

## Supplementary Materials

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membranome *Membrane Proteome* UNIVERSITY OF MICHIGAN | COLLEGE OF PHARMACY | LOMIZE GROUP  
of single-helix transmembran Search proteins by Uniprot ID or name search Search proteins

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**Proteins**

Types (1)  
Classes (15)  
Superfamilies (667)  
Families (1367)  
Species (6)  
Localizations (22)  
Proteins (5759)

**Protein Complexes**

Classes (14)  
Superfamilies (252)  
Families (518)  
Localizations (22)  
Complexes (1791)

**Mutations in TMH**

Types (4)  
Diseases (13)  
Mutations (1051)

**Pathways**

Classes (22)  
Subclasses (161)  
Pathways (1962)

**1TMNet**

1TMNet allows identifying structural and functional associations between bitopic proteins from Membranome based on their interactions, common complexes and pathways. Please select a single species and several proteins of interest for analyzing how they interact with each other in protein complexes and pathways.

Proteins can be selected

1. by using search for text (for example, phosphatase) or Uniprot codes (for example, P08575 or PTPRC\_HUMAN),
2. by selecting proteins that belong to certain families, or
3. by selecting proteins that are located in certain membranes.

An example  
One can click at "Family selection" below and select first superfamily in the list ("Protein-tyrosine phosphatase"). A table with proteins will appear. Then, one can click "select" for the first six proteins in the list. The list of selected proteins will appear under "Selected proteins". After submitting the task, 1TMNet will generate a set of interactions between the selected proteins, their complexes and biological pathways included to the Membranome database. The list includes indirect interactions of proteins A and B through an intermediate protein X.

**Select proteins**  
No proteins selected.

**Proteins**  
[Family selection](#)  
[Membrane selection](#)

Species:

[Show all](#)

**FMAP Server**




Figure S1. 1TMnet input page.

Direct protein-protein Interactions (10 results)	
Protein 1	Protein 2
CD44 antigen (CD44_HUMAN <a href="#">↗</a> )	Receptor tyrosine-protein kinase erbB-2 (ERBB2_HUMAN <a href="#">↗</a> )
Disintegrin and metalloproteinase domain-containing protein 17 (ADA17_HUMAN <a href="#">↗</a> )	Protransforming growth factor alpha (TGFA_HUMAN <a href="#">↗</a> )
Epidermal growth factor receptor (EGFR_HUMAN <a href="#">↗</a> )	Receptor-type tyrosine-protein phosphatase eta (PTPRJ_HUMAN <a href="#">↗</a> )
Epidermal growth factor receptor (EGFR_HUMAN <a href="#">↗</a> )	Receptor tyrosine-protein kinase erbB-4 (ERBB4_HUMAN <a href="#">↗</a> )
Epidermal growth factor receptor (EGFR_HUMAN <a href="#">↗</a> )	Mucin-1 (MUC1_HUMAN <a href="#">↗</a> )
Probetacellulin (BTC_HUMAN <a href="#">↗</a> )	Receptor tyrosine-protein kinase erbB-2 (ERBB2_HUMAN <a href="#">↗</a> )
Protransforming growth factor alpha (TGFA_HUMAN <a href="#">↗</a> )	Receptor tyrosine-protein kinase erbB-2 (ERBB2_HUMAN <a href="#">↗</a> )
Receptor tyrosine-protein kinase erbB-2 (ERBB2_HUMAN <a href="#">↗</a> )	Receptor-type tyrosine-protein phosphatase kappa (PTPRK_HUMAN <a href="#">↗</a> )
Receptor tyrosine-protein kinase erbB-2 (ERBB2_HUMAN <a href="#">↗</a> )	Receptor-type tyrosine-protein phosphatase eta (PTPRJ_HUMAN <a href="#">↗</a> )
Receptor tyrosine-protein kinase erbB-2 (ERBB2_HUMAN <a href="#">↗</a> )	Receptor tyrosine-protein kinase erbB-4 (ERBB4_HUMAN <a href="#">↗</a> )

Visualization of Direct Protein-Protein Interactions

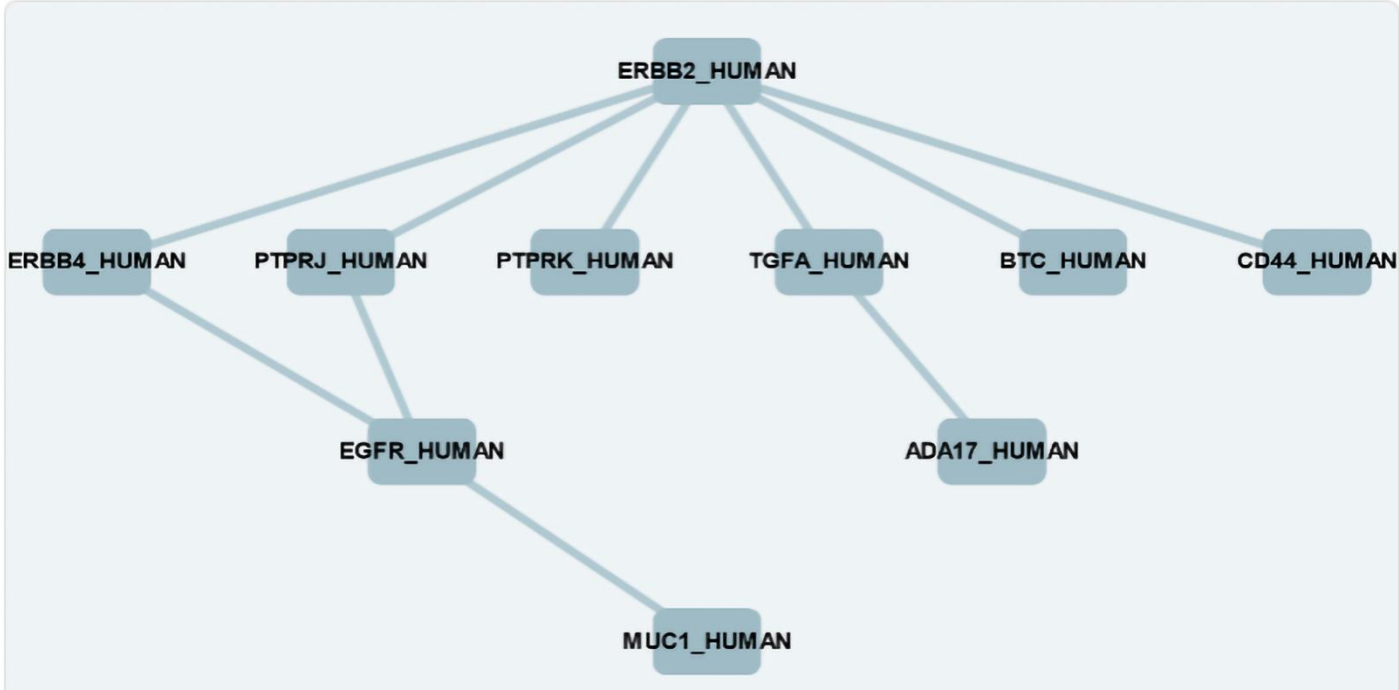


Figure S2. Direct protein-protein interactions for EGFR\_HUMAN produced by 1TMnet.



**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB.

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
4F2_HUMAN	7CCS	A	469	162-630	2.2	100	93	74	100
A4_HUMAN	3NYL	A	195	370:372-515:517-522:524-567	2.6	97	89	25	99
ABHD6_HUMAN	7OTS	A	292	43:46-335:337	1	99	93	87	100
ACBD5_HUMAN	3FLV	A	92	39-128:130:134	1.4	97	88	17	100
ACE_HUMAN	6EN5	D	613	30-159:163-644:706	1.1	99	94	47	100
ACE2_HUMAN	6M18	B	749	20-729:731-740:743-761:763-771:775	2.3	96	94	93	100
ACVL1_HUMAN	3MY0	N	300	162:195-493	1.7	100	94	60	100
ACVR1_HUMAN	6I1S	A	314	186-193:196:200-280:284-506:510	1.6	99	92	62	98
ADA10_HUMAN	6BE6	C	286	217-458:466-469:641-646:655:658-660:663-669:671-675:706-708:713:715:719-726:749-753	3.6	88	88	38	66
ADA17_HUMAN	2OIO	A	264	216-478:507	1.5	98	87	32	99
ADA22_HUMAN	5Y2Z	K	486	233-717:719	1.1	100	91	54	100
ADA33_HUMAN	1R54	A	205	205:207-410	1.1	99	88	25	100
ADAM8_HUMAN	4DD8	D	208	195-196:198-402:404	1.3	99	86	25	100
AL3A2_HUMAN	4QGK	A	460	2-461	0.5	100	98	95	100
ALK_HUMAN	4FOD	A	308	1083:1086-1136:1143-1277:1279-1280:1285:1288-1405	1.5	98	84	19	100
AMHR2_HUMAN	7L0J	B	105	24-128	1.5	100	80	18	96
AMNLS_HUMAN	6GJE	A	338	20-357	1.6	100	91	75	100
AMPE_HUMAN	4KXD	A	875	76-607:610:612-614:616-954	0.3	99	98	91	100
AMPN_HUMAN	5LHD	C	905	63-967	1.7	100	95	94	100
ANPRC_HUMAN	1JDN	A	407	50-85:92-95:97-463	1.1	100	93	75	100
ANTR1_HUMAN	6CX1	E	180	43-203:209:212-226:245:310-311	1.9	89	93	32	99
ANTR2_HUMAN	7N1O	A	188	77-78:80-82:98:101-102:105-106:109-286	1.7	94	85	38	73
AOC3_HUMAN	4BTY	A	710	53-470:472-763	0.7	100	97	93	100



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AOFA_HUMAN	2Z5Y	A	513	12-524	0.4	100	98	97	100
AOFB_HUMAN	6YT2	A	500	2-500:502	0.6	100	97	96	100
APLP1_HUMAN	4RDA	A	201	287-290:295:299-487:489-495	2.5	94	89	31	99
APLP2_HUMAN	5TPT	A	197	373-569	1.7	100	90	26	100
AREG_HUMAN	2RNL	A	46	142-145:147-188	1.8	94	83	18	92
ASAH2_HUMAN	4WGK	B	672	99-638:643-757:763-779	0.3	100	97	86	100
ASB11_HUMAN	4UUC	A	219	66-284	0.7	100	95	68	99
ASGR1_HUMAN	5JQ1	A	130	152-281	0.2	100	97	45	100
ASPH_HUMAN	7E6J	A	429	330-758	0.5	100	96	57	100
ASTRC_HUMAN	6GN5	A	174	322-323:325-341:343-352:354-381:383-499	1.1	99	90	26	100
AVR2A_HUMAN	4ASX	B	306	164:167-171:188-487	1.6	97	92	60	100
AVR2B_HUMAN	2QLU	A	297	188-484	1.2	99	93	58	100
B2CL1_HUMAN	1LXL	A	173	5-32:34-37:41-44:62-71:73-77:112-229:231-232:235-236	3.7	88	82	74	78
B2CL2_HUMAN	1O0L	A	175	18-68:70-81:83-180:182-187:189-191:195-198:200	2.2	88	86	91	93
B2L10_HUMAN	4B4S	A	148	13-116:132-174:179	0.6	97	92	73	100
B3GA1_HUMAN	1V82	A	247	83-156:162-334	0.4	100	96	74	100
B3GA2_HUMAN	2D0J	A	242	78-146:148:152-323	0.8	100	96	75	100
B3GA3_HUMAN	3CU0	A	250	75-140:143:153-335	0.8	99	96	75	100
B3GN2_HUMAN	7JHO	A	331	55-74:76-77:89-397	0.4	99	97	83	100
B4GT1_HUMAN	4L41	C	273	126-398	0.4	99	97	69	100
B4GT7_HUMAN	4IRQ	C	249	79-327	1	99	97	76	100
BACE1_HUMAN	4LC7	A	397	58-220:222-229:231-450:452-457	1.8	96	96	79	99
BACE2_HUMAN	3ZKQ	A	376	75-236:246-385:387-460	0.9	100	95	73	100
BAK_HUMAN	5VWZ	A	166	21-186	1.7	99	86	79	100

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BASI_HUMAN	6LZ0	B	198	37:139-150:153-163:165-175:177-185:187:189-202:204-339:341-342:347	3.8	77	93	51	92
BAX_HUMAN	2LR1	A	186	6-13:15-40:42-45:47-194	2.5	95	88	97	97
BCAM_HUMAN	2PF6	A	231	32-261:297	1.4	100	93	37	100
BCL2_HUMAN	2O22	A	153	3-35:97-216	2.5	96	87	64	93
BGAT_HUMAN	6GX2	A	296	59:61-355	0.8	98	97	84	100
BMPR2_HUMAN	3G2F	A	302	197-287:289-364:373:375-396:398-495:497-507:509:511-512	1.2	99	92	29	100
BMR1A_HUMAN	2QJA	D	93	53-54:56-144:146-147	1.5	85	82	17	100
BMR1B_HUMAN	3MDY	A	320	170:175-358:366:369-502	0.9	99	92	64	100
BOC_HUMAN	3N1M	C	104	710-813	0.7	100	76	9	100
BOK_HUMAN	6CKV	A	156	22-177	2.1	97	89	74	100
BST2_HUMAN	3MQB	A	108	50-151:153-158	1.9	96	95	60	99
BT3A1_HUMAN	4F9L	A	214	30-243	0.8	100	93	42	100
BT3A2_HUMAN	4F8Q	A	208	29-181:186-211:213:216-240:242-244	1.9	98	95	62	100
BT3A3_HUMAN	4F8T	A	210	30-212:216-242	1	100	93	36	100
BTC_HUMAN	1IOX	A	49	60-63:66-86:88-91:93-109:112-113:116	3.6	80	85	28	98
BTLA_HUMAN	2AW2	A	110	34-143	1.4	94	92	38	100
C163B_HUMAN	6K0O	A	104	793-896	0.9	98	76	7	100
C2C2L_HUMAN	5TOD	D	153	89-117:119-149:151-176:178-223:234-252:255-256	0.8	99	87	22	100
CABP7_HUMAN	2LV7	A	72	57-128	2.3	100	76	33	72
CAD17_HUMAN	6ULM	B	209	27-235	1.6	100	90	25	100
CAD23_HUMAN	5TFM	A	305	886-918:924-944:948-961:964-1028:1030-1034:1037-1043:1045-1046:1049-1149:1151-1154:1156-1176:1178:1180:1183-1186:1189-1204:1206-1215	2.7	31	84	22	95

