



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 01:33 AM UTC

PDB ID : 4BOG / pdb_00004bog
EMDB ID : EMD-2376
Title : The structure and super-organization of acetylcholine receptor-rapsyn complexes
Authors : Zuber, B.; Unwin, N.
Deposited on : 2013-05-20
Resolution : 50.00 Å(reported)
Based on initial model : 2BG9

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

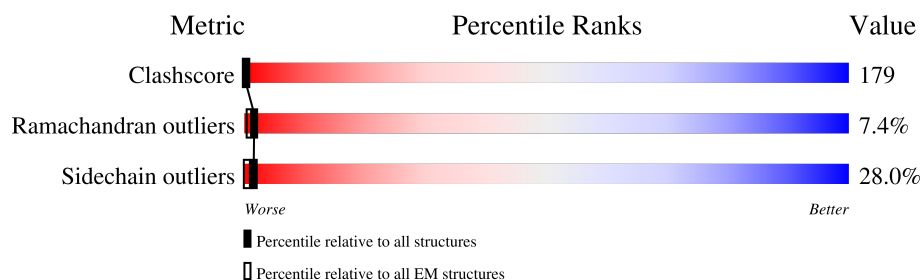
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 50.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



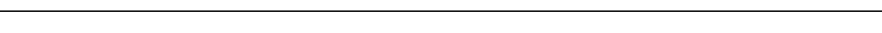
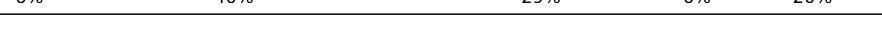
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	0	493	
1	B	493	
1	G	493	
1	L	493	
1	Q	493	
1	V	493	
2	1	522	
2	C	522	
2	H	522	

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Mol	Chain	Length	Quality of chain
2	M	522	
2	R	522	
2	W	522	
3	2	461	
3	A	461	
3	D	461	
3	F	461	
3	I	461	
3	K	461	
3	N	461	
3	P	461	
3	S	461	
3	U	461	
3	X	461	
3	Z	461	
4	3	505	
4	E	505	
4	J	505	
4	O	505	
4	T	505	
4	Y	505	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 89544 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Acetylcholine receptor beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	370	Total	C	N	O	S	0	0
			2972	1938	465	554	15		
1	B	370	Total	C	N	O	S	0	0
			2972	1938	465	554	15		
1	G	370	Total	C	N	O	S	0	0
			2972	1938	465	554	15		
1	L	370	Total	C	N	O	S	0	0
			2972	1938	465	554	15		
1	Q	370	Total	C	N	O	S	0	0
			2972	1938	465	554	15		
1	V	370	Total	C	N	O	S	0	0
			2972	1938	465	554	15		

- Molecule 2 is a protein called Acetylcholine receptor delta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	370	Total	C	N	O	S	0	1
			2983	1944	489	536	14		
2	C	370	Total	C	N	O	S	0	1
			2983	1944	489	536	14		
2	H	370	Total	C	N	O	S	0	1
			2983	1944	489	536	14		
2	M	370	Total	C	N	O	S	0	1
			2983	1944	489	536	14		
2	R	370	Total	C	N	O	S	0	1
			2983	1944	489	536	14		
2	W	370	Total	C	N	O	S	0	1
			2983	1944	489	536	14		

- Molecule 3 is a protein called Acetylcholine receptor subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	370	Total	C	N	O	S	0	0
			2991	1954	478	540	19		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	370	Total 2991	C 1954	N 478	O 540	S 19	0	0
3	D	370	Total 2991	C 1954	N 478	O 540	S 19	0	0
3	F	370	Total 2991	C 1954	N 478	O 540	S 19	0	0
3	I	370	Total 2991	C 1954	N 478	O 540	S 19	0	0
3	K	370	Total 2991	C 1954	N 478	O 540	S 19	0	0
3	N	370	Total 2991	C 1954	N 478	O 540	S 19	0	0
3	P	370	Total 2991	C 1954	N 478	O 540	S 19	0	0
3	S	370	Total 2991	C 1954	N 478	O 540	S 19	0	0
3	U	370	Total 2991	C 1954	N 478	O 540	S 19	0	0
3	X	370	Total 2991	C 1954	N 478	O 540	S 19	0	0
3	Z	370	Total 2991	C 1954	N 478	O 540	S 19	0	0

