

Supplementary Materials

Spatial arrangement of proteins in planar and curved membranes by PPM 3.0

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Table S1. Parameters of biological and artificial membranes: average hydrophobic thicknesses (D_0) and stretching stiffness coefficients (f_{mism}).

Membrane type	D_0, Å^a	f_{mism} kcal/mol/Å^b
Plasma membrane (mammalian)	32.0	0.02
Plasma membrane (plants)	30.6	0.02
Plasma membrane (Fungi)	30.6	0.02
Endoplasmic reticulum membrane (fungi)	28.7	0.02
Endoplasmic reticulum membrane (mammalian)	28.7	0.02
Golgi membrane	30.0	0.02
Lysosome membrane	30.7	0.02
Endosome membrane	30.0	0.02
Vacuole membrane	30.4	0.02
Outer mitochondrial membrane	22.7	0.01
Inner mitochondrial membrane	28.4	0.01
Thylakoid membrane (plants)	30.2	0.02
Thylakoid membrane (bacteria)	30.8	0.02
Gram-negative bacteria outer membrane	23.9	0.015
Gram-negative bacteria inner membrane	30.1	0.015
Gram-positive bacteria inner membrane	30.3	0.015
Archaeobacteria cell membrane	30.2	0.015
Generic membrane with TM α-helical/TM β-barrel proteins	30.0/23.9	0.001
DLPC (diC12:0 PC) bilayer	21.7 ^c	0.02

DMPC (diC14:0 PC) bilayer	25.7 ^c	0.02
DOPC (diC18:1Δ9c PC) bilayer	28.8 ^c	0.02
DEuPC (diC22:1Δ13c PC) bilayer	35.8 ^d	0.02
DPC(C12PC) micelle	39.0 ^e	N/A

^a D_0 values of biological membranes were estimated previously¹ and refined here as average hydrophobic thicknesses of their TM proteins.

^b from Ref.²

^c D_0 values correspond to $2D_{HC}$ values determined from small-angle neutron and X-ray scattering data.^{3;4}

^d from Ref.⁵

^e The hydrophobic diameter of *n*-dodecyl-phosphocholine (DPC) micelles was based on small-angle neutron scattering studies.⁶

Abbreviations: DOPC, 1,2-dioleoyl-*sn*-glycero-3-phosphocholine; DLPC, 1,2-dilauroyl-*sn*-glycero-3-phosphocholine; DMPC, 1,2-dimyristoyl-*sn*-glycero-3-phosphocholine; DEuPC, 1,2-dierucoyl-*sn*-glycero-3-phosphocholine DPC, *n*-dodecyl-phosphocholine.

Table S2. Characteristics of 46 structures of peripheral membrane protein positioned in sphere-shaped vesicles