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

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CADH1_HUMAN	6CXY	C	213	155-367	1	100	93	24	100
CADH3_HUMAN	6ZTB	I	215	110-323:363	1.6	100	93	26	99
CADH6_HUMAN	5VEB	Y	100	492-591	1.8	100	89	13	93
CADM1_HUMAN	4H5S	B	100	45-143:227	0.8	99	95	23	100
CADM3_HUMAN	1Z9M	B	105	26:28-130:211	0.8	98	96	26	100
CAH12_HUMAN	6RPS	A	262	30-291	0.7	100	98	74	100
CAH14_HUMAN	5CJF	A	267	21-287	0.5	100	97	79	100
CAH4_HUMAN	5KU6	C	264	21-284	0.3	100	97	85	100
CAH9_HUMAN	6Y74	A	258	137-394	0.8	100	97	56	100
CANT1_HUMAN	2H2U	B	317	85-401	0.6	100	98	79	100
CBPD_HUMAN	5AQ0	B	82	382-463	0.6	96	91	6	100
CC90B_HUMAN	6H9M	B	93	61-62:64-100:102-106:108-156	2.4	66	93	37	99
CCD47_HUMAN	6W6L	7	256	152-154:156-176:180-188:194-196:198-202:204-216:218-230:233-242:244-287:296-301:303-341:361-372:374-379:381-436:438-439:499-510:512-513	3.6	68	92	53	88
CD166_HUMAN	5A2F	A	218	28-245	1	100	95	37	100
CD180_HUMAN	3B2D	A	601	26-626	1.4	100	96	91	100
CD19_HUMAN	6AL5	A	232	21-39:48-137:153-176:183:185-278:281-284	1.2	98	85	42	99
CD1A_HUMAN	7KP1	A	274	25-121:125:127-302	1.5	96	94	84	100
CD1B_HUMAN	2H26	A	278	22-299	0.7	100	96	83	98
CD1C_HUMAN	5C9J	A	277	24-299:308	1	91	94	83	99
CD1D_HUMAN	1ZT4	C	278	22-299	1.3	100	95	83	100
CD1E_HUMAN	3S6C	A	271	134-250:254-403:405-408	1.4	98	94	70	73
CD2_HUMAN	1HNF	A	179	27:29-206	1.2	99	95	51	100
CD209_HUMAN	6GHV	C	133	212:253-384	0.7	99	95	33	100
CD22_HUMAN	5VKJ	A	310	21-330	2.5	98	88	37	99



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CD226_HUMAN	6ISB	A	220	21-128:130-133:135-242	2.3	99	92	65	100
CD27_HUMAN	5TL5	A	99	23-121	0.9	100	95	38	100
CD28_HUMAN	1YJD	C	118	19-136	0.7	100	93	54	100
CD302_HUMAN	2NAN	A	136	22-81:83-86:88-121:123-127:129-161	2	93	92	59	97
CD320_HUMAN	4ZRQ	D	51	34-36:38-43:71-72:77-116	3	35	75	18	68
CD33_HUMAN	5J06	B	215	18-232	0.9	98	95	59	100
CD38_HUMAN	6VUA	A	255	44:47-300	1.3	98	95	85	100
CD3D_HUMAN	6JXR	d	77	22-98	1.8	100	88	45	71
CD3E_HUMAN	6JXR	f	124	33-156	1.8	100	87	60	100
CD3G_HUMAN	1SY6	A	88	24-28:31-105:113:116:160-165	2.7	85	82	48	52
CD4_HUMAN	3TOE	E	365	26-382:384-390:392	2.6	97	93	80	100
CD40L_HUMAN	1ALY	A	144	113-115:121-214:216-218:220-263	1.5	96	94	55	99
CD44_HUMAN	4PZ4	A	154	18-171	0.9	99	96	21	100
CD5_HUMAN	2JP0	A	107	29:32-137	2.5	98	77	22	97
CD6_HUMAN	5A2E	A	303	43-100:122-366	0.7	99	94	45	100
CD69_HUMAN	3HUP	A	121	79-199	1.2	100	96	61	100
CD79B_HUMAN	3KG5	A	101	45-68:70-72:74-146:148	1.4	96	89	44	98
CD80_HUMAN	1DR9	A	198	34-42:44-149:151-155:157-179:181-186:188-236	3.3	90	95	69	99
CD83_HUMAN	5MJ2	A	81	18-53:56:86-129	1.1	94	90	40	100
CD86_HUMAN	5YXK	A	110	25-134	1	99	96	33	100
CD8A_HUMAN	3QZW	G	114	22-135	0.8	100	94	49	100
CDHR2_HUMAN	5CZR	B	216	20-235	1.1	100	89	16	100
CDHR3_HUMAN	7KNV	A	121	14:18:20:22-134:220-224	2.9	92	84	14	96
CDHR5_HUMAN	6OAE	A	204	26:28-230	1	100	95	24	100
CDON_HUMAN	3N1F	D	102	823-924	0.8	98	77	8	100

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CEAM1_HUMAN	6GBG	D	110	34-143	0.5	98	95	21	100
CEAM3_HUMAN	6AW3	A	108	34-141	0.5	99	96	43	100
CGRF1_HUMAN	2EA5	A	56	252-255:279-330	2.3	89	85	17	82
CISD1_HUMAN	6DE9	A	75	30-31:33-105	1.9	97	93	69	100
CISD2_HUMAN	3FNV	B	68	68-135	0.5	98	93	50	100
CLC10_HUMAN	6PY1	A	130	165:180-308	0.6	98	95	41	100
CLC1B_HUMAN	3WWK	C	122	100-221	0.7	100	96	53	100
CLC2A_HUMAN	4IOP	A	117	56-172	0.8	100	96	67	100
CLC2D_HUMAN	4QKH	A	122	68-69:72-191	0.6	98	95	64	99
CLC4A_HUMAN	5B1X	A	130	105-234	0.6	99	97	55	100
CLC4C_HUMAN	4ZET	A	147	67-213	0.8	99	95	69	100
CLC4D_HUMAN	3WHD	C	148	58:61-70:79-215	1.3	99	93	69	100
CLC4E_HUMAN	3WH2	A	131	68:79-173:175-176:178-210	1.1	97	98	60	99
CLC4K_HUMAN	3KQG	A	169	159-327	0.9	99	96	52	100
CLC4M_HUMAN	1SL6	A	168	219-234:245:247-397	0.8	99	89	42	100
CLC5A_HUMAN	2YHF	A	118	70-187	0.5	99	98	63	100
CLC6A_HUMAN	5VYB	A	143	63-70:75-209	0.2	99	97	68	100
CLC9A_HUMAN	3VPP	B	122	111-200:202-203:208-237	0.8	98	93	51	100
CLIC1_HUMAN	4K0G	A	237	5-241	0.9	100	95	98	100
CLIC3_HUMAN	3KJY	A	217	10-51:62-236	0.9	100	96	92	97
CLIC4_HUMAN	2D2Z	B	237	10-14:17-165:174-256	1.4	98	94	94	99
CLIC5_HUMAN	6Y2H	A	223	173-215:218:227-323:327-407:410	1.1	99	93	54	100
CLM1_HUMAN	2NMS	A	112	17:19-128:130	1.2	96	97	39	100
CLM8_HUMAN	2Q87	B	103	22-66:71-93:95-110:112-115:117-131	1.7	96	94	34	97
CMTD1_HUMAN	2AVD	A	219	44-262	0.2	100	98	84	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
CNTP2_HUMAN	5Y4M	A	150	34-183	0.4	98	95	11	100
COL12_HUMAN	2OX8	C	129	606-734	0.9	99	91	17	100
COMT_HUMAN	4XUE	B	215	51-265	0.8	100	97	79	100
COQ8A_HUMAN	4PED	A	372	255:257:260-279:281-308:310-311:314-348:350-356:358-375:377-380:382:384-484:486-543:545-554:556-588:590-612:614-631:633-644	2.5	97	86	58	100
COX41_HUMAN	5Z62	D	144	26-169	0.9	100	96	85	100
COX6C_HUMAN	5Z62	I	73	3-75	1.6	100	96	97	100
COX7B_HUMAN	5Z62	K	49	30-78	0.9	100	97	61	100
COX7C_HUMAN	5Z62	L	47	15:18-63	0.7	98	95	75	100
CP17A_HUMAN	5IRV	C	470	16:20:37-39:42-43:45-226:229-507:509-510	2.3	98	93	93	99
CP19A_HUMAN	5JL9	A	452	45-496	0.5	100	96	90	100
CP1A1_HUMAN	6UDL	B	477	36-512	0.4	100	97	93	100
CP1A2_HUMAN	2HI4	A	480	34-513	0.4	99	97	93	100
CP1B1_HUMAN	6IQ5	A	459	68-307:312-526:528-530:532	1	99	95	85	100
CP21A_HUMAN	4Y8W	C	442	28-265:274-324:332-484	0.5	100	96	89	100
CP2A6_HUMAN	4EJJ	A	465	30-494	0.4	100	98	94	100
CP2AD_HUMAN	4EJG	D	465	30-494	0.6	100	97	94	100
CP2B6_HUMAN	5WBG	B	464	27-273:275-491	0.9	98	96	94	100
CP2C8_HUMAN	2VNO	A	463	28-490	1.2	100	93	94	100
CP2C9_HUMAN	4NZ2	A	464	27-490	1.4	98	94	95	100
CP2CJ_HUMAN	4GQS	A	461	29-136:139-491	1.6	100	95	94	99
CP2D6_HUMAN	5TFT	A	467	31-497	0.5	99	95	94	100
CP2E1_HUMAN	3T3Z	A	463	31-493	0.3	100	97	94	100
CP2R1_HUMAN	3DL9	A	464	38-501	0.3	100	98	93	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
CP3A4_HUMAN	5TE8	B	468	26-211:213-220:222-282:284-285:289-290:292-500	2.3	98	94	93	99
CP3A5_HUMAN	5VEU	C	469	27-495	0.6	100	95	93	100
CP3A7_HUMAN	7MK8	B	462	25-200:204-214:216-218:220:222-244:246:249-268:270-271:273-282:284-285:287:289-500	1.7	90	94	92	99
CP46A_HUMAN	4J14	A	436	56-491	1	100	97	87	100
CP51A_HUMAN	3JUV	A	446	55-235:237-238:240-249:252-504	1.6	98	95	89	100
CP7A1_HUMAN	3V8D	A	476	24-37:39:41-48:51-472:475:477-506	1.2	97	96	94	99
CR1_HUMAN	5FO9	F	193	491-683	2.1	98	71	9	100
CR2_HUMAN	1GHQ	C	134	20-152:200	1	98	83	13	100
CRLF2_HUMAN	5J11	C	190	29-218	0.4	100	95	51	100
CRTAM_HUMAN	3RBG	D	100	24-123	1.5	96	94	25	97
CSF1_HUMAN	5LXF	B	149	32:35-182	1.2	98	92	27	100
CSF1R_HUMAN	4LIQ	E	469	20-88:94-143:145-146:148-150:152-344:346-351:353-356:359-500	1.2	97	91	48	100
CSF2R_HUMAN	4RS1	B	267	35-74:78-100:102:105-229:232-260:266:268-315	0.8	98	94	67	100
CSF3R_HUMAN	2D9Q	B	299	26-237:245-331	1.5	99	88	36	100
CSMD1_HUMAN	2EHF	A	70	13:80:689-691:736-797:846-848	2.7	33	75	5	96
CSPG4_HUMAN	7ML7	B	137	409:411-412:414-477:479-488:490-549	1.5	90	77	6	99
CTLA4_HUMAN	3OSK	B	123	38-156:158-159:161-162	1.4	98	91	55	100
CX6A1_HUMAN	5Z62	G	73	33:35-58:60-63:66-68:70-110	1.4	90	94	67	97
CX7A2_HUMAN	5Z62	J	56	24:26-80	1.1	98	96	67	100
CXAR_HUMAN	3J6N	K	209	24:26-233	1.2	90	94	57	100
CYB5_HUMAN	2I96	A	85	11-94:96	1.9	99	91	63	79
CYB5B_HUMAN	3NER	A	85	27-111	1.2	100	93	57	94

