pancreatic Trypsin Inhibitor (BPTI) II. Semi-empirical Energy Calculations.

Hetzl R, Wüthrich K, Deisenhofer J, Huber R, *Biophysics of Structure and Mechanism* 1976 2 159-80

Crystallographic Structural Studies of a Human Fc-Fragment I. An Electron Density Map at 4 Å Resolution and a Partial Model.

Deisenhofer J, Colman PM, Huber R, Haupt H, Schwick G, *Hoppe-Seyler's Zeitschrift fuer Physiologische Chemie* 1976 357 435-45

Crystallographic structural studies of a human Fc fragment II. A complete model based on a Fourier map at 3.5 Å resolution.

Deisenhofer J, Colman PM, Epp O, Huber R, *Hoppe-Seyler's Zeitschrift fuer Physiologische Chemie* 1976 357 1421-34

Structure of the Human Antibody Molecule Kol (Immunoglobulin G1): An Electron Density Map at 5 Å Resolution.

Colman PM, Deisenhofer J, Huber R, Palm W, *J. Mol. Biol.* 1976 100 257-82

1975

Crystallographic refinement of the structure of bovine pancreatic trypsin inhibitor at 1.5 Å resolution.

Deisenhofer J, Steigemann W, *Acta Cryst* 1975 B31 238-50

1974

Structure of the Complex Formed by Bovine Trypsin and Bovine Pancreatic Trypsin Inhibitor II. Crystallographic Refinement at 1.9 Å Resolution.

Huber R, Kukla D, Bode W, Schwager P, Bartels KS, Deisenhofer J, Steigemann W, *J. Mol. Biol.* 1974 89 73-101

1971

Imprisonment of resonant phonons observed with a new technique for the detection of 10^{12} -Hz phonons.

Renk KF, Deisenhofer J, *Physical Review Letters* 1971 26 764-66

Book chapters, editorials

2001

Proteins (editorial).

Deisenhofer J, Smith JL, *Current Opinion in Structural Biology* 2001 11 6 701-02.

1997

Structural analysis of bovine heart mitochondrial cytochrome b/c1 complex by X-ray crystallography.

Xia D, Kim H, Deisenhofer J, Yu CA, Kachurin A, Xia JZ, Yu L (1997). In Namba K (Ed.), *Structure and Function of Macromolecular Assembly. Proceeding of the 22nd International Symposium, Division of Biophysics, The Taniguchi Foundation* (pp. 10-22): Matsushita Electric Industrial Co., Ltd.

The structure of *Escherichia coli* GroES.

Hunt JF, Deisenhofer J (1997). In Gething MJ (Ed.), *Guidebook to Molecular Chaperones and Protein-Folding Catalysis* (pp. 179-181): Oxford University Press.

Proteins (editorial).

Brändén CI, Deisenhofer J, *Current Opinion in Structural Biology* 1997 7 819-20

1994

Recent developments in studies of macromolecular structure by X-ray crystallography.

Deisenhofer J (1994). In Deisenhofer J, Helliwell JR, Sakabe N (Eds.), *Synchrotron Radiation in the Biosciences* (pp. 3-11). Oxford: Oxford University Press.

1993

Three-dimensional structure of the reaction center of *Rhodospseudomonas viridis*.

Deisenhofer J, Michel H (1993). In Deisenhofer J, Norris JR (Eds.), *The Photosynthetic Reaction Center Volume II* (pp. 541-558). San Diego: Academic Press.

1992

The 3-D structure of the reaction center from *Rhodospseudomonas viridis*.

Deisenhofer J, Michel H (1992). In Breton J, Vermeglio A (Eds.), *The photosynthetic bacterial reaction center II. Structure, spectroscopy and dynamics* (pp. 1-11). New York: Plenum Press.

High-resolution crystal structures of bacterial photosynthetic reaction centers.

Deisenhofer J, Michel H (1992). In Ernster L (Ed.), *Molecular Mechanisms in Bioenergetics* (pp. 103-120): Elsevier Science Publishers.

1991

Crystallography of chlorophyll proteins.

Deisenhofer J, Michel H (1991). In Scheer H (Ed.), *Chlorophylls* (pp. 613-625). Boca Raton: CRC Press.

Structures of bacterial photosynthetic reaction centers.

Deisenhofer J, Michel H. (1991). In Palade GE, Alberts BM, Spudich JA (Eds.), *Annual Review of Cell Biology* 7 1-23

High-resolution structures of photosynthetic reaction centers.

Deisenhofer J, Michel H. (1991) In Engelmann DM, Cantor CR, Pollard TD (Eds.) *Annual Review of Biophysics and Biophysical Chemistry* 20 247-66

1990

The photosynthetic reaction center from the purple bacterium *Rhodospseudomonas viridis*: Aspects of membrane protein structure.

Michel H, Deisenhofer J (1990). In Claudio T (Ed.), *Current Topics in Membranes and Transport Volume 36: Protein-Membrane Interactions* (pp. 53-69). San Diego: Academic Press.