- Molecule 4 is a protein called Acetylcholine receptor gamma subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	371	Total 2987	C 1948	N 478	O 551	S 10	0	1
4	E	371	Total 2987	C 1948	N 478	O 551	S 10	0	1
4	J	371	Total 2987	C 1948	N 478	O 551	S 10	0	1
4	O	371	Total 2987	C 1948	N 478	O 551	S 10	0	1
4	T	371	Total 2987	C 1948	N 478	O 551	S 10	0	1
4	Y	371	Total 2987	C 1948	N 478	O 551	S 10	0	1

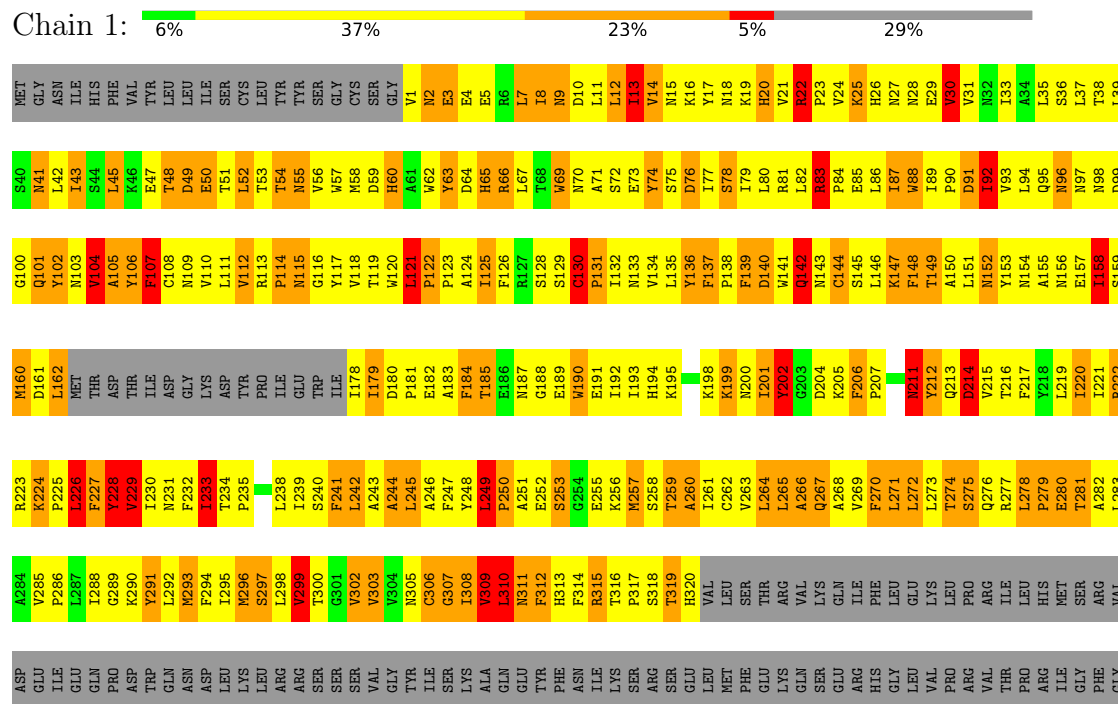
L37	D97	I157	P217	V277	THR	LEU	D457
T38	G98	L158	L218	P278	THR	PRO	A458
S39	S99	L159	F219	I279	PRO	GLN	S459
L40	F100	H160	Y220	I280	SER	ASP	H460
L41	E101	A161	I221	I281	PRO	LEU	N461
L42	I102	L162	V222	S282	ASP	LYS	V462
L43	T103	D163	Y223	Y283	SER	E403	P463
L44	T104	A164	T224	L284	LYS	A404	P464
N45	H105	LYS	I225	M285	PRO	V405	D465
K46	V106	GLY	V226	F286	THR	E406	N466
N47	I107	GLY	P227	L287	ILE	A407	P467
E48	V108	ARG	C228	M288	ILE	I408	F468
E49	L109	GLU	I229	L289	SER	K409	A469
M50	V110	VAL	L230	L290	ARG	V410	
T51	Q111	LYS	I231	V291	ALA	I411	
T52	H112	GLU	S232	A292	ASN	A412	
S53	T113	ILE	L233	F293	ASP	E413	
V54	G114	M174	L234	S294	GLU	Q414	
F55	I115	I175	A235	V295	TVR	L415	
L56	V116	H176	T236	L296	PHE	E416	