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
DAF_HUMAN	1OK9	A	254	33-285:287	1.5	99	96	67	100
DAG1_HUMAN	5LLK	A	226	61-162:181-304	0.5	100	90	25	100
DCC_HUMAN	4URT	B	204	844-870:872-876:878-888:890-902:904-1049:1051-1052	1.9	89	81	14	99
DDR1_HUMAN	4AG4	A	340	30-369	0.6	99	93	37	100
DDR2_HUMAN	6FER	D	280	553-582:602-851	1.6	100	87	33	100
DHI1_HUMAN	4IJU	B	271	32-302	1.1	98	96	93	96
DJB12_HUMAN	2CTP	A	73	111-180:182-184	2	89	86	19	94
DJC30_HUMAN	2YUA	A	91	40-124:126-131	2.2	90	82	40	92
DLL1_HUMAN	4XBM	B	401	22-95:97-99:106-131:133-134:136:139:142-430:432:439-440:444:463	2.9	98	90	55	100
DLL4_HUMAN	5MVX	A	251	26-44:49-53:56-57:59-66:68-71:73-74:76-91-94-132:134-145:147-159:161-191:193-199:201-267:269-274:276-287:289-293:296:299-300	4.7	55	94	37	84
DMA_HUMAN	2BC4	C	193	38-230	1.2	98	96	74	99
DMB_HUMAN	2BC4	D	196	21-212:214-216:218	2	98	94	75	99
DMPK_HUMAN	2VD5	A	383	11-300:305-357:360-364:370-388:393:395-409	1.5	98	92	61	98
DNJC1_HUMAN	2CQR	A	65	168-169:171-172:175:189:192:497-500:502-553:556-557	3.2	74	88	12	89
DOA_HUMAN	4I0P	C	180	27-76:78-83:85-208	1.4	97	94	72	99
DOB_HUMAN	4I0P	D	188	29:31-217	2.3	100	96	69	100
DOPO_HUMAN	4ZEL	A	550	45:47-108:110-592:606-609	1.3	99	93	89	100
DPA1_HUMAN	4P4K	E	180	34-213	1.3	100	96	69	99
DPB1_HUMAN	4P5M	B	186	45-46:48-231	2.5	97	93	72	93
DPP10_HUMAN	4WJL	B	719	64-65:67-783	0.7	100	94	90	100
DPP4_HUMAN	5KBY	B	732	36-767	0.8	100	98	96	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
DPP6_HUMAN	1XFD	A	723	127-849	0.9	100	94	84	100
DQA1_HUMAN	1JK8	A	180	27-76:78-207	1.3	91	94	71	99
DQB1_HUMAN	1JK8	B	189	35-138:140-142:144-225	1.8	95	94	72	99
DRA_HUMAN	4I5B	D	184	27-210	1.5	100	95	72	98
DRB1_HUMAN	5NIG	B	195	30-220:223-226	0.9	89	95	73	99
DRB3_HUMAN	2Q6W	B	188	32-219	0.9	100	96	71	100
DRB5_HUMAN	1H15	B	189	30-32:34-219	1.7	98	95	71	100
DSC1_HUMAN	5IRY	A	539	135-673	2.7	100	91	60	100
DSC2_HUMAN	5J5J	A	482	135:137-333:335-468:470-485:488-534:536-546:548-559:563-579:581-589:617-626:652-660:716:723-724:726-729:732:738-741:755-759:762-763	4.3	43	92	54	87
DSCAM_HUMAN	6ZR7	AAA	273	516:595-620:622-633:635-661:663-676:678-694:700-707:710-718:720-784:786-793:795-800:802-808:813-825:827-834:836-840:842-866:872-883:886-890:892-896	4.9	63	81	14	93
DSCL1_HUMAN	1VA9	A	111	728:962:987:989-1095:1180	2.2	96	82	5	91
DSG2_HUMAN	5ERD	A	551	50-526:528-536:539-552:555-565:567-606	3.4	94	93	49	99
DSG3_HUMAN	5EQX	A	438	50-448:450-455:457-488:520	3.2	98	92	44	100
DYSF_HUMAN	7KRB	A	128	8-114:116-119:121-137	2.3	98	85	6	93
E2AK3_HUMAN	4X7L	A	260	585-663:881-957:982-983:986-1087	1.7	98	87	23	100
E41L3_HUMAN	6IBE	A	284	107-389:413	1.2	100	93	26	100
ECE1_HUMAN	3DWB	A	660	101-421:431:433-770	0.9	100	97	86	100
EDA_HUMAN	1RJ7	E	149	241-244:246-390	1.1	97	93	38	100
EFNB1_HUMAN	6THG	F	137	31-164:166-168	1.4	98	93	40	100
EFNB2_HUMAN	6PDL	D	139	27-92:95-167	1.9	100	93	42	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
EFNB3_HUMAN	4BKF	C	140	28:30-118:120-122:124-170	1.2	96	92	41	99
EGF_HUMAN	2KV4	A	46	971-978:981:984-1019:1025	3.7	96	68	4	87
EGFR_HUMAN	3QWQ	A	613	25:27-638	1.3	100	92	51	100
EGLN_HUMAN	5HZW	A	319	200-201:204:354:359-368:370-371:373-434:436:438:441-679	2	95	87	48	48
EMC1_HUMAN	6WW7	A	927	23-24:26-341:367-500:502-503:519-521:523:525-993	2.1	99	91	93	100
EMC10_HUMAN	6Z3W	I	156	50-114:116-120:123-126:129-133:135-178:180-193:196-200:204-216:218	2.7	72	92	60	95
EMC7_HUMAN	6WW7	G	111	43-152:154	1.5	99	90	46	100
EMD_HUMAN	2ODG	C	46	3-48	0.7	100	91	18	98
EMRE_HUMAN	6K7Y	F	54	48-100:102	1.3	98	85	50	100
ENPP1_HUMAN	6WEW	AbA	817	105-921	0.4	100	97	88	100
ENPP3_HUMAN	6C01	A	819	53-871	0.3	100	98	94	100
ENPP4_HUMAN	4LR2	A	379	24-402	0.2	100	98	84	100
ENPP5_HUMAN	5VEM	B	383	19-401	1.2	98	96	80	100
ENPP7_HUMAN	5UDY	A	388	30-417	0.2	100	98	85	100
ENTK_HUMAN	6ZOV	B	234	787-1020	0.8	97	87	23	100
EPCAM_HUMAN	4MZV	A	239	25-263	1.7	98	91	76	99
EPCR_HUMAN	3JTC	B	173	25-197	0.4	100	96	73	100
EPHA1_HUMAN	3KKA	A	64	911-974	1	100	77	7	100
EPHA2_HUMAN	3FL7	A	481	25-58:61:63-108:111:114-153:160-238:241-380:382-464:466:468-477:479-487:489-500:502-513:517-526:529-531	2.8	90	90	49	100
EPHA3_HUMAN	3FXX	A	285	606-772:777:779:784-892:894-895:897:899:903:906-907	1.4	98	87	29	99
EPHA4_HUMAN	4M4R	A	513	27-539	2.3	100	91	52	99
EPHA5_HUMAN	2R2P	A	272	661:663-824:843-951	1.5	97	88	26	96
EPHA7_HUMAN	2REI	A	277	607-779:799-900:902:907	0.9	99	89	28	100



**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
EPHA8_HUMAN	3KUL	B	271	627-792:794-795:797-899	1.3	100	85	27	100
EPHB1_HUMAN	5MJB	A	270	605:608-609:611-646:648-767:787-897	1.2	98	90	27	98
EPHB2_HUMAN	3ZFM	A	248	615-627:632-655:660-765:789-891:893-894	0.6	99	90	24	100
EPHB3_HUMAN	5L6P	A	260	632-778:807-919	1.3	100	87	26	95
EPHB4_HUMAN	6FNK	A	274	600-601:604:607-760:762-766:778-889	1.1	96	89	28	100
EPOR_HUMAN	6MOJ	B	219	28:31-248	1.9	98	90	43	100
ERAP1_HUMAN	6RQX	A	862	46-485:515-554:557-936:939-940	0.6	100	97	92	100
ERBB2_HUMAN	6J71	A	617	22-277:279-284:286-638:644-645	1.1	99	90	49	100
ERBB3_HUMAN	4LEO	C	593	27-38:41:43-112:114-128:130-144:146-155:157:160-171:174:177-187:189:191-204:207-214:217-638	3.8	91	92	44	99
ERBB4_HUMAN	2AHX	B	615	25-639	2	100	91	47	100
EREG_HUMAN	5WB7	E	47	64-109:111	1.4	98	81	28	100
ERN1_HUMAN	6XDB	A	404	561-964	1.2	100	91	41	100
ESYT2_HUMAN	4P42	B	431	192-255:257:259-260:263-371:379-397:414-463:466-524:532-658	1.8	99	90	47	100
FBCD1_HUMAN	4M7F	A	220	239-458	0.3	100	98	48	100
FCAR_HUMAN	1OVZ	A	193	27-219	1.4	98	92	67	100
FCER2_HUMAN	4GKO	L	136	158-293	1.1	100	92	42	100
FCERA_HUMAN	1J86	B	173	26-197:199	0.9	99	93	67	100
FCG2A_HUMAN	1H9V	A	172	37-208	1.3	99	95	54	100
FCG2B_HUMAN	2FCB	A	173	46-218	1.6	99	95	56	100
FCG2C_HUMAN	3WJL	C	160	48-72:81-215	0.5	100	97	50	100
FCG3A_HUMAN	5MN2	A	172	22-191:193-194	2.6	99	97	68	100
FCGR1_HUMAN	4X4M	E	259	21-219:223-282	1.9	94	94	69	100
FCGRN_HUMAN	6QIP	B	267	26-291:293	0.6	100	95	73	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
FDFT_HUMAN	3WEK	A	335	35-368:370	0.9	99	96	80	100
FGFR1_HUMAN	4RWK	A	300	457-646:655-660:663:670-770:772-773	2.2	96	87	36	97
FGFR2_HUMAN	4J96	B	305	446-447:464-766	1.7	99	87	37	100
FGFR3_HUMAN	6PNX	B	294	442-443:457-575:581:585-755:757	1.9	98	87	36	100
FGFR4_HUMAN	4TYG	A	284	438-442:445:447:451-567:583-635:645-648:658-760	2.1	97	87	35	97
FICD_HUMAN	6I7J	A	337	100:103:105-432:434-440	0.7	97	96	74	100
FIS1_HUMAN	1PC2	A	129	5-6:9-125:128:136:138-143:147-148	2.7	94	83	85	85
FKBP8_HUMAN	5MGX	G	266	91-356	0.7	100	96	65	100
FKRP_HUMAN	6KAM	A	446	46-491	0.4	100	97	90	100
FLRT3_HUMAN	5CMP	A	324	29-349:351:353-354	0.6	99	96	50	100
FLT3_HUMAN	3QS9	E	403	79-95:98-101:103-111:113-116:118-119:121:123:125:127-147:149:151-162:164:169-201:215-347:350-436:438-447:452-470:476-481:484-489:496-507:509-531	2.8	89	84	41	100
FLT3L_HUMAN	7NBI	B	135	28-29:31-163	1.6	98	96	57	98
FND3A_HUMAN	1WK0	A	119	257-296:298-300:302-375:453-454	2	93	78	10	87
FNDC5_HUMAN	4LSD	F	97	33-75:77-129:132	1	99	94	46	100
FOLH1_HUMAN	6SKH	A	696	52:56-750	0.6	100	97	93	100
FURIN_HUMAN	5JMO	B	470	108-576:579	0.8	99	96	59	100
FUT8_HUMAN	6VLD	B	469	107-575	0.4	100	97	82	100
G6B_HUMAN	6ROX	E	99	20-36:38-39:41-51:54-68:70:72-76:78-79:81:83-88:91-124:126:128-131	1.4	66	91	41	100
GALT2_HUMAN	4D0T	A	496	75-569:571	1.3	100	96	87	100
GALT4_HUMAN	6H0B	B	521	58-578	1.2	100	96	90	100
GALT7_HUMAN	6IWR	A	546	112-657	1	100	97	83	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
GDAP1_HUMAN	7AIA	AAA	234	22:24-58:60-62:86-171:173-174:177:222-326:328	2.1	97	95	65	90
GFRAL_HUMAN	6WMW	B	192	129-320	0.6	100	92	49	100
GGT1_HUMAN	4GG2	A	343	33-373:439-440	0.9	99	97	60	100
GHR_HUMAN	1HWH	B	196	50-70:81-255	0.9	100	92	31	100
GIMA1_HUMAN	3V70	A	217	26-53:63-251	0.4	100	96	71	100
GIMA4_HUMAN	3LXX	A	165	29-58:66-89:91:96-139:141-148:150-159:172-178:180-220	1.4	99	92	50	99
GLCE_HUMAN	6I02	B	516	102-617	0.4	100	97	84	100
GLDN_HUMAN	5YBY	A	245	299:302-545	0.4	100	96	44	100
GLIP1_HUMAN	3Q2U	A	193	21:23-214	1	100	97	73	100
GLT10_HUMAN	2D7R	A	536	68-603	0.5	100	96	89	100
GLT12_HUMAN	6PXU	B	532	50-581	0.5	100	97	92	100
GP1BA_HUMAN	1OOK	G	280	17-286:632:635-637:639-642:644-645	2	96	93	43	99
GP1BB_HUMAN	3RFE	A	119	25-143	0.3	99	95	58	100
GPIX_HUMAN	3REZ	A	111	18:20-28:34-103:106-111:113-137	1.3	57	91	63	98
GPVI_HUMAN	5OU9	A	176	20-121:124:127-148:150-159:164-171:175-207	2.2	89	94	52	98
GPX8_HUMAN	3CYN	A	173	37-38:40-210	1.6	96	97	83	99
HAVR1_HUMAN	5DZO	A	107	21-127	0.9	99	93	29	100
HAVR2_HUMAN	6TXZ	A	109	22-130	0.9	100	92	36	100
HEPS_HUMAN	1Z8G	A	364	49-159:167-419	0.6	100	96	87	99
HERP2_HUMAN	2KDB	A	77	9-85	1.2	100	89	19	100
HFE_HUMAN	1A6Z	A	270	26-41:46-299	1.6	100	94	78	99
HLAB_HUMAN	6UJ7	A	279	25-303	1.3	100	97	77	100
HLAC_HUMAN	1EFX	A	278	25-299:301-303	1.9	91	96	76	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
HLAE_HUMAN	3BZF	A	276	20:23-297	1.4	99	96	77	100
HLAF_HUMAN	5KNM	A	276	22-297	0.8	100	97	80	100
HLAG_HUMAN	6AEE	A	275	26-300	0.8	99	97	81	100
HMOX1_HUMAN	1NI6	C	223	1-223	1.1	100	95	77	100
HMOX2_HUMAN	2RGZ	B	219	28:31-247:249	0.8	99	96	69	100
HMR1_HUMAN	6PUM	C	269	22-269:271:273-292	1	99	96	79	100
HS3S5_HUMAN	3BD9	A	258	85-306:311-346	0.7	98	96	75	100
HS3SA_HUMAN	1T8U	B	271	27:31:34:136:140-406	1.4	98	96	67	100
HTRA2_HUMAN	5FHT	A	296	142-279:281:291-346:360-460	1	99	92	65	99
I10R1_HUMAN	1LQS	R	207	21:24-229	1.2	97	94	36	100
I10R2_HUMAN	3LQM	A	199	20-218	1.3	97	95	61	99
I11RA_HUMAN	6O4P	A	295	23-24:26-153:162-323:325-327	1.3	98	93	70	100
I12R1_HUMAN	6WDP	A	207	27-31:33-36:39:41-45:47-58:60-66:68-74:76-123:125-129:131-242:244	3.4	84	84	31	98
I13R1_HUMAN	5E4E	C	303	32-191:198-340	0.8	100	91	71	100
I13R2_HUMAN	3LB6	D	284	29-58:63:65-81:83-98:100-160:164:166-248:253-297:302-331	0.8	100	94	75	100
I15RA_HUMAN	2Z3Q	B	81	28-108	1.8	96	93	30	100
I17RA_HUMAN	4HSA	C	272	33-304	1.4	99	90	31	100
I17RC_HUMAN	6HG4	B	427	80-94:107-169:188-536	1.9	95	83	54	100
I18RA_HUMAN	3WO4	C	270	28-35:37:39-51:77-79:101-102:104-127:138-356	1.2	95	87	45	100
I20RA_HUMAN	4DOH	R	204	39-242	1.1	99	94	37	100
I20RB_HUMAN	4DOH	B	193	34-226	1	99	95	62	100
I22R1_HUMAN	3DGC	S	207	19-225	0.7	99	94	36	100
ICAM1_HUMAN	1Z7Z	I	430	28-334:348-349:353-423:425-433:437-444:448-456:458-481	3	94	94	81	99
ICAM2_HUMAN	1ZXQ	A	192	25-216	1.2	100	94	70	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
ICAM3_HUMAN	1TOP	B	86	30-115	0.9	99	92	16	100
ICAM5_HUMAN	4OI9	A	378	32-406:476-478	1.7	99	92	41	100
ICOS_HUMAN	7JOO	C	102	30-73:77-85:87:90-137	1.9	92	86	51	94
ICOSL_HUMAN	6X4T	A	210	17:19-144:146-150:154-231	1.6	97	93	70	100
IGF1R_HUMAN	5U8Q	A	800	31-64:67:69:71:73-170:172-177:179-184:190-197:199-219:223-674:715-716:718-723:726-734:775-929	3.3	96	88	59	100
IGHD_HUMAN	1ZVO	C	213	390-395:446-476:478-482:484-493:495-497:499-510:513-540:542-553:555-570:572-575:578:580-609:611-620:622-653:655-658:660-668	3.9	66	80	55	42
IGHM_HUMAN	2RCJ	O	229	401:455-463:466-472:475:478:482:485:508-527:529-543:545-554:556-572:574-616:618-636:638-667:670-680:682-683:685-725	3.9	27	90	51	44
IL18R_HUMAN	3WO4	B	301	18-318	1.3	99	89	56	100
IL1AP_HUMAN	3O4O	B	321	24-48:50-57:59-76:78-87:89-339:341-349	1.7	92	93	56	99
IL1R1_HUMAN	1ITB	B	310	23-332	1.2	100	93	54	100
IL1R2_HUMAN	3O4O	C	315	28-299:301-319:321-343:345	1.7	94	90	79	100
IL21R_HUMAN	3TGX	C	209	20-228	0.6	98	93	39	100
IL23R_HUMAN	6WDQ	C	293	23-24:26-316	1.7	99	94	47	100
IL2RA_HUMAN	6VWU	A	136	13-16:139-207:246-308	2.4	94	90	50	53
IL2RB_HUMAN	2ERJ	B	204	32-234:236	0.6	98	93	37	100
IL2RG_HUMAN	2ERJ	C	195	54-248	0.7	100	93	53	100
IL3RA_HUMAN	6NMY	F	270	25:27-294:296	1.2	99	94	71	100
IL3RB_HUMAN	4NKQ	A	410	24-38:41-52:54-90:92-102:104-438	2.7	91	92	46	100
IL4RA_HUMAN	3BPL	B	202	23-224	0.9	96	93	24	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
IL5RA_HUMAN	6H41	A	309	27-335	1.2	99	94	74	100
IL6RA_HUMAN	1N26	A	299	20-318	0.8	100	94	64	100
IL6RB_HUMAN	3L5H	A	585	24-48:50-104:106-111:113-122:124-612	2.6	100	92	64	100
IL7RA_HUMAN	3UP1	A	201	32-232	0.8	100	94	44	100
ILRL1_HUMAN	4KC3	B	200	21-50:53:56-116:118-125:127-210:214-216:261-263:291-293:326-327:354-358	2.7	88	91	36	72
ILRL2_HUMAN	6U6U	R	195	21-27:29-35:37-123:125-131:133-219	1.7	92	83	34	99
INAR1_HUMAN	3SE4	A	283	32-34:36-48:59-82:84-94:96-108:110-114:116-274:277-329:331-332	1.9	93	92	51	99
INAR2_HUMAN	1N6V	A	205	34-38:41-163:165-168:170-238:241:244-245:248	3.1	96	87	40	97
INGR1_HUMAN	1FG9	C	210	29-154:157-161:163-240:242	1.4	98	91	43	100
INGR2_HUMAN	6E3L	E	213	28-240	0.9	100	95	63	100
INLR1_HUMAN	3OG6	B	200	24-223	0.8	100	92	38	100
IRPL1_HUMAN	5WY8	B	323	27-349	0.8	100	93	46	100
ITA1_HUMAN	1PT6	B	195	171-362:367-369	0.9	97	92	17	100
ITA2_HUMAN	1AOX	A	201	168-364:367-370	1.3	98	89	17	100
ITA2B_HUMAN	3FCS	A	913	32-698:700-793:795:806-870:905-989:991	0.6	100	93	88	100
ITA4_HUMAN	3V4V	A	580	34-524:526-538:540-561:563-574:576-588:594-620:673:719	3.1	96	91	56	100
ITA5_HUMAN	7NWL	A	603	42-644	1.5	100	91	57	100
ITA6_HUMAN	7CEC	A	553	24-221:234-240:251-254:294-567:574-579:586-609:612:615-629:631:638:640-661	1.8	99	91	49	100
ITAL_HUMAN	5E6U	A	583	26-331:337:341-614:752-753	0.8	99	92	50	100
ITAM_HUMAN	1NA5	A	195	114:147-335:337-338:344-346	0.9	97	90	17	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
ITAV_HUMAN	4G1E	A	941	31-649:651-868:870:872-876:878:885:897-992	2.4	100	93	90	98
ITAX_HUMAN	4NEH	A	1084	20-1103	0.8	99	90	93	100
ITB1_HUMAN	4WK4	B	435	24-98:102:105-436:438:440-465	1.5	99	92	55	100
ITB2_HUMAN	5ES4	B	674	22:24-696	2.4	100	89	88	100
ITB3_HUMAN	3IJE	B	695	26:28-716:718-721:723	2	99	90	88	100
ITB4_HUMAN	3F7R	A	200	1126-1325	2.4	100	82	11	93
ITB6_HUMAN	4UM9	D	455	22-47:49:56:58-458:460-481:488-491	0.9	99	90	58	100
ITB7_HUMAN	3V4V	B	375	100-474	1.2	100	91	47	100
ITB8_HUMAN	6UJC	B	359	104-439:441:446-467	1.1	100	90	47	100
IZUM1_HUMAN	5JK9	A	240	18-257	1.6	98	93	69	100
JAG1_HUMAN	4CC1	A	306	32-337	1.3	99	88	25	100
JAG2_HUMAN	5MW7	A	289	27-51:62:65-113:116-117:122-156:160-161:163-337	2.8	99	85	23	99
JAM1_HUMAN	1NBQ	A	209	25-233	1.2	100	96	70	100
JTB_HUMAN	2KJX	A	60	48-102:104-106:108-109	2.2	90	85	41	92
K0319_HUMAN	2E7M	A	103	331-333:335-431:433-435	2.3	94	77	10	91
KCNE1_HUMAN	2K21	A	79	3-24:26-28:33-36:38-39:51-52:54-84:89:91-99:102-106	3.6	70	74	61	61
KCNE3_HUMAN	2NDJ	A	54	36-38:41-44-46:48-56:58-67:69-70:75:82:86-87:90-91:94-95:98-102:104-115:118	4.2	7	65	52	52
KI2L1_HUMAN	1NKR	A	195	27-221	1.8	100	95	56	100
KI2L2_HUMAN	2DL2	A	197	25-221	1.6	100	94	57	100
KI2L3_HUMAN	1B6U	A	199	26-223:225	1.1	100	94	58	100
KI2L4_HUMAN	3WYR	A	189	30-218	1.6	99	91	50	100
KI2S2_HUMAN	1M4K	A	191	29-176:181-223	2.2	100	95	63	99
KI2S4_HUMAN	3H8N	A	195	27-221	1.2	100	96	64	100