Protein name	PDB ID	D , Å	R , Å	DG_{curv} , kcal/mol	DG_{flat} , kcal/mol	Curvature	Membrane type	Comment	Resolution, Å	Organism
BAR domains^a										
Endophilin-A1	2c08	1.1	80	-2.6	-2.0	positive	END	N-BAR	2.00	<i>Rattus norvegicus</i>
Endophilin-A	1uru	1.0	160	-4.7	-1.8	positive	END	N-BAR	2.60	<i>Drosophila melanogaster</i>
Endophilin-A1	1zww	5.5	140	-7.6	-3.3	positive	END	N-BAR	2.30	<i>Mus musculus</i>
Endophilin-A1	2d4c	0.6	170	-5.9	-2.7	positive	END	N-BAR	2.40	<i>Homo sapiens</i>
Endophilin-A3	2z0v	3.4	80	-4.7	-3.2	positive	END	N-BAR	2.49	<i>Homo sapiens</i>
Bin1/Amphiphysin	2fic	3.1	100	-5.2	-2.1	positive	END	N-BAR	1.99	<i>Homo sapiens</i>
BAR protein	3caz	0.4	100	-2.9	-2.4	positive	undefined	N-BAR	3.32	<i>Galdieria sulphuraria</i>
Bridging integrator 2	4avm	4.7	100	-11.8	-5.8	positive	PM	N-BAR	1.91	<i>Homo sapiens</i>
F-BAR domain of FCHo2	2v0o	0.4	330	-4.1	-2.5	positive	VES	F-BAR	2.30	<i>Homo sapiens</i>
PACSIN 2	3lll	2.5	500	-8.3	-5.9	positive	END	F-BAR	3.30	<i>Mus musculus</i>
Cdc42-interacting protein 4	2efk	0.4	300	-3.6	-2.4	positive	LYS	F-BAR	2.30	<i>Homo sapiens</i>
Formin-binding protein 1	2efl	0.4	320	-4.8	-2.3	positive	LYS	F-BAR	2.30	<i>Homo sapiens</i>
Syndapin	3i2w	4.3	180	-6.8	-4.9	positive	PM	F-BAR	2.67	<i>Drosophila melanogaster</i>
PACSIN 2	4bne	2.1	390	-6.9	-5.4	positive	END	F-BAR	2.57	<i>Gallus gallus</i>
Cell division control protein 15	6xj1	0.4	600	-6.0	-3.9	positive	ER	F-BAR	3.52	<i>Schizosaccharomyces pombe</i>
Cytokinesis protein 2	4wpe	1.9	370	-6.3	-5.8	positive	ER	F-BAR	2.70	<i>Saccharomyces cerevisiae</i>
Septation protein imp2	5c1f	2.3	590	-6.9	-6.5	positive	ER	F-BAR	2.36	<i>Schizosaccharomyces pombe</i>
PACSIN 3	3qe6	2.4	460	-7.7	-5.4	positive	PM	F-BAR	2.60	<i>Mus musculus</i>

PACSIN 1	3qni	4.0	590	-8.1	-6.7	positive	PM	F-BAR	2.80	<i>Homo sapiens</i>
PACSIN 2	3q0k	3.6	220	-7.1	-6.5	positive	END	F-BAR	2.60	<i>Homo sapiens</i>
PACSIN 1	2x3v	1.9	320	-6.5	-4.3	positive	PM	F-BAR	2.45	<i>Mus musculus</i>
Growth arrest-specific protein 7	6ikn	0.4	600	-3.3	-2.6	positive	PM	F-BAR	3.00	<i>Mus musculus</i>
BAR-PH domain of ACAP1	4nsw	3.6	110	-7.9	-4.5	positive	END	BAR-3 of APPL	2.20	<i>Homo sapiens</i>
BAR-PH domain of ACAP1 (tetramer)	4ckh	5.0	80	-11.2	-6.9	positive	END	BAR-3 of APPL	17.00 (EM)	<i>Homo sapiens</i>
BAR-PH domain of APPL2	4h8s	3.2	600	-8.8	-8.3	positive	END	BAR-3 of APPL	3.50	<i>Homo sapiens</i>
RCB domain of IRSp53	1wdz	0.4	600	-4.6	-4.0	negative	PM	I-BAR	2.63	<i>Homo sapiens</i>
Annexins^b										
Annexin	4mdv	2.8	70	-7.8	-5.9	negative	PM		2.50	<i>Schistosoma mansoni</i>
Annexin 24	1dk5	0.9	60	-3.5	-3.3	negative	PM		2.80	<i>Capsicum annuum</i>
Annexin A11	6tu2	2.3	90	-9.3	-4.8	negative	PM		2.30	<i>Rattus norvegicus</i>
Annexin D1	2q4c	1.8	110	-3.4	-3.1	negative	PM		2.51	<i>Arabidopsis thaliana</i>
Annexin GH1	3brx	1.7	60	-4.9	-4.4	negative	PM		2.50	<i>Gossypium hirsutum</i>
Annexin I	1hm6	1.8	250	-5.6	-5.6	negative	VES		1.80	<i>Sus scrofa</i>
Annexin II	1xjl	2.8	150	-4.8	-4.4	negative	PM		2.59	<i>Homo sapiens</i>
Annexin III	1axn	3.8	80	-9.3	-5.9	negative	PM		1.78	<i>Homo sapiens</i>
Annexin IV	1aow	3.1	120	-7.5	-5.9	negative	PM		3.00	<i>Bos taurus</i>
Annexin IV	2zoc	5.4	90	-11.4	-7.8	negative	PM		2.00	<i>Homo sapiens</i>
Annexin IV	2zhj	4.9	100	-11.5	-7.9	negative	PM		1.35	<i>Rattus norvegicus</i>
Annexin V (trimer)	2ie6	3.9	130	-21.0	-8.7	negative	PM		1.83	<i>Rattus norvegicus</i>
Annexin V	1anx	4.5	80	-8.1	-4.6	negative	PM		1.90	<i>Homo sapiens</i>