1989

The photosynthetic reaction centre from the purple bacterium *Rhodospseudomonas viridis*.

Deisenhofer J, Michel H (1989). In Frangsmyr T (Ed.), *Les Prix Nobel 1988* (pp. 134-188). Stockholm: Nobel Foundation.

The 3-D Structure of the Photosynthetic Reaction Center from *Rhodospseudomonas viridis*.

Deisenhofer J, Michel H (1989). In Carter FL, Siatkowski RE, Wohltjen H (Eds.), *Molecular Electronic Devices: Proceedings of the 3rd International Symposium on Molecular Electronic Devices* (pp. 621-631). Amsterdam: Elsevier Science Publishers.

The Crystal Structure of the Photosynthetic Reaction Center from *Rhodospseudomonas viridis*.

Deisenhofer J, Michel H (1989). In Norris JR, Meisel M (Eds.), *Photochemical Energy Conversion: Proceedings of the Seventh International Conference of Photochemical Conversion and Storage of Solar Energy* (pp. 232-237). New York: Elsevier Science Publishers.

The Structure of the Photochemical Reaction Center of *Rhodospseudomonas viridis* and Its Implications for Function.

Deisenhofer J, Huber R, Michel H (1989). In Fasman GD (Ed.), *Prediction Of Protein Structure And The Principles Of Protein Conformation* (pp. 99-116): Plenum Publishing. 1988

Electrostatic Control of Electron Transfer in the Photosynthetic Reaction Center of *Rhodospseudomonas viridis*.

Treutlein H, Schulten K, Niedermeier C, Deisenhofer J, Michel H, Devault D (1988). In Breton J, Vermeglio A (Eds.), *The Photosynthetic Bacterial Reaction Center: Structure and Dynamics* (pp. 369-377). New York: Plenum Press.

Molecular Dynamics Simulation of the Primary Processes in the Photosynthetic Reaction Center of *Rhodospseudomonas viridis*.

Treutlein H, Schulten K, Deisenhofer J, Michel H, Brünger AT, Karplus M (1988). In Breton J, Vermeglio A (Eds.), *The Photosynthetic Bacterial Reaction Center: Structure and Dynamics* (pp. 139-150). New York: Plenum Press.

Molecular Dynamics Simulation of the Primary Processes in the Photosynthetic Reaction Center from *Rhodospseudomonas viridis*.

Treutlein H, Niedermeier C, Schulten K, Deisenhofer J, Michel H, Brünger AT, Karplus M (1988). In Pullman A, Jortner J, Pullman B (Eds.), *Transport through membranes: carriers, channels, and pumps: Proceedings of the 21st Jerusalem Symposium on Quantum Chemistry and Biochemistry* (pp. 513-525). Dordrecht: Kluwer Academic Publishers.

The crystal structure of the photosynthetic reaction center from *Rhodospseudomonas viridis*.

Deisenhofer J, Michel H (1988). In Pullman A, Jortner J, Pullman B (Eds.), *Transport through membranes: carriers, channels, and pumps: Proceedings of the 21st Jerusalem Symposium on Quantum Chemistry and Biochemistry* (pp. 507-512). Dordrecht: Kluwer Academic Publishers.

The crystal structure of the photosynthetic reaction center from *Rhodospseudomonas viridis*.

Deisenhofer J, Michel H (1988). In Breton J, Vermeglio A (Eds.), *The Photosynthetic Bacterial Reaction Center: Structure and Dynamics* (pp. 1-3). New York: Plenum Press.

1987

The Structural Organization of Photosynthetic Reaction Centers.

Michel H, Deisenhofer J (1987). In Biggins J (Ed.), *Progress in Photosynthesis Research, Vol 1* (pp. I.4.353-I.354.362). Dordrecht: Martinus Nijhoff.

The Crystal Structure of the Photosynthetic Reaction Center From *Rhodospseudomonas Viridis*.

Deisenhofer J, Michel H (1987). In Moras D, Drenth J, Strandberg B, Stuck D, Wilson K (Eds.), *Crystallography in Molecular Biology* (pp. 421-423). New York and London: Plenum.

1986

X-ray diffraction studies on a crystalline bacterial photosynthetic reaction center: A progress report and conclusions on the structure of photosystem II reaction centers. Michel H, Deisenhofer J (1986). In Staehelin LA, Arntzen CJ (Eds.), *Encyclopedia of Plant Physiology, (New Series) Vol. 19 Photosynthesis III: Photosynthetic Membranes and Light Harvesting Systems* (pp. 371-381). Berlin: Springer.

1985

Spin Dipolar Interaction of Radical Pairs in Photosynthetic Reaction Centers. Ogrodnik A, Lersch W, Michel-Beyerle ME, Deisenhofer J, Michel H (1985). In Michel-Beyerle ME (Ed.), *Springer Series in Chemical Physics Vol 42: Antennas and Reaction Centers of Photosynthetic Bacteria: Structure, Interactions, and Dynamics* (pp. 198-206). Berlin: Springer.