N57	S117	Q177	L237	L297	ILE	S417	
L65	R125	A183	V238	S298	ARG	A418	
L66	Q185	D178	F239	V299	LYS	S419	
Q66	K186	A179	Y240	V300	PRO	E420	
N67	S127	F180	L241	V301	ALA	F421	
D68	C128	T181	P242	L302	GLY	D422	
P69	I129	E182	P243	L303	ASP	P423	
A70	H130	M183	D244	N304	PHE	L424	
A71	K131	G184	A245	H305	VAL	K425	
Y72	P192	Q185	G246	H306	CYS	K426	
E73	M133	Q193	E247	R307	PRO	D427	
G74	Y134	E194	T248	S308	VAL	K428	
I75	F136	K195	M249	P309	ASP	Q429	
K76	P136	M196	L256	N310	ASN	V430	
D77	F137	N197	L257	T311	ALA	V431	
L78	D138	R198	A258	H312	ARG	A432	
S79	W139	S199	L259	THR	VAL	M433	
T80	Q140	D200	T260	THR	ALA	V434	
P81	N141	D201	V261	MET	VAL	A435	
S82	C142	P202	F262	PRO	VAL	D436	
D83	T143	S203	L263	ASN	GLN	D437	
D84	M144	Y204	L264	TRP	PRO	R437	
V85	V145	E205	L265	ILE	GLU	L438	
K86	F146	D206	L266	ARG	ARG	F439	
Q87	K147	V207	A267	LEU	LEU	L440	
P88	T208	V207	D268	TRP	HIS	C447	
D89	Y149	T208	K269	LEU	LEU	S448	
I90	T150	F209	Y210	ASN	ASN	I449	
V91	Y151	Y210	P271	GLY	GLY	G450	
L92	D152	L212	E272	TRP	TRP	T451	
H93	T153	L212	T273	ILE	THR	F452	
N94	S154	Q214	S274	GLN	GLN	S453	
N95	E155	R215	L275	PRO	PRO	L454	
N96	V156	K216	S276	VAL	THR	L456	