Annexin V	1yii	3.4	110	-6.5	-5.5	negative	PM		1.42	<i>Gallus gallus</i>
Annexin VIII	1w45	3.4	100	-9.3	-6.4	negative	PM		3.40	<i>Homo sapiens</i>
Annexin XII (trimer)	1dm5	3.7	110	-26.3	-10.1	negative	PM		1.93	<i>Hydra vulgaris</i>
Annexin A13 (dimer)	6b3i	1.0	110	-4.4	-4.0	negative	PM		2.60	<i>Homo sapiens</i>
α-synuclein										
α-synuclein	1xq8	11.3	70	-25.8	-16.5	positive	PM		NA(NMR)	<i>Homo sapiens</i>
Mitochondrial proteins										
Trifunctional protein, (trimer)	6dv2	6.4	90	-12.5	-6.7	positive	MIM		3.60	<i>Homo sapiens</i>
NADH-ubiquinone oxidoreductase (dimer)	4g6h	6.0	90	-26.1	-14.9	positive	MIM		2.26	<i>Saccharomyces cerevisiae</i>

^a form dimers, except PDB ID: 4ckh (tetramer)

^b form monomers, except PDB IDs: 2ie6 (dimer), 1dm5 (trimer), 6b3i (dimer).

Abbreviations: EM, cryo-electron microscopy; END, endosomal membrane; LYS, lysosomal membrane; MIM, mitochondrial inner membrane; NA, not applicable; PM, plasma membrane; VES, membrane of vesicles.

Table S3. Characteristics of 75 structures of transmembrane proteins positioned in sphere-shaped vesicles

Protein name and oligomeric state	PDB ID	D , Å	R , Å	DG_{curv} , kcal/mol	DG_{flat} , kcal/mol	Curvature	Membrane type	Resolution, Å	Method	Organism
Dimeric mitochondrial ATP synthases (protozoa)										
F₁F₀ ATP synthase	6yny	28	180	-251.4	-12.1	positive	MIM	2.70	EM	<i>Tetrahymena thermophila</i>
F₁F₀ ATP synthase	6tmk	28.8	160	-231.9	-32.4	positive	MIM	2.90	EM	<i>Toxoplasma gondii</i>
F₁F₀ ATP synthase	6rd4	27.6	90	-99.7	-30.6	positive	MIM	2.90	EM	<i>Polytomella sp</i>
Trimeric mechanosensitive Piezo channels (mammalia)										
Piezo-1 channel	6b3r	31.2	120	-168.1	-46.1	positive	PM	3.80	EM	<i>Mus musculus</i>
Piezo-1 channel	6bpz	32.2	120	-343.4	-66.4	positive	PM	3.80	EM	<i>Mus musculus</i>
Piezo-1 channel	5z10	31.2	100	-134.4	-29.0	positive	PM	3.97	EM	<i>Mus musculus</i>
Piezo-1 channel	6lqi	31.8	110	-190.1	-61.5	positive	PM	4.50	EM	<i>Mus musculus</i>
Piezo-2 channel	6kg7	31.6	120	-227.1	-57.7	positive	PM	3.80	EM	<i>Mus musculus</i>
Heptameric mechanosensitive channels of small conductance, MscS (bacteria)										
YnaI channel, closed	5y4o	29.7	80	-81	-76	positive	G- IM	3.80	EM	<i>Escherichia coli</i>
YnaI channel, open	6urt	30.5	80	-157.6	-112.2	positive	G- IM	3.27	EM	<i>Escherichia coli</i>
YnaI channel, open	6zyd	29.9	80	-143.9	-116.2	positive	G- IM	3.00	EM	<i>Escherichia coli</i>
YbiO channel, open	7a46	30.7	100	-123.9	-121	positive	G- IM	3.00	EM	<i>Escherichia coli</i>
MscS channel, closed	7onl	31.7	80	-119.3	-107.6	positive	G- IM	3.90	EM	<i>Escherichia coli</i>
MscS channel, closed	7oo8	31.3	80	-107.4	-93.9	positive	G- IM	3.70	EM	<i>Escherichia coli</i>
MscS channel, closed	7oo6	29.1	80	-89.8	-75.2	positive	G- IM	3.10	EM	<i>Escherichia coli</i>
MscS channel, closed	4hw9	31.3	80	-150.9	-142.5	positive	G- IM	4.14	EM	<i>Helicobacter pylori</i>
MscS channel, closed	6vyk	31.9	80	-109.8	-104.7	positive	G- IM	3.20	EM	<i>Escherichia coli</i>