**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
KI3L1_HUMAN	7K80	G	289	27-66:68-78:80-317	1.6	96	89	65	100
KIRR3_HUMAN	2CRY	A	116	379-383:398:412-521	2.4	94	90	15	95
KIT_HUMAN	2E9W	B	469	32:34-317:320-444:446-447:449-450:452-467:469-506:508	1.9	95	89	48	100
KLOT_HUMAN	5W21	A	914	34-97:116-956:959-967	1.8	99	92	90	99
KLOTB_HUMAN	5VAQ	A	861	52:54-62:75-119:126-537:576-969	0.8	100	96	82	100
KLRB1_HUMAN	5MGS	H	129	90-218	1.6	100	95	57	100
KLRD1_HUMAN	3CDG	J	123	57-179	0.7	100	96	69	100
KLRF2_HUMAN	4IOP	B	121	76-196	0.6	100	96	58	100
KLRG1_HUMAN	3FF7	C	112	75-186	0.4	99	96	57	100
KREM1_HUMAN	5FWV	A	294	29-322	0.7	100	97	62	100
LAIR1_HUMAN	3KGR	A	99	25-123	0.6	99	97	34	100
LAMP3_HUMAN	4AKM	B	157	222-377:379	1.2	99	95	38	100
LCAP_HUMAN	5MJ6	A	860	151:153-154:160-639:649-1025	0.5	100	97	84	99
LDLR_HUMAN	1N7D	A	500	236-239:252-280:282-286:292-295:297-300:395-434:436-547:549-597:599-612:615-853	4.1	82	87	58	78
LEPR_HUMAN	3V6O	B	184	430-451:453-454:460-559:566-588:595-631	0.9	99	88	16	100
LFA3_HUMAN	1CCZ	A	167	28:30-135:138-145:148:150-152:155-164:166-170:175-180:183-186:188-207:210:212-213	2	61	93	67	98
LIFR_HUMAN	3E0G	A	478	51:53-115:119-130:132-180:182-195:197-535	1.8	94	89	44	100
LIGO1_HUMAN	4OQT	A	475	42-516	0.9	100	97	77	100
LIRA2_HUMAN	2OTP	B	142	26-66:69-76:79-160:163:165-172:210-211	2.2	89	92	29	73
LIRA5_HUMAN	2D3V	A	177	43:45-105:107-146:158-176:180-210:212-236	1.2	99	94	59	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
LIRB1_HUMAN	6ZDX	B	396	25-420	1.2	100	92	61	100
LIRB2_HUMAN	6AED	A	385	24:26-63:68-78:81-82:85-162:169-423	2	96	91	64	99
LIRB4_HUMAN	3P2T	A	193	25-163:165-174:176-219	2.5	95	89	43	99
LMAN1_HUMAN	3LCP	A	234	41-274	0.3	100	96	46	100
LMTK3_HUMAN	6SEQ	A	278	128:130:132-227:229:232-235:237-318:321-413	1.1	97	90	19	100
LRBA_HUMAN	1T77	A	414	875:877-1289	0.8	100	94	30	100
LRC32_HUMAN	6GFF	I	551	18:21-280:290-299:312-587:589-592	1	99	91	83	100
LRC4C_HUMAN	3ZYJ	A	393	45-341:343:346-367:369-413:416-423:426-433:435-446	3.2	90	94	61	99
LRFN5_HUMAN	5XNP	A	361	13-14:16-374	1	99	94	50	100
LRIG1_HUMAN	4U7L	A	453	40:42-492:552	1.1	98	94	41	100
LRP1_HUMAN	2FYJ	A	71	258:291-301:304-310:312-316:318-322:324-334:336:338-341:344-348:351-362:365-373	3.9	37	72	5	87
LRP6_HUMAN	4DG6	A	614	20-632:649	1.5	100	90	38	100
LRP8_HUMAN	5B4X	B	441	175:186:188-190:200:203-206:217-226:228-230:235-238:241-243:317:322-324:326:332:337-341:375-380:382-775	2.9	90	90	46	92
LRRC4_HUMAN	3ZYI	A	395	44-319:323-441	0.7	100	96	60	100
LRRT2_HUMAN	5Z8Y	A	328	34-361	0.6	100	96	64	100
LYAM1_HUMAN	3CFW	A	156	39-194	0.8	100	95	42	100
LYAM2_HUMAN	4C16	B	279	21-32:34-273:275-280:282-295:297-302:352	3.5	91	92	46	100
LYAM3_HUMAN	1G1R	D	160	42-198:222:244-245	1.4	98	89	19	100
MA1B1_HUMAN	5KK7	A	455	245-699	0.2	100	98	65	100
MADCA_HUMAN	1BQS	A	206	23-62:64-67:69-164:166-177:179-232	2	94	91	54	99