Experience with Various Techniques for the Refinement of Protein Structures. Deisenhofer J, Remington SJ, Steigemann W (1985). In Wyckoff HW, Hirs CHW, Timasheff SN (Eds.) *Methods in Enzymology* 115 303-23
The Crystal Structure of the Photosynthetic Reaction Center from *Rhodospseudomonas viridis*. Deisenhofer J, Michel H (1985). In Michel-Beyerle ME (Ed.), *Springer Series in Chemical Physics, Vol. 42* (pp. 94-96). Berlin: Springer.

1983

Crystallization of Membrane Proteins and Actual State of Structure Analysis of Photosynthetic Reaction Centre Crystals. Michel H, Deisenhofer J, Miki K, Weyer KA, Lottspeich F (1983). In Quagliariello E, Palmieri F (Eds.), *Structure and Function of Membrane Proteins* (pp. 191-197). Amsterdam: Elsevier.

The Contribution of X-Ray Crystallography to Our Understanding of Immunoglobulin Function. Deisenhofer J, Huber R (1983). In Yamamura Y, Tada T (Eds.), *Progress in Immunology V* (pp. 47-59). Tokyo: Academic Press.

1981

The Structures of the Intact Immunoglobulin Kol, Its Fab Fragment, a Human Fc Fragment and Fc-Protein-A Complex After Crystallographic Refinement at 3.0, 1.9, 2.9, and 2.8 Å Resolution.

Marquart M, Deisenhofer J, Huber R (1981). *Structural Aspects of Recognition and Assembly in Biological Macromolecules* (pp. 253-261): Balaban ISS.

1980

Conformational Flexibility and Its Functional Significance in Some Protein Molecules. Deisenhofer J, Huber R (1980). In Jaenicke R (Ed.), *Protein Folding* (1 ed., pp. 565-582): Elsevier/North-Holland Biomedical Press.

1976

X-Ray Diffraction Analysis of Immunoglobulin Structure. Huber R, Deisenhofer J, Colman PM, Matsushima M, Palm W (1976). In Melchers F, Rajewski K (Eds.), *27. Mosbacher Colloquium* (pp. 26-40). Berlin, Heidelberg: Springer.

1975

Constrained Crystallographic Refinement of Three Protein Structures. Steigemann W, Deisenhofer J, Huber R (1975). In Ahmed FR, Huml K, Sedlacek B (Eds.), *Crystallographic Computing Techniques (Summer School Prague)* (pp. 302-306). Copenhagen: Munksgaard.

1974

Structure of the Complex Formed by Bovine Trypsin and Bovine Pancreatic Trypsin Inhibitor. Refinement of the Crystal Structure Analysis. Huber R, Kukla D, Steigemann W, Deisenhofer J, Jones TA (1974). In Fritz H, Tschesche H, Greene LJ, Truscheit E (Eds.), *Bayer Symposium V: Proteinase Inhibitors* (pp. 497-512). Berlin, Heidelberg, New York: Springer.

The Model of the Basic Pancreatic Trypsin Inhibitor Refined at 1.5 Å Resolution. Deisenhofer J, Steigemann W (1974). In Fritz H, Tschesche H, Greene LJ, Truscheit E (Eds.), *Bayer Symposium V: Proteinase Inhibitors* (pp. 484-496). Berlin, Heidelberg, New York: Springer.

Journal articles with members of the JD lab as co-authors

2010

Induced polymerization of mammalian acetyl-CoA carboxylase by MIG12 provides a tertiary level of regulation of fatty acid synthesis.

Kim CW, Moon YA, Park SW, Cheng D, Kwon HJ, Horton JD, *Proc. Natl. Acad. Sci. U.S.A.* 2010 107 21 9626-31

2009

Secondary structure of Huntingtin amino-terminal region.

Kim MW, Chelliah Y, Kim SW, Otwinowski Z, Bezprozvanny I, *Structure* 2009 17 9 1205-012

Antagonism of Secreted PCSK9 Increases Low Density Lipoprotein Receptor Expression in HepG2 Cells.

Mcnutt MC, Kwon HJ, Chen C, Chen JR, Horton JD, Lagace TA, *J. Biol. Chem.* 2009 284 16 10561-70

2008

NPC2 facilitates bidirectional transfer of cholesterol between NPC1 and lipid bilayers, a step in cholesterol egress from lysosomes.

Infante RE, Wang ML, Radhakrishnan A, Kwon HJ, Brown MS, Goldstein JL, *Proc. Natl. Acad. Sci. U.S.A.* 2008 105 40 15287-92

2007

Sterol-regulated transport of SREBPs from endoplasmic reticulum to Golgi: oxysterols block transport by binding to Insig.

Radhakrishnan A, Ikeda Y, Kwon HJ, Brown MS, Goldstein JL, *Proc. Natl. Acad. Sci. U.S.A.* 2007 104 16 6511-18

2004

Direct binding of cholesterol to the purified membrane region of SCAP: mechanism for a sterol-sensing domain.

Radhakrishnan A, Sun LP, Kwon HJ, Brown MS, Goldstein JL, *Molecular Cell* 2004 15 2 259-68