MscS channel, open	7oo0	28.1	80	-101.2	-76.3	positive	G- IM	3.10	EM	<i>Escherichia coli</i>
MscS channel, open	7ooa	29.1	90	-105.8	-73	positive	G- IM	2.70	EM	<i>Escherichia coli</i>
MscS channel, open	7onj	28.7	100	-100.7	-78.4	positive	G- IM	2.30	EM	<i>Escherichia coli</i>
MscS channel, open	2oau	31.1	80	-181.5	-166.2	positive	G- IM	3.70	EM	<i>Escherichia coli</i>
MscS channel, closed	6rld	32.5	80	-131.3	-116.2	positive	G- IM	2.90	EM	<i>Escherichia coli</i>
MscS channel, open	5aji	27.9	80	-135.6	-116.6	positive	G- IM	2.99	EM	<i>Escherichia coli</i>
MscS channel, open	2vv5	28.5	100	-151.3	-139.8	positive	G- IM	2.99	EM	<i>Escherichia coli</i>
MscS channel, open	4age	28.7	90	-145.8	-125.9	positive	G- IM	2.99	EM	<i>Escherichia coli</i>
MscS channel, open	4agf	28.7	90	-147.4	-127.4	positive	G- IM	2.99	EM	<i>Escherichia coli</i>
MscS channel, open	4hwa	27.7	90	-104.5	-73.1	positive	G- IM	2.99	EM	<i>Escherichia coli</i>
MscS channel, closed	6pwn	32.1	90	-142.9	-133.3	positive	G- IM	3.10	EM	<i>Escherichia coli</i>
MscS channel, closed	6pwo	30.9	80	-88.4	-79.1	positive	G- IM	3.40	EM	<i>Escherichia coli</i>
MscS channel, closed	6pwp	28.1	80	-108.3	-87.9	positive	G- IM	4.10	EM	<i>Escherichia coli</i>
MscS channel, open	6uzh	29.7	80	-148.5	-126.6	positive	G- IM	3.30	EM	<i>Escherichia coli</i>
MscS channel, open	6vym	22.3	80	-106.4	-86.2	positive	G- IM	3.70	EM	<i>Escherichia coli</i>
MscS channel, open	6vyl	22.5	90	-157.7	-149.1	positive	G- IM	3.40	EM	<i>Escherichia coli</i>
MscS channel, closed	3t9n	30.1	80	-133.7	-125.9	positive	G+ PM	3.46	Xray	<i>Caldanaerobacter subterraneus</i>
MscS channel, closed	3udc	29.9	90	-118.4	-103.9	positive	G+ PM	3.36	Xray	<i>Caldanaerobacter subterraneus</i>
Dimer/tetramers of mitochondrial TOM complexes (yeast, mammalia)										
TOM complex (dimer)	6ucu	22.5	180	-120.7	-108.7	negative	MOM	3.06	EM	<i>Saccharomyces cerevisiae</i>
TOM complex (dimer)	6jnf	21.1	80	-100.0	-37.4	negative	MOM	3.81	EM	<i>Saccharomyces cerevisiae</i>
TOM complex (tetramer)	6ucv	21.7	220	-133.9	-48.9	negative	MOM	4.10	EM	<i>Saccharomyces cerevisiae</i>
TOM complex (dimer)	7ck6	22.7	100	-151.5	-98.8	negative	MOM	3.40	EM	<i>Homo sapiens</i>