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
MANEA_HUMAN	6ZJ5	AAA	360	99-458	0.8	100	97	78	99
MARC1_HUMAN	6FW2	A	285	52-129:289-495	0.4	99	97	85	64
MAVS_HUMAN	2MS8	A	100	3-102	1.7	100	94	19	98
MCL1_HUMAN	6YBL	A	167	338-339:400-407:489-490:492-493:514-515:517-667	2.6	90	88	48	33
MCP_HUMAN	3O8E	B	252	35-286	1.3	100	96	64	100
MEP1B_HUMAN	4GWM	A	561	25-193:200-301:308-596:598	1	100	95	80	100
MERTK_HUMAN	7AAZ	A	286	574-623:625-632:634-751:754-755:758-761:763-764:766-867	2.5	95	88	29	99
MET_HUMAN	7MO7	B	697	25-31:33-104:106-107:110-302:306-307:311-619:621-627:634-659:661-670:672-715:717-720:722-729:731-739:770-771:773:797	3.2	94	88	50	100
MGA_HUMAN	3TOP	A	890	960-1849	0.7	100	95	48	100
MGAT2_HUMAN	5VCM	B	354	84-87:90-298:301-403:410-418:420:422-449	1.6	99	95	79	99
MGT5A_HUMAN	5ZIB	A	572	75-84:131-133:147-151:153:156-174:179-180:182-190:192-213:216-217:219-285:302-336:344-346:352-487:491-748	3.2	89	90	77	99
MICA_HUMAN	1HYR	C	271	23-60:62-63:65-75:77:79-244:246-251:253-276:278-290:292:294-302	3.5	85	93	71	99
MICB_HUMAN	1JE6	A	275	23-297	2.6	98	92	72	100
MICU1_HUMAN	6XJX	Q	361	104-254:256:258-275:277-281:283-337:339:341:344-356:361-475:477	1.7	90	88	76	98
MICU2_HUMAN	6LB7	D	303	76:85-208:210:215:235-409:411	2.2	99	89	70	97
MICU3_HUMAN	6AGI	B	321	135-181:183-270:273-291:336:338-500:502:504-505	1.8	99	89	61	100
MID49_HUMAN	5WP9	B	328	126-283:285-295:297-455	1.8	98	91	72	100
MID51_HUMAN	4NXV	C	333	134-466	1.5	100	94	72	99
MIRO1_HUMAN	5KU1	A	398	181-479:484-582	0.7	100	96	64	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
MIRO2_HUMAN	5KUT	A	172	414-450:455-479:482-487:490-588:591-595	2	94	84	28	96
MMP14_HUMAN	6CM1	A	196	316-511	1.1	100	94	34	100
MMP16_HUMAN	1RM8	A	169	123:125-292	1.2	99	88	28	100
MPEG1_HUMAN	6U2K	B	604	28-435:437:447-544:547:551-646	1.2	100	89	84	100
MPRI_HUMAN	6P8I	A	663	43-117:119:122:124-331:336-346:351-367:369-371:374:377-388:391-491:493-502:504:510-518:520-523:528-532:542-543:548:550:552-554:557-570:572:582-603:607:609-765:819:822	3.5	94	78	27	100
MPZL1_HUMAN	6IGO	C	122	37-156:159-160	0.7	98	92	45	100
MRC1_HUMAN	6INN	A	588	21:23-30:32-41:43-67:69-131:133-156:158-349:352-433:435-466:468-488:490-492:500:502-505:507-522:524-592:594-604:606-619:621-632	3.3	93	87	40	100
MRC2_HUMAN	5EW6	A	442	37-99:103-138:154:156:158-363:365:375:378:380-511	1.6	98	85	30	100
MSPD2_HUMAN	6TQT	A	130	313:315-319:321-341:344-446	1.6	96	85	25	99
MUC1_HUMAN	2ACM	A	57	1041-1097	1.2	100	86	5	100
MUC18_HUMAN	6LYN	C	178	306-311:342-395:397-411:413:415-429:431-446:448-458:460-469:471-480:483-495:497-522:524	3.9	61	91	28	97
MUL1_HUMAN	6M2D	B	56	294:297-351	1.6	98	88	16	98
MXRA8_HUMAN	6JO8	O	258	31-36:38-46:48-79:82-292	3	94	90	58	100
MYOF_HUMAN	2DMH	A	130	8-80:82-85:87-138:349	1.8	95	86	6	93
MYP0_HUMAN	3OAI	A	121	397-516:518	1.1	98	95	49	25
MYRF_HUMAN	5YHU	A	191	342-532	0.3	100	93	17	100
NALD2_HUMAN	3FED	A	690	46-132:136-328:330-739	0.8	100	97	93	100
NALDL_HUMAN	4TWE	A	706	34:36-740	0.7	100	96	95	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
NB5R3_HUMAN	1UMK	A	271	31-301	0.7	100	98	90	100
NCAM1_HUMAN	3MTR	A	197	411-607	0.8	98	94	23	100
NCAM2_HUMAN	2JLL	A	376	300:302-345:347:349-462:464-467:469-620:622-634:638-639:641-647:650:652-656:658-662:664-666:668-691	3.6	85	94	45	99
NCLN_HUMAN	6W6L	5	465	45-59:61-72:84-119:126:130-135:145-181:193-194:197-209:221-224:226:228-325:329-334:336-337:340-362:364:367-368:370-384:386-399:405-465:468:471-476:479-483:486-501:503-505:518-536:539-548:554-606:608-609:612	4.8	72	90	83	90
NCPR_HUMAN	5EMN	A	607	67-237:242-677	0.7	100	95	90	100
NCTR1_HUMAN	1P6F	A	188	25-212	0.3	100	97	62	100
NCTR2_HUMAN	1HKF	A	108	23-130	0.9	100	96	39	100
NCTR3_HUMAN	3NOI	A	115	20-134	1.2	98	95	57	97
NDST1_HUMAN	1NST	A	282	579-586:601-664:670-879	0.6	100	96	32	100
NDUA1_HUMAN	5XTI	S	70	1-70	0.9	100	97	100	100
NDUA3_HUMAN	5XTI	U	83	2-84	0.9	100	97	99	100
NDUA4_HUMAN	5Z62	N	77	1:4-44:46-51:53-75:77-82	2	58	93	95	97
NDUAD_HUMAN	5XTI	W	132	13-16:20-21:23-33:35-38:40-150	1.8	92	96	92	96
NDUB1_HUMAN	5XTI	n	55	3-51:53-55:57-59	1.6	96	93	95	98
NDUB3_HUMAN	5XTI	Z	79	10-51:53-57:59-89:91	0.9	94	93	81	99
NDUB4_HUMAN	5XTI	o	128	2-129	1.4	100	95	99	100
NDUB5_HUMAN	5XTI	a	138	52-189	1.1	100	95	73	100
NDUB6_HUMAN	5XTI	b	101	40:45:49-110:112-114:116-130:132-134:136-151	2.7	76	89	79	81
NDUB8_HUMAN	5XTI	c	152	33:35-178:180-184:186-187	1.2	97	95	82	99
NDUBB_HUMAN	5XTI	e	97	53-54:56-149:151	1.9	97	90	63	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
NDUC2_HUMAN	5XTI	g	118	1:3-5:7-120	1.4	98	91	99	99
NECT1_HUMAN	4MYW	B	303	33-334:336	2	100	94	59	100
NECT2_HUMAN	5V52	D	127	33-108:110-116:119-160:162:187	1.5	92	89	24	100
NECT3_HUMAN	4FOM	A	302	58-357:359-360	1.4	100	94	55	100
NECT4_HUMAN	4FRW	A	215	32-244:321-322	1.4	99	93	42	100
NEO1_HUMAN	3P4L	A	198	852-898:900:903-1052	1.7	99	81	14	100
NEP_HUMAN	6SUK	A	698	53-750	0.2	100	98	93	100
NFASC_HUMAN	3P40	A	390	37-426	1.4	100	88	29	100
NICA_HUMAN	7D8X	A	667	34-699:701	1.6	100	91	94	100
NKG2A_HUMAN	3CDG	F	120	110-111:115-232	1	98	93	52	100
NKG2D_HUMAN	1MPU	A	128	85-86:88-89:91:93-215	1	97	94	59	100
NLGN1_HUMAN	5OJ6	A	547	50:52-164:205:207-208:211-317:327-599:607-656	0.7	99	95	63	100
NLGN2_HUMAN	5XEQ	A	525	42-149:175-392:401-552:563-609	0.8	100	95	63	100
NLGNX_HUMAN	2WQZ	A	545	35-36:38-160:164-539:543:555:557-596:598-599	1.1	98	94	67	100
NOTC1_HUMAN	6PY8	F	249	1555-1556:1566:1569-1573:1732:1735:1741:1744-1745:1748:1878:1880-1896:1906:1909-2124	2.3	94	80	10	98
NOTC2_HUMAN	2O04	A	226	1424-1426:1428-1594:1617-1672	1.3	98	77	9	100
NOTC3_HUMAN	4ZLP	A	241	1385-1562:1575-1637	1.7	100	79	10	100
NPTN_HUMAN	6A69	B	127	236-361:364	1.3	100	95	32	100
NR3L1_HUMAN	6YJP	C	224	22:24-151:153-157:159-248	1.2	96	92	49	100
NRCAM_HUMAN	1UEN	A	123	574-577:619-620:623-624:759-760:842-895:898-952:954-956:977	2.4	90	86	9	98
NRG1_HUMAN	1HRE	A	57	172-174:177:179-200:202-205:207-218:220:222-229:231-233:235-236:628	3.1	79	76	9	85

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
NRP1_HUMAN	2QQM	A	436	145-197:200-201:204-270:273-586	1	99	92	47	100
NRP2_HUMAN	2QQL	A	554	26-196:208-508:516:518-595:597:600:602	1.2	99	93	60	100
NSDHL_HUMAN	6JKG	A	193	35-150:165:167:169-203:211:228:234-237:261-291:293:374:377	2.1	94	96	52	89
NTRK1_HUMAN	2IFG	B	343	35-44:46-61:63-67:69-81:83-92:94-233:235-242:244-320:322-326:328-383:385:391-392	4.2	88	86	43	99
NTRK2_HUMAN	4AT5	A	288	524-560:566-816	2.2	99	86	35	98
NTRK3_HUMAN	6KZD	A	276	528-636:649-712:729-831	1.3	100	87	33	98
OLR1_HUMAN	6TL7	B	133	142-274	1	98	94	49	99
OSBL8_HUMAN	1V88	A	126	150-274:277	2.4	94	82	14	97
OST48_HUMAN	6S7O	G	411	42-452	0.7	100	95	90	100
OSTM1_HUMAN	7JM7	B	195	81-135:137:146-208:210:221-282:286-287:289-297:300-301	2.4	92	90	58	89
OTULL_HUMAN	6DRM	A	270	87-356	1.1	100	95	76	100
P4HTM_HUMAN	6TP5	A	370	107-180:182:187-481	0.6	100	92	74	100
PAR16_HUMAN	6HXS	A	248	3-225:227-228:252-274	1.6	98	92	77	100
PCD15_HUMAN	6E8F	C	249	9-13:295-301:316-322:359-364:377-381:383-386:415-419:454-461:463-464:466-471:473-510:518-595:606-650:653-658:661-687	4.4	76	85	13	75
PCD17_HUMAN	6VFT	C	420	17:19-41:44-46:60-393:408-464:500:504	2.2	98	90	36	100
PCD18_HUMAN	6VFR	A	428	27:29-455	2.5	100	89	38	100
PCD19_HUMAN	6VFU	C	427	22-49:51-57:59-448:483-484	2.7	97	91	37	100
PCDGF_HUMAN	6MEQ	A	416	30:32-445:539	2	99	91	45	100
PCDH1_HUMAN	6VFP	A	439	59-497	2.6	100	88	41	100



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UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
PCDH7_HUMAN	2YST	A	108	276:310-341:343:347-348:351-399:401-403:405-420:466:522-524	2.4	92	92	10	91
PCDH8_HUMAN	6VFX	A	222	489-491:493-711	1.8	99	90	21	100
PCDH9_HUMAN	2EE0	A	113	218-219:240-245:247-279:281-285:287-353	1.9	89	90	9	99
PD1L1_HUMAN	3FN3	A	215	17:19-232	1.4	100	95	74	100
PD1L2_HUMAN	6UMT	B	99	20-63:65:68-121	1	99	93	36	100
PDCD1_HUMAN	6JJP	F	118	29-146	1	100	92	41	100
PECA1_HUMAN	5GNI	B	198	31-65:67-212:214-224:226-231	1.2	90	90	27	100
PEX14_HUMAN	2W84	A	57	17:19-20:22:24-73:75-77	2	88	85	15	100
PGAM5_HUMAN	5MUF	A	210	56-63:65-67:91-289	0.5	99	97	73	100
PGFRA_HUMAN	5K5X	A	343	554-697:776-785:787-975	1.1	97	84	32	99
PGFRB_HUMAN	3MJG	X	274	32-36:38-104:110-111:113-312	1.6	98	86	25	100
PGRC1_HUMAN	4X8Y	A	111	70-180	0.9	97	96	57	99
PIGR_HUMAN	6UE9	C	536	20-507:509-514:525-565:567	1.9	99	89	70	100
PILRA_HUMAN	5XOF	B	120	31-150	0.5	98	95	40	100
PILRB_HUMAN	4NFD	A	120	31-150	0.5	98	97	53	100
PLA2R_HUMAN	6JLI	A	118	1117-1234	0.8	100	81	8	100
PLAT2_HUMAN	4DPZ	X	108	2-39:52-105:111-112:114-127	1.6	100	90	67	100
PLAT3_HUMAN	2KYT	A	122	5-42:44-54:56-128	2.3	92	87	75	98
PLAT4_HUMAN	2LKT	A	117	1-39:52-53:56-59:61-63:65-133	3.1	94	85	71	94
PLM_HUMAN	2JO1	A	59	31-32:37-73:79-80:83:86-88:90-91:93-103:105	3.4	70	72	64	82
PLXA2_HUMAN	3Q3J	A	100	1288:1291:1494-1495:1498-1540:1546-1576:1581-1602	1.5	96	85	5	98
PLXA4_HUMAN	4.00E+74	A	101	1496-1507:1512-1574:1578-1602:1604	1	99	85	5	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
PLXB1_HUMAN	3SU8	X	524	1558-1559:1562-1757:1764-1854:1879:1881-1896:1898-1899:1929-2144	1.8	99	84	25	97
PLXB2_HUMAN	4.00E+71	A	90	1459-1500:1510-1519:1521-1535:1539-1561	1	100	86	5	100
PLXC1_HUMAN	6VXK	B	737	37-87:89-93:96:112-520:529-544:546:548:551:553:556-559:564-565:567:582-595:668-797:799:802-822:829-845:847-859:871-891:903-917:934-945	3	93	82	47	99
PLXD1_HUMAN	3H6N	A	101	1553-1564:1566-1574:1576-1651:1653-1656	1.5	98	86	5	100
PMGT1_HUMAN	5GGI	B	551	97-647	0.5	100	97	83	100
PMGT2_HUMAN	6XFI	A	511	52-278:285-465:477:479-580	1.5	100	95	88	100
PPAP_HUMAN	1ND6	B	343	33-374:376	0.3	100	98	89	100
PREB_HUMAN	5TF2	A	337	8-35:37-40:42-55:57-99:138-236:239-387	1.3	99	95	81	100
PRLR_HUMAN	3NCF	B	206	25-230	0.4	99	94	33	100
PRSS8_HUMAN	3E0N	B	249	49-297	1.2	99	94	73	99
PTCRA_HUMAN	3OF6	E	104	23-126	0.9	100	88	37	100
PTGIS_HUMAN	2IAG	A	470	23-319:328-500	0.7	100	96	94	100
PTK7_HUMAN	6VG3	B	279	786:789-1066	1.8	100	85	26	100
PTN1_HUMAN	7LOC	A	299	1-299	0.3	100	97	69	100
PTN2_HUMAN	1L8K	A	273	5-276:278	1.3	100	96	66	100
PTPR2_HUMAN	2QEP	A	288	723:725-968:970-1012	1	99	93	28	100
PTPRA_HUMAN	6UZT	A	587	215-801	1.3	100	96	73	100
PTPRB_HUMAN	2I4G	A	288	1678-1749:1754-1853:1856-1971	1.3	100	89	14	100
PTPRC_HUMAN	1YGU	B	567	623:626-627:629-738:740-749:751-768:770-868:870-894:896-931:933-989:993:1015-1023:1025-1031:1033-1048:1050-1059:1061-1139:1141-1153:1156-1159:1162-1212:1214-1232	1.4	98	92	43	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
PTPRD_HUMAN	4RCA	A	297	21-232:234-248:250-272:275-282:285-308:311-324:402	3.2	88	85	16	99
PTPRE_HUMAN	2JJD	F	542	111-129:132-181:183-281:288-406:425-472:479-574:581-691	1.5	100	95	77	100
PTPRF_HUMAN	6KR4	A	575	1328-1650:1654-1903:1905-1906	0.8	99	91	30	100
PTPRG_HUMAN	2NLK	A	553	827-897:903-1142:1148-1160:1167-1173:1175-1196:1204-1250:1260-1412	0.6	99	94	38	100
PTPRJ_HUMAN	2NZ6	A	279	1024:1026-1027:1030-1155:1166-1241:1247-1318:1322:1325	1.5	96	93	21	94
PTPRK_HUMAN	2C7S	A	289	864-932:935-1147:1176-1177:1180-1184	1	97	92	20	100
PTPRM_HUMAN	2V5Y	A	564	22-525:528:530-582:614-618:671	3.4	99	91	39	100
PTPRN_HUMAN	2I1Y	B	290	687-976	0.5	100	94	30	100
PTPRO_HUMAN	2GJT	A	295	914-1208	0.8	99	93	24	100
PTPRQ_HUMAN	4IKC	A	274	2013-2137:2145-2293	1.1	99	85	12	100
PTPRR_HUMAN	2A8B	A	283	373-655	1.1	99	95	43	100
PTPRS_HUMAN	2FH7	A	568	1367-1688:1697-1942	1	100	91	29	100
PTPRT_HUMAN	2OOQ	B	281	866-1146	1	99	93	20	100
PTPRU_HUMAN	6SUB	A	253	872-903:926-1146	1.3	100	91	18	100
PTPRZ_HUMAN	5AWX	A	283	1696-1727:1731-1732:1734:1738-1877:1888-1995	0.9	96	91	12	100
PVR_HUMAN	3J8F	7	306	28-330:332-333:335	1.2	99	94	73	100
PYRD_HUMAN	6IDJ	A	367	28-29:31-395	1.1	100	97	93	100
QCR10_HUMAN	5XTI	AG	51	2-48:50-53	0.7	92	92	91	100
QCR8_HUMAN	5XTI	AA	78	2-71:73-74:76:78-82	1.2	90	95	95	96
QCR9_HUMAN	5XTI	AD	62	2-63	1.3	100	95	98	100
QPCTL_HUMAN	3PB8	X	313	69:71-382	0.5	100	97	82	100
QSOX1_HUMAN	3LLI	A	250	294-517:520-545	1.5	100	95	33	100