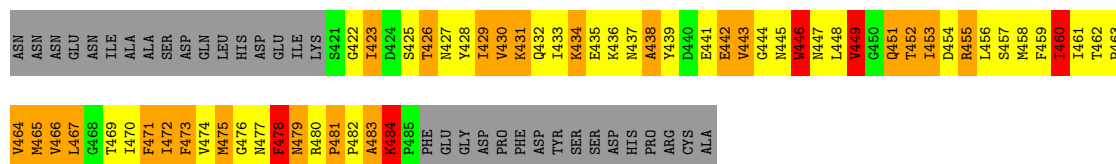
• Molecule 1: Acetylcholine receptor beta subunit

Chain Q: 5% 41% 24% 5% 25%

MET	THR	THR	V277	THR	LEU	S459
GLU	THR	PRO	P278	THR	PRO	H460
ASP	PRO	GLN	I279	PRO	ASP	N461
VAL	SER	ASP	I280	SER	ASP	V462
ARG	PRO	LEU	I281	PRO	LEU	P463
ARG	PRO	LYS	S282	ASP	LYS	D465
MET	MET	E403	Y283	SER	E404	M466
ALA	ALA	A404	T224	LYS	A405	F468
LEU	LEU	V405	V226	PRO	E406	A469
GLY	GLY	E406	P227	THR	A407	
LEU	LEU	A407	L287	ILE	A407	
VAL	VAL	I408	C228	ILE	I408	
VAL	VAL	K409	I229	SER	K409	
MET	MET	V410	L230	ARG	V410	
MET	MET	I411	I231	ALA	I411	
ALA	ALA	A412	S232	ASN	A412	
LEU	LEU	E413	L233	ASP	F293	
ALA	ALA	Q414	L234	GLU	S294	
LEU	LEU	L415	A235	TVR	V295	
SER	SER	E416	T236	PHE	L296	
GLY	GLY	S417	L237	ILE	L297	
VAL	VAL	A418	V238	ARG	S298	
GLY	GLY	S419	F239	LYS	V299	
ALA	ALA	E420	Y240	PRO	V300	
S1	S1	F421	L241	ALA	V301	
V2	V2	D422	P242	GLY	L302	
M3	M3	P423	P243	ASP	N303	
D5	D5	L424	D244	PHE	L304	
T6	T6	H305	A245	VAL	H305	
T6	T6	K426	G246	CYS	H306	
L7	L7	D427	E247	PRO	R307	
L8	L8	K428	T248	VAL	S308	
S9	S9	Q429	M249	ASP	P309	
V10	V10	S250	S250	ASN	N310	
L11	L11	L251	L251	ALA	T311	
F12	F12	S252	S252	ARG	H312	
E13	E13	I253	I253	VAL	V434	
H14	H14	S254	S254	ALA	A435	
Y15	Y15	A255	A255	VAL	D436	
M16	M16	L256	L256	GLN	R437	
P17	P17	L257	L257	PRO	F439	
K18	K18	A258	A258	GLU	L440	
V19	V19	L259	L259	ARG	Y441	
R20	R20	T260	T260	LEU	K442	
P21	P21	Q140	Q140	PHE	F443	
S22	S22	N141	N141	SER	T444	
Q23	Q23	P202	P202	GLU	M446	
T24	T24	C142	C142	MET	C447	
V25	V25	T143	T143	LYS	S448	
G26	G26	Y204	Y204	TRP	I449	
D27	D27	E205	E205	HIS	G450	
K28	K28	D206	D206	LEU	T451	
V29	V29	F146	F146	LEU	F452	
T30	T30	V207	V207	TRP	I454	
V31	V31	K147	K147	TRP	T454	
R32	R32	T208	T208	ILE	F455	
V33	V33	Y149	Y149	THR	L456	
G34	G34	F209	F209	GLN	D457	
L35	L35	Y210	Y210	VAL	A458	
T36	T36	T150	T150	THR		
		D152	D152			
		L92	L92			
		H93	H93			
		N94	N94			
		E155	E155			
		V156	V156			