TOM complex (dimer)	7cp9	22.9	130	-132.9	-89.1	negative	MOM	3.40	EM	<i>Homo sapiens</i>
Dimeric cation-chloride cotransporters, inward-facing state (zebrafish, mammalia)										
KCC1, SLC12A4	6kkt	31.8	80	-125.3	-90.5	positive	PM	2.9	EM	<i>Homo sapiens</i>
KCC1, SLC12A4	6kkr	32	80	-124.8	-89.9	positive	PM	2.9	EM	<i>Homo sapiens</i>
KCC1, SLC12A4	6kku	32.4	90	-125.5	-94.3	positive	PM	3.5	EM	<i>Homo sapiens</i>
KCC2, SLC12A5	6m23	30.8	100	-105.3	-61.2	positive	PM	3.2	EM	<i>Homo sapiens</i>
KCC2, SLC12A5	7d8z	30.4	90	-103.7	-55.7	positive	PM	3.4	EM	<i>Homo sapiens</i>
KCC2, SLC12A5	7d14	32	100	-88.5	-68.9	positive	PM	3.8	EM	<i>Mus musculus</i>
KCC3, SLC12A6	6y5v	32	90	-147.0	-112.3	positive	PM	4.08	EM	<i>Homo sapiens</i>
KCC3, SLC12A6	6y5r	31.6	90	-144.3	-112.6	positive	PM	3.76	EM	<i>Homo sapiens</i>
KCC3, SLC12A6	7d90	32	120	-140.6	-114.4	positive	PM	3.6	EM	<i>Homo sapiens</i>
KCC3, SLC12A6	6m22	32	110	-153.8	-118.9	positive	PM	2.7	EM	<i>Homo sapiens</i>
KCC3, SLC12A6	6m1y	32.2	100	-141.9	-101.7	positive	PM	3.2	EM	<i>Homo sapiens</i>
KCC4, SLC12A7	7d99	32	100	-137.2	-98.9	positive	PM	2.9	EM	<i>Homo sapiens</i>
NKCC1, SLC12A2	6npl	31.8	130	-166.3	-140.7	positive	PM	2.9	EM	<i>Danio rerio</i>
NKCC1, SLC12A2	6nph	31.8	130	-165.2	-137.7	positive	PM	2.9	EM	<i>Danio rerio</i>
NKCC1, SLC12A2	6npk	32.2	130	-153.4	-132.4	positive	PM	3.6	EM	<i>Danio rerio</i>
NKCC1, SLC12A2	7d10	32.8	120	-145.0	-138.3	positive	PM	3.52	EM	<i>Homo sapiens</i>
NKCC1, SLC12A2	6pzt	32	130	-141.0	-130.5	positive	PM	3.46	EM	<i>Homo sapiens</i>
KCC1, SLC12A4	7aip	32	100	-129.6	-94.6	positive	PM	3.12	EM	<i>Homo sapiens</i>
KCC1, SLC12A4	7aiq	32.2	100	-136.7	-101.7	positive	PM	3.72	EM	<i>Homo sapiens</i>
KCC1, SLC12A4	7air	32.4	100	-128.2	-93.3	positive	PM	3.66	EM	<i>Homo sapiens</i>
KCC3, SLC12A6	7ain	32	90	-141.1	-112.9	positive	PM	3.2	EM	<i>Homo sapiens</i>