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UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
R144A_HUMAN	1WIM	A	94	13-102:104-107	1.9	86	90	32	100
RAGE_HUMAN	4LP5	A	301	20-273:275-293:295-322	2.5	93	92	74	100
RAMP1_HUMAN	7KNU	E	115	29-142:144	1	99	96	78	100
RAMP2_HUMAN	6UUN	E	107	60-129:131-134:136-139:141-144:147-171	2.4	69	95	61	99
RAMP3_HUMAN	6UVA	E	111	31:34-137:139-141:143-144:147	2.5	94	95	75	100
RET_HUMAN	6Q2R	E	572	29-128:137-207:211-246:251-379:387-622	0.9	100	91	51	100
RMD3_HUMAN	7CC7	A	227	239-334:337-391:393-468	0.9	100	93	48	100
RN128_HUMAN	3ICU	A	169	38-203:205:207:210	1.5	97	92	39	99
RNF13_HUMAN	5ZC4	A	73	215-287	0.9	99	88	19	100
RNF24_HUMAN	2EP4	A	55	87-137:139-140:142-143	1.7	93	79	37	74
RNF43_HUMAN	4KNG	E	147	44-177:180-192	1.3	91	88	19	99
ROBO1_HUMAN	5OPE	A	382	60:62:65-68:70-115:117-124:126:128-137:139-449	3.3	94	90	23	99
ROBO2_HUMAN	6IAA	A	804	22-82:84-188:190-199:201-207:209-283:285-291:293-301:303-593:595-608:610-670:672-721:723-741:743-750:753-756:758-840	2.1	98	90	58	100
ROBO3_HUMAN	6POK	A	195	668-709:713-833:835-840:842-867	2.8	97	84	14	99
RON_HUMAN	4QT8	B	629	28-357:361-580:583-597:600-603:606-612:614-618:620-621:634-646:648:652-682:684	1.2	96	89	45	100
ROR1_HUMAN	6TU9	A	267	460-568:588-647:652-749	1.3	100	89	28	100
ROR2_HUMAN	4GT4	A	274	464-493:501-511:513-515:517-577:582:584-751	1.4	99	88	29	100
ROS1_HUMAN	4UXL	A	288	1932-1933:1936-2111:2120-2229	0.8	100	84	12	100
RPN1_HUMAN	6S7O	E	552	29-90:92:96-106:109-462:465-467:469-498:501-507:515-516:518-520:522-543:545-574:578-579:585:588-590:594-614	3.9	77	93	91	99

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
RYK_HUMAN	6TUA	A	294	298-302:310-351:358-498:502-607	0.7	100	94	48	100
SARAF_HUMAN	6O2V	A	134	30-88:91-147:150:324-340	2.1	87	94	40	99
SC22B_HUMAN	3EGD	C	137	1-23:29-128:131-132:134-135:148-157	1	96	89	64	100
SC61G_HUMAN	6W6L	2	62	25020	0.9	100	94	91	100
SCAR5_HUMAN	7C00	A	107	390-496	1.5	97	95	22	99
SCF_HUMAN	1EXZ	B	139	27-154:157-160:162-168	2.6	94	84	51	99
SCN1B_HUMAN	6J8J	B	173	20-191:194	1.5	99	93	79	100
SCN2B_HUMAN	6VRR	A	127	27-153	1.5	96	95	59	100
SCN3B_HUMAN	4L1D	A	113	24:26-51:56-126:134-148	0.9	96	92	53	100
SCN4B_HUMAN	4MZ3	A	117	40-59:61-157	2.5	99	95	51	98
SCO1_HUMAN	2GT6	A	167	139-304:307	1.6	100	94	55	97
SCO2_HUMAN	2RLI	A	163	105-264:266-268	2.7	98	95	61	96
SDK2_HUMAN	1WFO	A	116	1253-1256:1258:1284-1285:1309-1411:1443-1446:1449:1470	2.2	90	84	5	89
SE6L1_HUMAN	2YRA	A	74	662-664:741-805:850-851:855:857-859	1.5	80	83	7	100
SEM4D_HUMAN	1OLZ	A	621	24-220:223:226-648	0.8	100	95	72	100
SEM6A_HUMAN	6WTS	A	536	19-44:54-454:459-563:565-568	0.9	99	95	52	100
SEM7A_HUMAN	3NVQ	A	588	46-632:634	0.6	100	95	88	100
SEPR_HUMAN	6Y0F	C	722	36-757	0.9	100	97	95	100
SGMR1_HUMAN	6DK1	C	205	19:26:32-33:36-236	2.1	100	95	92	93
SGPL1_HUMAN	4Q6R	B	443	110-352:354-553	0.4	100	97	78	100
SHPS1_HUMAN	2WNG	A	307	31-94:98-127:129-318:326-348	1	96	95	61	100
SIA7B_HUMAN	6APL	C	301	65-66:68-140:144-203:205-238:240-297:299-308:310-341:343-374	1.1	98	95	80	100
SIA8C_HUMAN	5CXY	A	292	89-380	0.9	100	96	77	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
SIAT1_HUMAN	4JS2	A	318	89-406	0.3	100	98	78	100
SIGL5_HUMAN	2ZG2	A	214	19-218:220:222-234	1.7	99	89	39	100
SIGL7_HUMAN	1O7V	A	123	24-75:78-148	1.3	100	90	26	97
SIGL8_HUMAN	2N7B	A	145	17-154:156:225-227:234-236	2.1	94	89	29	100
SIRB1_HUMAN	2D9C	A	124	35-151:238-240:242-245	2	93	94	31	91
SIRPG_HUMAN	4I2X	E	314	30-322:325-345	1.6	100	94	81	100
SLAF5_HUMAN	2PKD	E	109	23-131	1.4	100	93	32	100
SLAF6_HUMAN	2IF7	D	192	23-24:26-215	1.7	100	91	58	100
SLC31_HUMAN	6LI9	A	621	61-65:68:71-81:84-687	2.2	98	93	91	100
SLIK1_HUMAN	4RCA	B	241	22-262	0.8	100	91	35	100
SLMAP_HUMAN	6AR0	A	138	2-139	0.9	100	85	17	100
SORC2_HUMAN	1WGO	A	104	362-363:793-893:964	2.2	93	89	9	85
SORL_HUMAN	3WSY	A	653	86-690:699-704:714-722:725:729-735:737-753:755:2152-2153:2156-2158:2161:2220	2.9	94	85	29	99
SORT_HUMAN	5MRI	A	662	87-748	1.1	100	94	80	100
SPAST_HUMAN	6PEN	D	293	318-610	2	100	92	48	100
SPIT1_HUMAN	5H7V	A	319	46:48-147:149-153:155-157:165:168-225:233-307:324:331:336-337:339-340:351:354:366-367:369-370:372-374:377:379:381:383-385:387-389:391-442	1.8	89	88	60	100
SPIT2_HUMAN	4U32	X	54	130-183	0.5	46	95	21	100
SPTC1_HUMAN	7K0P	E	435	60-61:64-65:67-72:74-75:77-86:89-90:92-502	2.1	95	96	92	94
SPTC2_HUMAN	7CQI	T	495	49-52:55-431:435:437-549	2	99	93	88	99
SRPRB_HUMAN	7NFX	v	186	65-207:229-271	1.1	100	94	69	100
ST14_HUMAN	5LYO	B	251	601-613:615:618-795:797-802:804-856	2.1	96	87	29	100
STAB2_HUMAN	5N86	A	139	2311-2449	1.4	99	76	5	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
STIM1_HUMAN	2K60	A	145	35-37:43-45:62:65-175:177-179:181-184:186-188:190-206	2.7	91	84	21	97
STIM2_HUMAN	2L5Y	A	147	50:53:56:65-208	2.9	98	85	20	98
STX10_HUMAN	4DND	A	92	5-31:41-94:96-101:103-105:107:112	1	99	93	37	100
STX12_HUMAN	2DNX	A	119	25-140:143-144:147	1.8	98	91	43	92
STX17_HUMAN	7BV6	F	50	20:91-92:94-136:138-141	2.5	6	74	17	82
STX6_HUMAN	4J2C	A	108	1-108	1.4	98	87	42	100
SUIS_HUMAN	3LPP	A	871	61-931	0.3	100	96	48	100
SUN1_HUMAN	6R2I	A	179	139-143:148:605-607:642-675:696-831	2.6	96	86	22	90
SUN2_HUMAN	6WMD	A	196	521:523-717	1.5	100	87	27	100
SYCY1_HUMAN	5HA6	B	49	451-452:454-456:458-501	2.7	4	71	9	62
SYCY2_HUMAN	6RX3	C	98	354-360:375:379-468	2.8	92	60	18	99
SYJ2B_HUMAN	2ENO	A	108	10-117	1.7	98	87	74	90
SYNE1_HUMAN	6XF2	A	117	944-945:947-949:951-985:987-988:991-998:1000-1030:1039-1040:1042-1074:1076	3.2	3	92	8	99
SYNE2_HUMAN	6XF1	A	223	172-174:177:234:236-306:308-309:312:314-369:371-372:375-383:386-422:426:428-466	3.5	12	88	16	97
SYT1_HUMAN	2R83	A	167	102-103:155-157:242-245:248-249:334-336:379-531	3.1	92	92	40	60
SYT13_HUMAN	1WFM	A	128	164-255:258-260:262:264-291:294:297:299-300	1.7	94	85	30	93
SYT4_HUMAN	1UGK	A	134	151-284	1.7	93	89	32	97
SYT5_HUMAN	5H4Z	A	129	105-233	1	98	91	33	100
SYT7_HUMAN	2D8K	A	135	137-266:271-274:298	1.6	96	92	34	96
TACT_HUMAN	6ARQ	A	109	27-93:96-136:138	1.3	98	82	19	100
TEN2_HUMAN	6VHH	A	753	624-876:878:881:886-992:1001-1057:1067-1400	1.7	100	94	54	44



**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
TF_HUMAN	6R2W	T	209	35-243	0.8	100	95	71	100
TFR1_HUMAN	6D05	A	641	120-760	1.4	100	94	84	100
TGBR3_HUMAN	7LBG	D	156	47-71:81-211	0.7	100	90	18	100
TGFA_HUMAN	1MOX	C	49	41-88:90	2	98	75	31	100
TGFR1_HUMAN	3KCF	E	330	169:171-173:175-500	1.5	99	92	66	100
TGFR2_HUMAN	7DV6	A	304	240-542:544	0.8	98	94	54	100
TIE1_HUMAN	5N06	A	79	643-685:689-724	1.2	100	86	7	85
TIE2_HUMAN	4K0V	A	514	23-486:488-491:493-537:539	1.1	91	91	46	100
TIGIT_HUMAN	3Q0H	A	109	21-128:130	1.1	99	96	45	100
TIMD4_HUMAN	5DZN	A	114	20:22-134	1.8	99	94	30	100
TLR1_HUMAN	6NIH	B	518	26-484:487-506:529:531-545:547-551:555-561:565-566:568-570:572-574:576:579-580	2.2	89	93	66	100
TLR10_HUMAN	2J67	A	141	627:629-658:660-715:717:724-776	1.1	97	79	17	100
TLR2_HUMAN	6NIG	C	548	27-540:542-558:562-567:572-577:579-581:586-587	1.9	90	93	70	100
TLR3_HUMAN	7C76	A	691	29-32:34-336:343-725:727	1.6	99	96	76	100
TLR4_HUMAN	4G8A	B	605	23-627	1.3	100	95	72	100
TLR5_HUMAN	3J0A	A	594	12-13:16:19-24:32-87:89-195:197:199-210:213-221:223-270:279-443:445-456:458-497:500:503-507:509-524:527:530-531:533-635:637-643	4.8	72	95	69	75
TLR6_HUMAN	4OM7	A	143	640-782	1	100	82	18	100
TLR7_HUMAN	7CYN	A	786	30-31:33-435:471-476:490-856:860-861:863-868	1.2	98	94	75	100
TLR8_HUMAN	4QBZ	A	754	31-100:113-434:457-818	1.1	100	91	72	100
TM11E_HUMAN	2OQ5	A	231	194-424	0.8	100	93	55	100
TMED2_HUMAN	5AZW	A	94	20-113	1.2	100	90	47	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
TMPS2_HUMAN	7MEQ	A	325	148-162:166-202:208-215:217:221-247:249-250:258-492	1.2	99	91	66	100
TMX1_HUMAN	1X5E	A	120	31-143:146-152	1.7	91	94	43	95
TMX2_HUMAN	2DJ0	A	129	140-268	1.3	96	94	44	94
TN13B_HUMAN	4ZCH	A	164	80-81:95-98:108-118:147-150:247:394-472:481-543	3.5	87	93	58	39
TNF10_HUMAN	1D4V	B	162	119-135:137-142:144-282	1.4	97	90	58	99
TNF11_HUMAN	5BNQ	A	156	161:163-317	0.4	99	96	49	100
TNF12_HUMAN	4HT1	T	131	105-114:121-194:202:204-249	0.6	99	95	53	100
TNF14_HUMAN	4RSU	G	150	91-240	1.7	99	94	62	100
TNF15_HUMAN	2RE9	A	164	88-251	1.4	100	92	65	100
TNF18_HUMAN	3B93	A	123	77-199	1.3	100	94	62	100
TNFA_HUMAN	7KPB	A	153	81-233	1.4	100	95	66	100
TNFC_HUMAN	4MXW	D	135	87-147:155-165:169-171:173-187:199-243	1.2	90	93	55	100
TNFL4_HUMAN	2HEV	F	126	58-183	0.7	98	93	69	100
TNFL6_HUMAN	5L19	A	145	141-146:148-286	1.3	94	95	52	97
TNFL9_HUMAN	6MGE	B	153	90-111:113:115-118:121-246	1.8	97	92	60	99
TNR14_HUMAN	4RSU	D	105	38-141:143	1.7	98	96	37	100
TNR16_HUMAN	2N80	A	94	333:335-427	2.1	100	82	22	100
TNR17_HUMAN	2KN1	A	48	3-7:9-47:49-51:54	2.5	81	83	26	98
TNR18_HUMAN	7KHD	C	98	39-51:71-155	1.2	100	92	41	100
TNR1A_HUMAN	1EXT	A	159	42-183:185-201	2.7	90	93	35	99
TNR1B_HUMAN	3ALQ	S	164	37-200	0.8	100	97	36	100
TNR21_HUMAN	3U3V	A	164	51-214	0.9	100	96	25	100
TNR3_HUMAN	4MXW	R	149	42:44-106:108:111-112:114-126:128:130-132:142-154:156:158:160-161:163:165-211	2.1	93	91	34	100
TNR4_HUMAN	6OGX	G	140	31-170	1	100	97	51	100