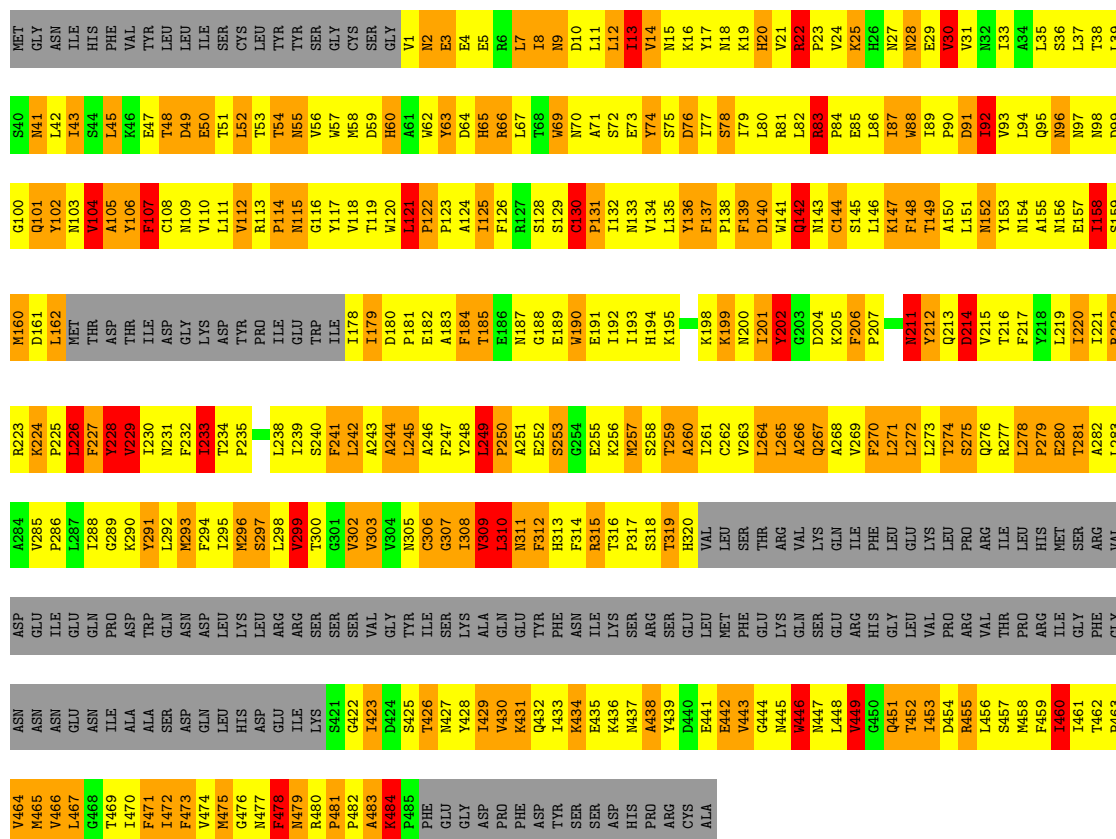
• Molecule 1: Acetylcholine receptor beta subunit





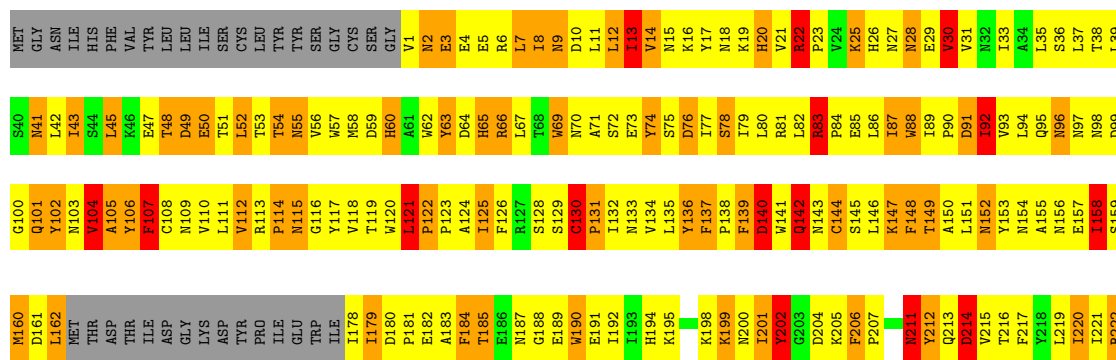
• Molecule 2: Acetylcholine receptor delta subunit