KCC3, SLC12A6	7aio	32.2	90	-148.4	-120.3	positive	PM	3.31	EM	<i>Homo sapiens</i>
KCC3, SLC12A6	7ngb	31.8	100	-146.5	-124.6	positive	PM	3.64	EM	<i>Homo sapiens</i>
Dimeric proton-coupled K⁺ transporter, inward-facing state (KUP family)										
KimA transporter	6s3k	29.5	70	-131.4	-68.8	positive	G+ PM	3.7	EM	<i>Bacillus subtilis</i>
Mitochondrial (plant, yeast, mammalian) and bacterial respiratory complex I										
Plant mitochondrial respiratory complex I	7a23	26.8	380	-138.2	-105.0	negative	MIM	3.70	EM	<i>Brassica oleracea</i>
Mitochondrial respiratory complex I	7b0n	28.6	420	-281.4	-245.1	negative	MIM	3.70	EM	<i>Yarrowia lipolytica</i>
Mitochondrial respiratory complex I	6h8k	28.4	410	-155.9	-126.6	negative	MIM	3.79	Xray	<i>Yarrowia lipolytica</i>
Mitochondrial respiratory complex I	7b93	27.6	530	-304.2	-274.1	negative	MIM	3.04	EM	<i>Mus musculus</i>
Mitochondrial respiratory complex I	6ztq	27.8	480	-287.9	-262.1	negative	MIM	3.00	EM	<i>Mus musculus</i>
Mitochondrial respiratory complex I	6zka	27.4	480	-274.4	-250.8	negative	MIM	2.50	EM	<i>Ovis aries</i>
Bacterial respiratory complex I	3rko	30.3	270	-261.8	-229.3	negative	G- IM	3.00	Xray	<i>Escherichia coli</i>
Bacterial respiratory complex I (Mrp)	6z16	29.9	600	-373.4	-345.2	negative	G+ PM	2.98	EM	<i>Anoxybacillus flavithermus</i>
Photosystems dimers/tetramers (algae, cyanobacteria)										
PSII-FCP supercomplex (dimer)	6jlu	30.4	530	-495.4	-189.2	positive	THYL	3.02	EM	<i>Chaetoceros gracilis</i>
Bacterial PSI (tetramer)	6tcl	31.2	390	-622.0	-538.7	positive	THYL	3.20	EM	<i>Nostoc sp.</i>
PSI-LHCI-LHCII (dimer)	7d0j	30.4	550	-500.6	-434.1	positive	THYL	3.42	EM	<i>Chlamydomonas reinhardtii</i>

Abbreviations: EM, cryo-electron microscopy; G- IM, inner membrane of Gram-negative bacteria; G+ PM, plasma membrane of Gram-positive bacteria; MIM, mitochondrial inner membrane, MOM, mitochondrial outer membrane; PM, plasma membrane; THYL, thylakoid membrane,

Table S4. Characteristics of 35 structures of transmembrane proteins positioned in two flat membranes

Protein name	PDB ID	1 st membrane		2 nd membrane		Membrane type	Oligomer	Resolution, Å	Method	Organism
		D, Å	DG _{flat} , kcal/mol	D, Å	DG _{flat} , kcal/mol					
Mitochondrial ATP synthase (two flat intersecting membranes)										
Yeast mitochondrial ATP synthase, F1F0	6b2z	28.8	-134.1	29.2	-132.1	MIM	dimer	3.60	EM	<i>Saccharomyces cerevisiae</i>
Yeast mitochondrial ATP synthase, F1F0	6b8h	30.2	-152.4	29.4	-147.2	MIM	dimer	3.60	EM	<i>Saccharomyces cerevisiae</i>
Mitochondrial calcium uniporter (two flat intersecting membranes)										
MCU-EMRE complex	6o58	28.8	-80.7	29.6	-79.6	MIM	dimer	3.80	EM	<i>Homo sapiens</i>
MCU-EMRE-MICU complex	6wdo	28.4	-59.9	28.0	-56.1	MIM	dimer	3.80	EM	<i>Homo sapiens</i>
MCU-EMRE-MICU complex	6xjv	29.0	-76.0	29.2	-81.6	MIM	dimer	4.17	EM	<i>Homo sapiens</i>
MCU-EMRE complex	6k7x	29.0	-78.9	29.0	-78.7	MIM	dimer	3.27	EM	<i>Homo sapiens</i>
MCU-EMRE-MICU complex	6k7y	28.2	-84.6	29.0	-85.2	MIM	dimer	3.60	EM	<i>Homo sapiens</i>
Multidrug efflux pumps of Gram-negative bacteria (two flat parallel membranes)										
AcrAB-ToIC complex	5v5s	23.9	-50.9	29.5	-174.0	OM/IM	trimer	6.50	EM	<i>Escherichia coli</i>
AcrABZ-ToIC complex	5o66	25.1	-51.1	29.5	-197.1	OM/IM	trimer	5.90	EM	<i>Escherichia coli</i>
AcrAB-ToIC complex	5ng5	25.3	-59.3	29.1	-143.2	OM/IM	trimer	6.50	EM	<i>Escherichia coli</i>
MacAB-ToIC complex	5nik	25.3	-68.8	31.9	-92.7	OM/IM	dimer/trimer	3.30	EM	<i>Escherichia coli</i>
MexAB-OprM complex	6iol	24.9	-69.6	28.9	-147.9	OM/IM	trimer	3.64	EM	<i>Pseudomonas aeruginosa</i>
MexAB-OprM complex	6ta5	25.3	-68.3	29.3	-167.0	OM/IM	trimer	3.20	EM	<i>Pseudomonas aeruginosa</i>
MexAB-OprM complex	6iok	25.1	-72.6	30.1	-163.5	OM/IM	trimer	3.64	EM	<i>Pseudomonas aeruginosa</i>