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
TNR5_HUMAN	5IHL	H	130	22:24-125:132-151:166-167:169-171:190-191	3.8	96	95	47	78
TNR6_HUMAN	1DDF	A	112	223-325:327:330-331:337-342	3.2	92	84	33	88
TNR9_HUMAN	6MGP	X	144	23:25:27-167:169	1.9	95	92	56	100
TOIP1_HUMAN	4TVS	A	224	72:361-583	1.3	100	93	38	100
TOIP2_HUMAN	5J1T	B	234	232:236:238-429:432-471	1.3	99	94	50	100
TOM22_HUMAN	7CP9	G	72	42-45:48:55:58-64:67:72-73:75-107:109-129:131-132	2.8	57	86	51	84
TOM7_HUMAN	7CP9	E	51	4-54	2	100	94	93	98
TOM70_HUMAN	7DHG	C	470	108:110-274:297-599:601	2.2	100	93	77	100
TPBG_HUMAN	4CNM	A	280	63-167:169:172:175-347	1.4	99	93	67	99
TPSN_HUMAN	6ENY	C	364	21-33:37-46:48-49:54-57:59-60:62-187:189:192:195:198-400:402	2.6	97	92	81	100
TPSNR_HUMAN	5WER	C	317	29:31-43:45-46:56-70:72:85-86:88:91-109:111-112:114-115:117-128:138-256:258:262-314:317-339:344-373:379-389:392-401	1.6	86	89	68	100
TPST1_HUMAN	5WRJ	A	275	64-338	0.3	100	98	74	100
TPST2_HUMAN	3AP2	A	300	51-56:60-353	0.3	100	97	80	100
TR10A_HUMAN	5CIR	E	102	128:130-230	1	97	92	22	100
TR10B_HUMAN	1D4V	A	114	75-188	1.6	99	92	26	97
TRAC_HUMAN	6JXR	m	132	108-109:111-152:154-162:164-213:222-223:226-227:229-252:255	3.9	72	92	94	53
TRBC1_HUMAN	4ZDH	B	129	113-241	0.5	95	96	73	54
TRBC2_HUMAN	3T0E	D	130	116-245	0.7	98	96	73	53
TRBM_HUMAN	1DX5	J	116	363-468:471-477:480-482	2.1	94	84	20	98
TRDC_HUMAN	1HXM	A	86	121-206	0.7	100	95	56	42
TREM1_HUMAN	1Q8M	B	119	20-138	2.3	98	89	51	98

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
TREM2_HUMAN	6XDS	A	130	111-114:144-153:334:337-338:365-415:424-427:432-487:490-491	2.7	81	90	57	27
TRGC1_HUMAN	4LFH	G	112	113-219:222-223:225:227-228	1.4	95	92	65	50
TRGC2_HUMAN	1HXM	B	106	127-232	1.4	96	94	56	46
TRML1_HUMAN	2FRG	P	103	19:21-67:69:74-75:77-128	2.1	96	94	33	97
TUTLA_HUMAN	1V5J	A	99	625-723	1.6	96	86	8	92
TYOBP_HUMAN	2L35	A	54	6-12:14-27:29-30:32:35:46-72:74-75	3.3	13	75	48	86
TYRO3_HUMAN	1RHF	A	173	49-69:71-200:202-222:253	2.1	99	86	19	99
TYRP1_HUMAN	5M8T	A	446	25-470	0.3	99	98	83	100
UB2J2_HUMAN	2F4W	B	152	11-95:105-171	0.4	100	97	59	100
UBP19_HUMAN	1WHO	A	119	276:281:284-396:514-515:579-580	2.3	96	85	9	89
UBP30_HUMAN	5OHP	A	315	64-104:113-181:216-290:302-358:430-502	0.9	96	93	61	100
UCRI_HUMAN	5XTI	AB	49	159-161:163-183:186-187:189-196:199:254-256:258-259:261-269	3.7	4	94	18	86
UD2B7_HUMAN	2O6L	B	160	282-291:293-310:316-389:391-405:407-419:421-442:444-451	0.6	98	97	30	100
UDB15_HUMAN	6IPB	A	170	280-281:283-311:313-316:318-452	1.3	96	98	32	99
UFO_HUMAN	5U6B	B	287	520-561:564-609:611:615-702:704-709:711:713-814:816	1.3	98	85	32	99
UNC5A_HUMAN	4V2A	A	248	43-289:292	1.5	99	91	29	100
UXS1_HUMAN	4GLL	A	305	88-343:345-351:353-356:359-396	2.3	96	96	73	99
VAMP7_HUMAN	2DMW	A	121	8-127:169	1.6	97	92	55	92
VAMP8_HUMAN	7BV6	A	66	9-74	1	100	94	66	100
VAPA_HUMAN	2RR3	A	127	10-136	1.7	98	93	51	99
VAPB_HUMAN	3IKK	A	124	1-96:98-101:103-126	1	97	91	51	99

**Table 1.** Verification of AF2-generated models of 788 bitopic proteins from *Homo sapiens* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID <sup>1</sup>	Chain	N <sub>over</sub> <sup>2</sup>	Overlapping segments <sup>2</sup>	RMSD, Å <sup>3</sup>	% identity <sup>4</sup>	Score <sup>5</sup>	%AF2 <sup>6</sup>	%PDB <sup>7</sup>
VAS1_HUMAN	6WM4	U	177	255-423:426-427:430-431:436-437:442:449	2.2	96	89	38	87
VCAM1_HUMAN	1VCA	A	199	25-222:250	1.6	100	89	27	100
VGFR1_HUMAN	5T89	Y	588	30-35:38-44:48-58:61-68:70-74:78-81:96-104:106:109-115:117-139:142-279:281-282:284-476:478-482:489:495-511:513-650:652-662:664-665	4.5	81	86	44	98
VGFR2_HUMAN	6GQO	A	308	805-808:813:816-944:955:995:997-1168	1.7	96	81	23	100
VGFR3_HUMAN	4BSJ	A	213	328-468:482:484-554	1.9	98	85	16	100
VISTA_HUMAN	6OIL	A	148	33-60:64-183	0.6	99	90	48	100
VRK2_HUMAN	5UU1	A	315	14-327:330	1	100	95	62	100
VSIG4_HUMAN	5IML	A	119	19-137	0.7	100	95	30	100
VTCN1_HUMAN	4GOS	A	115	35-149	0.8	99	97	41	100
VT11B_HUMAN	2V8S	V	91	2-3:6-7:10-96	0.8	94	83	39	98
X3CL1_HUMAN	1F2L	D	70	28:30-98	1.5	99	91	18	100
XYLT1_HUMAN	6EJ7	A	706	252-730:732-733:735-959	0.5	100	96	74	100

<sup>1</sup> One PDB entry with the largest number of overlapped residues was selected for each protein.

<sup>2</sup> Overlapped segments of AF2 models and PDB structures; residues were numbered as in the AF2 model file.

<sup>3</sup> Sequence identity of overlapped residues in the model and the corresponding experimental structure after their superposition. The sequence-independent superposition option of TM-align was used.

<sup>4</sup> Root-mean-square deviation of C<sup>α</sup>-atoms.

<sup>5</sup> Average AF2 confidence score (pLDDT) for overlapping residues.

<sup>6</sup> Percentage of the AF2 model that are overlapping with the PDB structure,  $(N_{over}/N_{AF2}) \times 100$ , where  $N_{AF2}$  is the number of residues in the full-length AF2 model

<sup>7</sup> Percentage of PDB structure covered by overlapping residues,  $(N_{over}/N_{PDB}) \times 100$ , where  $N_{PDB}$  is the number of residues in the PDB structure.

Same footnotes are used for Tables 2-5

UniProt ID	PDB ID	Chain	N <sub>over</sub>	Overlapping segments	RMSD, Å	% Identity	Score	% AF2	% PDB
AMPD_ARATH	2A3L	A	599	223-225:227-242:244-250:252-280:292-295:297-457:473-481:483:488-856	1.7	94	93	71	97
ANX1_ARATH	6FIG	A	386	25:27-411	0.6	100	93	45	100
ANX2_ARATH	5Y92	A	387	28-414	0.5	100	93	45	100
ARC6_ARATH	5D9R	A	132	668-799	0.6	100	91	16	100
BAK1_ARATH	3TL8	D	306	274-323:325-445:447-448:451-583	1	100	89	50	100
BRI1_ARATH	3RGZ	A	745	30-774	0.8	100	94	62	100
BRL1_ARATH	4J0M	A	724	31-60:64-757	0.7	100	93	62	100
CERK1_ARATH	4EBZ	A	200	25-224	0.7	100	91	32	100
CRL_ARATH	6LIX	B	196	42-237	0.9	100	97	73	100
ERL1_ARATH	5XJX	K	544	28-571	0.9	100	95	56	100
ERL2_ARATH	5XKN	A	540	29:31-566:568-570	1.2	99	95	56	100
FERON_ARATH	6A5B	A	376	34-65:70-201:207-209:216-424	0.4	100	93	42	100
FKB42_ARATH	2IF4	A	258	35-292	0.9	100	96	71	100
FLS2_ARATH	4MN8	A	759	26-784	1.2	100	96	65	100
FLU_ARATH	5CHE	E	119	196:198-315	0.6	99	96	38	100
FUT1_ARATH	5KWK	B	457	95-399:407-558	0.4	100	96	82	100
GLDH_ARATH	7A24	z	436	12-16:124-125:135:138-143:145-350:352-355:367-369:393-399:406:433-447:451:455-457:459-472:477-506:508-510:513-528:531:533-549:562-580:582:584:586-598:600:602-603:605-668	3.6	78	96	71	87
GSO1_ARATH	6S6Q	A	833	25-38:40-42:44-859	1.7	98	96	67	100
HAP2_ARATH	5OW3	C	445	25-75:86:88-142:145:147-263:275-494	1.3	99	92	63	100
HXK1_ARATH	4QS7	A	455	34-424:430-492:496	0.8	100	96	92	100

**Table 2.** Verification of AF2-generated models of 52 bitopic proteins from *Arabidopsis thaliana* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID	Chain	N <sub>over</sub>	Overlapping segments	RMSD, Å	% Identity	Score	% AF2	% PDB
NCPR2_ARATH	5GXU	A	532	104-140:145-147:154-163:167-173:180-188:190-191:193-195:198-205:207-208:211:213-219:223-240:242-243:245-247:249-255:258-259:261-263:265-280:324-400:416:418-731	3.8	80	94	75	96
NDADA_ARATH	7A24	Z	123	17-20:35:38:40-135:137-140:142-152:154-159	2.8	88	94	86	88
NDUA1_ARATH	7A24	V	57	2-57:59	0.8	98	92	88	100
OE64M_ARATH	6Q3Q	A	121	264-265:268:486-603	0.9	97	95	20	100
P2C57_ARATH	4YZH	A	294	58-349:351-352	1.1	99	96	76	100
P2C70_ARATH	1MZK	A	120	181-299:302	1.4	98	88	21	98
PDLP5_ARATH	6GRE	B	207	29-235	0.9	100	95	69	100
PDLP8_ARATH	6GRF	B	211	26-236	0.3	100	97	76	100
PDV1_ARATH	5U9O	E	46	1-24:27-29-30:49-50:54-55:59:162-163:166-168:170-171:174:177-178:181-182:316-317	4.5	9	88	17	32
PEPR1_ARATH	5GR8	A	710	29-733:735-738:740	1.9	99	96	63	100
PRK3_ARATH	5WLS	A	208	25-35:37-233	0.7	95	93	33	100
PRK6_ARATH	5YAH	B	215	27-241	1.5	100	91	33	100
PSBE_ARATH	5MDX	E	71	10-54:56-58:60-82	1.4	96	95	86	99
PSBH_ARATH	5MDX	H	52	13:15-64:66	1.7	96	97	71	100
PSKR1_ARATH	4Z63	A	610	30-634:637-641	1	99	94	61	100
RGI3_ARATH	5HZ3	B	623	56:58-84:92-686	1.2	99	94	57	100
RLK5_ARATH	5IYX	A	596	21-616	1	100	95	60	100
SBIR1_ARATH	6R1H	A	184	34-56:64-220:222-225	1.3	98	89	29	100
SCO11_ARATH	6N5U	A	161	172-332	0.7	100	94	48	100
SERK1_ARATH	6FG8	A	188	25-212	0.8	100	89	30	100
SERK2_ARATH	6G3W	A	185	30-213:215	0.5	100	91	29	100

**Table 2.** Verification of AF2-generated models of 52 bitopic proteins from *Arabidopsis thaliana* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID	Chain	N <sub>over</sub>	Overlapping segments	RMSD, Å	% Identity	Score	% AF2	% PDB
TBL29_ARATH	6CCI	A	354	133-486	0.9	100	95	73	100
TDR_ARATH	5GIJ	B	599	31-59:61:65-633	1.1	99	95	58	99
TIC40_ARATH	2LNM	A	60	385-387:389-445	1.6	97	77	13	97
TMK1_ARATH	4HQ1	A	424	24-447	0.3	100	97	45	100
TMK3_ARATH	7BRC	A	425	25:27-449:451	0.8	100	95	45	100
TMM_ARATH	5XJO	C	367	52-416:421:425	0.5	99	96	74	100
TO203_ARATH	1ZU2	A	145	5:7-150	2	99	93	72	92
U603_ARATH	3PW9	A	153	83-235	0.7	99	86	54	100
VSR1_ARATH	4TJV	A	155	25-28:30-130:133-134:137-140:142:146-184:186-189	2.2	92	92	25	94
XXT1_ARATH	6BSW	A	337	116-452	0.2	100	97	73	100
Y1719_ARATH	6G3W	B	189	25-213	1	100	91	31	100



**Table 3.** Verification of AF2-generated models of 69 bitopic proteins from *Saccharomyces cerevisiae* by comparison with experimental structures from PDB.