Gap-junction channels (two flat parallel membranes)										
Connexin 26	2zw3	32.4	-155.5	32.4	-158.8	PM/PM	6-mer	3.5	Xray	<i>Homo sapiens</i>
Connexin 26	5er7	33.0	-174.7	33.2	-174.6	PM/PM	6-mer	3.29	Xray	<i>Homo sapiens</i>
Connexin 26	6uvs	32.2	-97.3	32.2	-96.4	PM/PM	6-mer	4.2	EM	<i>Homo sapiens</i>
Connexin-46	7jkc	33.4	-204.5	33.4	-204.5	PM/PM	6-mer	1.9	EM	<i>Ovis aries</i>
Connexin-46	7jmd	34.0	-204.3	34.0	-204.4	PM/PM	6-mer	2.5	EM	<i>Ovis aries</i>
Connexin-46	7jn0	33.8	-212.5	33.8	-212.2	PM/PM	6-mer	2.5	EM	<i>Ovis aries</i>
Connexin-46	7jn1	33.0	-209.7	33.0	-209.9	PM/PM	6-mer	2.5	EM	<i>Ovis aries</i>
Connexin-50	7jip	32.6	-159.0	32.6	-159.4	PM/PM	6-mer	1.94	EM	<i>Ovis aries</i>
Connexin-50	7jlw	33.0	-172.1	33.0	-172.1	PM/PM	6-mer	2.5	EM	<i>Ovis aries</i>
Connexin-46	7jkc	33.4	-204.5	33.4	-204.5	PM/PM	6-mer	1.9	EM	<i>Ovis aries</i>
Connexin-50	7jm9	33.4	-185.9	33.4	-186.1	PM/PM	6-mer	2.5	EM	<i>Ovis aries</i>
Connexin-50	7jmc	33.0	-171.1	33.0	-169.4	PM/PM	6-mer	2.5	EM	<i>Ovis aries</i>
Connexin-46	6mhq	33.4	-193.9	33.6	-193.5	PM/PM	6-mer	3.4	EM	<i>Ovis aries</i>
Connexin-50	6mhy	33.2	-178.6	33.2	-178.1	PM/PM	6-mer	3.4	EM	<i>Ovis aries</i>
CALHM4	6ytl	33.0	-303.8	33.2	-305.7	PM/ORG	11-mer	3.82	EM	<i>Homo sapiens</i>
CALHM4	6ytk	32.8	-275.2	32.8	-278.3	PM/ORG	11-mer	3.82	EM	<i>Homo sapiens</i>
CALHM2	6uix	33.6	-335.3	33.6	-335.3	PM/PM	11-mer	3.5	EM	<i>Homo sapiens</i>
CALHM2	6vai	33.4	-328.4	33.4	-328.1	PM/PM	11-mer	3.68	EM	<i>Homo sapiens</i>
CLHM-1	6lom	33.4	-246.0	33.6	-246.1	PM/PM	10-mer	3.73	EM	<i>Caenorhabditis elegans</i>
Innexin-6	5h1r	33.0	-230.0	33.0	-226.4	PM/PM	8-mer	3.6	EM	<i>Caenorhabditis elegans</i>
Pannexin-1	6wbn	34.6	-291.5	34.6	-292.0	PM/PM	7-mer	2.83	EM	<i>Homo sapiens</i>

Abbreviations: MIM, mitochondrial inner membrane; IM, inner membrane; OM, outer membrane; PM, plasma membrane; ORG, organelle membrane.

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