UniProt ID	PDB ID	Chain	N <sub>over</sub>	Overlapping segments	RMSD, Å	% Identity	Score	% AF2	% PDB
ATG32_YEAST	5WLP	A	144	197-340	2	98	84	27	99
ATP18_YEAST	6B8H	i	59	1-59	1.1	100	95	100	100
ATPK_YEAST	6WTD	U	54	50:53-62:64-106	2.5	80	90	53	79
COX13_YEAST	6T15	k	118	10:12-128	1.7	99	95	91	100
COX5A_YEAST	6HU9	e	133	21-153	0.9	100	94	87	100
COX5B_YEAST	6T15	e	134	18-151	1.2	100	94	89	100
COX7_YEAST	6T15	g	59	2-60	1.1	100	96	98	100
COX8_YEAST	6YMX	h	51	28-78	1.5	100	95	65	100
COX9_YEAST	6T15	i	50	12-60:62	1.9	98	98	85	91
CP51_YEAST	5EQB	A	525	6-530	0.7	100	98	99	99
CUE1_YEAST	2MYX	A	70	50-52:54-120	1.9	96	82	34	93
CWH41_YEAST	4J5T	A	780	31-258:265-506:508-509:526-833	0.9	99	94	94	99
CYB2_YEAST	1KBI	A	504	81-380:387-388:390-591	0.5	100	94	85	100
EMC1_YEAST	7KRA	A	694	25-96:99:101-201:206-230:249-250:252-268:270:272-285:287-410:423-755:757-760	2.7	95	84	91	100
EMP46_YEAST	2A6X	B	219	53:55-272	0.3	99	92	49	100
EMP47_YEAST	2A6Y	A	224	36-257:259-260	0.7	98	94	50	97
ERV2_YEAST	1JRA	A	106	74-179	1.4	100	96	54	100
FET3_YEAST	1ZPU	A	529	22-531:533-540:542-543:545-553	0.4	97	98	83	100
FIS1_YEAST	1Y8M	A	135	7-134:136-138:140:147:150-151	2.3	96	92	87	94
GLRX6_YEAST	5J3R	A	114	112-225	0.2	100	98	49	100
HRD3_YEAST	5V7V	A	613	26-257:259-264:266-270:316:318-685:687	1.5	98	92	74	100
IRE1_YEAST	3SDJ	D	420	663-759:761-771:773-840:843-844:846-847:849-852:854-867:896-1117	1.2	96	88	38	100
KEX1_YEAST	1AC5	A	483	23-505	0.3	100	96	66	100
KEX2_YEAST	1R64	A	481	121-601	0.3	100	97	59	100

**Table 3.** Verification of AF2-generated models of 69 bitopic proteins from *Saccharomyces cerevisiae* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID	Chain	N <sub>over</sub>	Overlapping segments	RMSD, Å	% Identity	Score	% AF2	% PDB
KRE2_YEAST	1S4N	A	337	104-114:116:118-442	0.2	100	98	76	100
KTR4_YEAST	5A07	A	395	70-464	0.2	100	98	85	100
LAM4_YEAST	6BYM	A	197	946-1142	1	100	91	15	98
LAM6_YEAST	5YQR	A	112	312:314-424	1.7	96	86	16	42
MDM38_YEAST	3SKQ	A	227	182-408	0.3	100	92	40	100
MNN9_YEAST	3ZF8	A	288	95-189:202-394	0.7	100	93	73	100
MNS1_YEAST	1G6I	A	510	34-365:371-409:411-549	0.3	99	98	93	100
MSP1_YEAST	5W0T	A	196	50-111:114-140:142-158:160-162:164-176:178-199:206-216:218-229:231-259	1.4	100	88	54	68
NCPR_YEAST	2BF4	A	645	47-691	0.4	100	96	93	100
NYV1_YEAST	2FZ0	A	149	1-149	2.6	99	82	59	100
OST1_YEAST	6EZN	A	438	25-98:111-474	1.2	100	90	92	100
OSTB_YEAST	6C26	B	394	24-388:390:393-394:396-414:417-418:423-427	2.4	94	90	92	99
PEX13_YEAST	1JQQ	B	78	293-294:297:301-307:309-376	2.2	87	85	20	95
PEX15_YEAST	5VXV	A	211	43-64:66-80:82-92:94-166:168-177:179-210:212-259	0.9	97	95	55	100
PEX22_YEAST	2Y9P	B	122	57-147:152-182	1.1	100	90	68	98
QCR10_YEAST	6HU9	U	54	36:43:45-52:54-90:92-93:95-99	3.2	82	75	70	71
QCR8_YEAST	6YMX	H	88	12-99	1.6	100	91	94	95
QCR9_YEAST	6T15	T	57	1-2:4-58	1.8	96	95	86	100
SC61G_YEAST	2WWA	B	60	21-80	2.1	100	91	75	100
SCO1_YEAST	2B7J	B	173	108:114-283:285-286	1.6	98	89	59	96
SCS2_YEAST	6LP4	A	126	3-128	0.7	99	97	52	100
SEC12_YEAST	6X90	B	344	1-344	0.7	100	97	73	100
SEC66_YEAST	6ND1	E	139	29-80:82:91-157:159:162-169:171-180	1.7	86	94	67	100
SNC1_YEAST	3B5N	A	61	26-86	0.7	98	91	52	100

**Table 3.** Verification of AF2-generated models of 69 bitopic proteins from *Saccharomyces cerevisiae* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID	Chain	N <sub>over</sub>	Overlapping segments	RMSD, Å	% Identity	Score	% AF2	% PDB
SOP4_YEAST	7KTX	G	143	20-31:33-40:42-127:129-140:142-159:163-169	2	82	86	61	95
SRPB_YEAST	1NRJ	B	191	36-188:203-206:211-244	0.6	100	94	78	100
SSO1_YEAST	1FIO	A	188	30-166:168-179:184:186-221:223-224	1.8	93	87	65	99
SSO2_YEAST	5LG4	A	187	33-169:171-177:179:182-183:188-190:192-226:228-229	1.9	91	88	63	99
TIM14_YEAST	2GUZ	A	71	98-168	0.9	99	90	42	100
TIM21_YEAST	6K7D	A	147	141-148:152-154:232-233:235-242:244-248:444-446:448-496:503-570:572	3.9	76	90	62	29
TIM50_YEAST	4QQF	A	191	167-171:176-179:183-362:364-365	2.3	95	92	40	96
TIM54_YEAST	6LO8	B	175	36-62:64-80:82-150:153:240-264:371-378:385-386:388-413	0.9	85	94	37	99
TLG1_YEAST	2C5I	T	93	6-61:63-99	1.2	100	81	42	100
TOM22_YEAST	6UCV	J	55	77-131	1.2	9	95	36	100
TOM70_YEAST	2GW1	A	395	88-97:100-101:107-131:342-698:701	2.2	91	88	64	81
TOM71_YEAST	3FP3	A	498	107:109-120:122-138:140:146-254:261-534:544-627	1.2	97	93	78	100
UCRI_YEAST	6TOB	E	185	31-215	2.7	100	94	86	100
UPPS_YEAST	6JCN	A	206	151-248:261-262:264-369	1.5	98	92	55	100
USA1_YEAST	6VK0	D	64	12-15:28-29:38:41-44:47:75-77:80:88-102:165-166:170-173:197:207-211:213-219:221-222:225-226:228-231:256:266-270	4.9	8	78	8	66
VAM3_YEAST	1HS7	A	97	23-119	1.3	100	80	34	100
VOA1_YEAST	6PE4	B	47	212:214:216-250:252-261	3.1	79	71	18	89
VPS64_YEAST	6A8W	A	128	159-166:168-190:198-268:270-295	0.7	99	89	21	100
VTI1_YEAST	3ONJ	A	97	3-98:101	1	100	82	45	100

**Table 3.** Verification of AF2-generated models of 69 bitopic proteins from *Saccharomyces cerevisiae* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID	Chain	N <sub>over</sub>	Overlapping segments	RMSD, Å	% Identity	Score	% AF2	% PDB
YME1_YEAST	2MV3	A	87	98-181:183-185	1.7	92	85	12	99
YSP2_YEAST	5YQI	A	166	847-850:852-912:916-1015:1018	1.3	98	92	12	100

**Table 4.** Verification of AF2-generated models of 34 bitopic proteins from *Escherichia coli* by comparison with experimental structures from PDB.

UniProt ID	PDB ID	Chain	N <sub>over</sub>	Overlapping segments	RMSD, Å	% Identity	Score	% AF2	% PDB
ATPF_ECOLI	5T4P	I	136	2-129:131-135:140:155-156	3.1	93	94	87	88
BCSB_ECOLI	7LBY	B	650	68-78:80-85:88-449:451-459:475-609:623-633:652-653:672-754:757:759-785:788:791-792	2.6	90	91	83	98
CADC_ECOLI	3LY9	A	322	190-511	1.3	100	93	63	100
CCME_ECOLI	1SR3	A	98	38-135	1.6	100	90	62	86
DAMX_ECOLI	2LFV	A	90	103-106:359-444	2.5	96	88	21	85
DEGS_ECOLI	1TE0	A	307	37-180:183-223:232-275:288-365	2.6	99	90	86	97
DSBE_ECOLI	3K8N	A	153	30-33:35-182:184	1.8	98	94	83	100
EXBD_ECOLI	2PFU	A	75	79-153	1.8	100	87	53	76
FDNH_ECOLI	1KQF	B	284	2-285	1.6	100	94	97	98
FTSB_ECOLI	4IFF	C	65	25-38:42-91:93	2.2	8	84	63	79
FTSH_ECOLI	1LV7	A	248	138-143:146-147:149-177:183-221:225-227:231-398:443	2.5	95	87	39	99
FTSI_ECOLI	6HZQ	A	301	234-280:293:296-297:301-336:339-391:401-402:408-567	1.1	99	96	51	100
FTSN_ECOLI	1UTA	A	72	242-245:247-291:296-304:306:308-311:316-324	2.9	76	91	23	94
FTSQ_ECOLI	5Z2W	A	205	61-265	1.7	100	92	74	98
GSPH_ECOLI	2KNQ	A	136	31-32:34-84:89-171	2.2	98	83	80	96
KDPC_ECOLI	7BH2	C	190	1-190	1	100	95	100	100
LPTC_ECOLI	4B54	A	125	53:59-182	0.8	98	97	65	100

**Table 4.** Verification of AF2-generated models of 34 bitopic proteins from *Escherichia coli* by comparison with experimental structures from PDB (continuation).

UniProt ID	PDB ID	Chain	N <sub>over</sub>	Overlapping segments	RMSD, Å	% Identity	Score	% AF2	% PDB
MACA_ECOLI	5NIL	F	335	32-320:322-331:333:335-347:349-352:354-365:367-370:373:376	2.8	89	93	90	99
MBHS_ECOLI	4GD3	S	293	6:50-341	0.5	99	95	79	96
MBHT_ECOLI	6SZK	SSS	268	46-313	0.3	100	97	72	100
MLAD_ECOLI	7CGN	J	143	1-2:4-15:17-26:28-29:35:37:39-153	3.2	82	94	78	99
MRDA_ECOLI	6G9F	A	539	57-549:568-613	0.7	100	96	85	100
PBPB_ECOLI	5HLB	A	731	66-67:69-234:236-237:239-257:260-792:794-802	1.1	96	94	87	100
PPID_ECOLI	2KGJ	A	98	264-360:369	1.9	97	93	16	96
PQIB_ECOLI	5UVN	B	392	41-42:44-347:355-387:401:403-431:433:436-452:455-456:461:494:498	2.5	93	86	72	94
RSEA_ECOLI	1OR7	C	66	1-66	1.2	100	92	31	100
SPPA_ECOLI	3BF0	C	478	56-72:79:90:93-539:541-552	0.7	97	96	77	100
TAMB_ECOLI	5VTG	A	131	974-975:977-995:1024:1026-1106:1108:1111-1114:1118-1140	2	94	90	10	96
TATA_ECOLI	2LZS	B	48	1-3:5-42:44-46:48-49:51:53	2.4	83	88	54	100
TOLA_ECOLI	3QDR	A	92	328:330-350:352-421	1.2	99	90	22	100
TOLR_ECOLI	5BY4	A	105	37-141	1.3	100	79	74	100
YCBB_ECOLI	6NTW	A	502	51-62:64-68:70:73-74:76-78:80-266:315-457:460-467:469-472:474-478:480-600:604:608-617	2.4	91	94	82	99
YEBT_ECOLI	6V0C	C	820	49:52-60:62-65:67-77:80-107:111-123:126-127:129:131-132:134-146:150-346:348-365:367-369:371-383:385-889	4.8	87	85	94	99
ZIPA_ECOLI	1F47	B	144	185-328	0.9	99	96	44	100

**Table 5.** Verification of AF2-generated models of 4 bitopic proteins from *Methanococcus jannaschii* by comparison with experimental structures from PDB.

UniProt ID	PDB ID	Chain	N <sub>over</sub>	Overlapping segments	RMSD, Å	% Identity	Score	% AF2	% PDB
FLAB1_METJA	5YA6	A	159	59-217	0.4	100	92	73	98
MTRA_METJA	5L8X	A	170	3-172	0.2	100	95	71	99
SECE_METJA	2YXR	B	65	3-67	1.1	100	94	88	100
Y781_METJA	2JNQ	A	186	391-392:395-396:402-575:599-600:602:630-633:661	2.2	92	81	26	100

**Table 6.** AF2-generated models with coordinate R.M.S.D. larger than 5 Å from experimental structures

UniProt ID	PDB ID	Chain	N <sub>over</sub>	Overlapping segments	RMSD, Å	% Identity	Score	% AF2	% PDB
<b>Models compared with structures composed of multiple domains connected by flexible loops</b>									
BCS1_YEAST	6SH4	A	358	49-54:57-83:85-95:97-111:113:115-126:130:133-147:149-154:156-163:166-170:175-177:180-187:189-210:213-220:225-233:235-238:240-297:299:301-311:315-324:326-327:333-343:345-346:359-371:376-387:390-391:393-467	5.5	59	86	79	95
INSR_HUMAN	4ZXB	E	623	110-115:117:120-121:123-128:133-145:147-150:152-171:174-181:184-186:235-236:412-415:427-435:440-459:462-468:470-703:718:720-844:881:970-1126	5.1	84	88	45	78
LY75_HUMAN	7JPT	A	915	29:31-86:92:94-136:138-143:145-492:497:499-760:775-812:861:966-984:1010-1015:1020-1028:1031-1032:1035-1041:1108-1112:1131-1142:1182-1202:1231-1245:1248-1253:1266-1269:1299-1301:1304-1315:1359-1363:1401-1402:1419-1425:1461-1469:1562:1567-1568:1957-1963:2051-2052:2054-2055	5.2	79	79	53	69
PCD10_HUMAN	6VG4	A	633	19-29:33-41:46-49:54-55:59:62-70:72-109:114-219:236-237:239-592:594-607:609-657:659-663:665-693	5.3	92	93	61	98

VLDLR_HUMAN	6BYV	A	102	456-460:470-476:491-493:500-506:528-531:533-537:543-549:573-591:596-598:610:621-624:627:629-632:634:637-642:645:652-661:685:688-689:692-696:698-702:704	5.1	7	93	12	84
<b>Models compared with PDB entries representing proteins with hybrid sequences</b>									
ATG40_YEAST	7BRN	A	65	21-26:28-29:32-34:36:38-46:48-49:51-55:58:63-64:67:69-70:73:76-77:79-80:83:113:116:119-120:123:125-127:130:205-215:228:275:278-279:294	5.2	9	69	25	49
HG2A_HUMAN	4AH2	B	83	69:72-74:76-78:80-82:106:109-110:113-114:126:130:133:246-259:261:263:265:267-269:273-274:282-285:288:290:292:295:305-308:310-320:338-342:355-363:365-370	6.3	7	85	28	42
MIA40_YEAST	2ZXT	A	121	212-213:216-225:333-337:449-453:472-474:484-488:555-565:596-598:601:608-679:681-683:686	5.2	58	74	30	27
RENH_HUMAN	3LBS	B	157	28-33:36-37:40:51-57:59-62:64-68:77-81:83:86:88:94:98-102:126-133:135:137-144:146-147:150-154:163-166:171:174:179-180:183-185:190:194:199-216:239:270-275:277:308:310-321:324-326:329-330:341-352:378:400:404-410:412-415:453:456-457:460-462:487-492	6.8	6	85	45	42
SEM4C_HUMAN	6N5Z	A	90	214:240:253:296-321:328-350:358-362:373-377:463-465:467:469-479:499:505:507-511:517-522	5.2	6	96	11	57
TNR25_HUMAN	5YGP	D	145	32-40:45:48:50-55:63:87:89-95:117-119:122-124:126-134:141-150:197-234:238-239:462:465-490:500-513:524:528-529:556:559-567	7.6	6	88	35	32