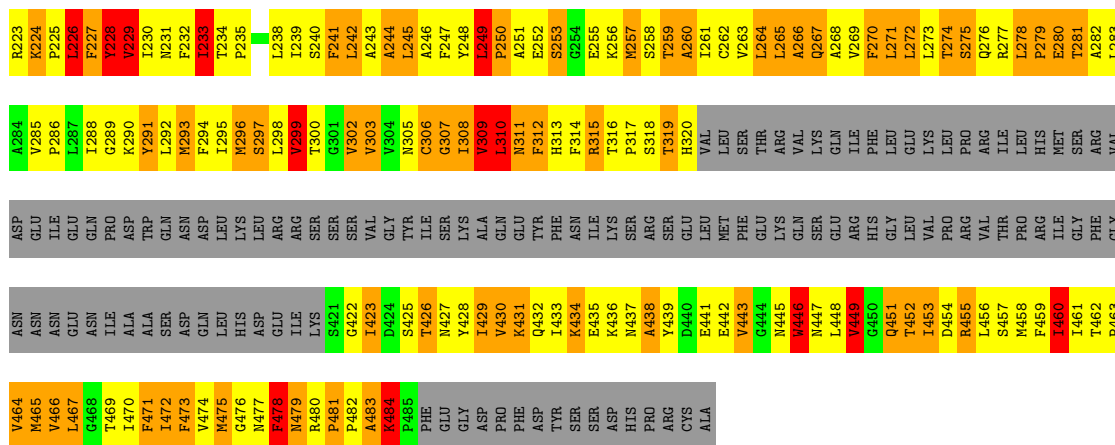
Chain C: 6% 36% 24% 5% 29%



• Molecule 2: Acetylcholine receptor delta subunit

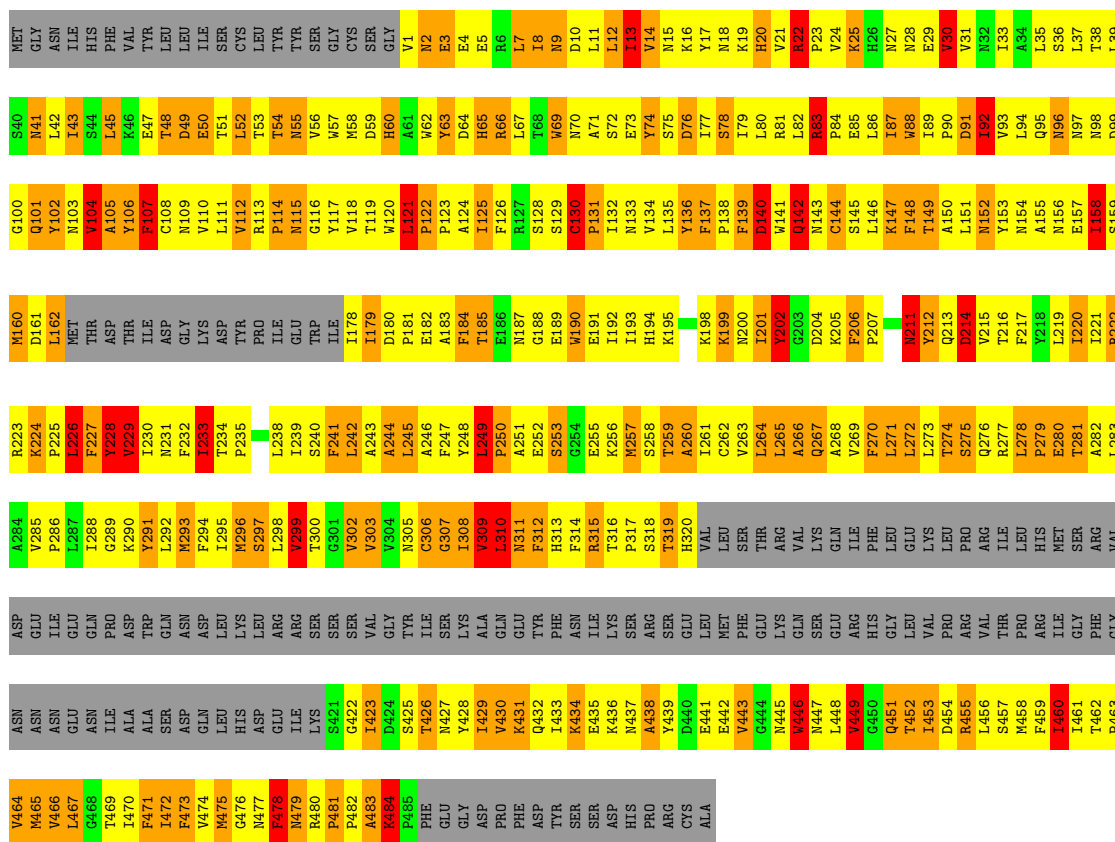
Chain H: 6% 36% 23% 5% 29%





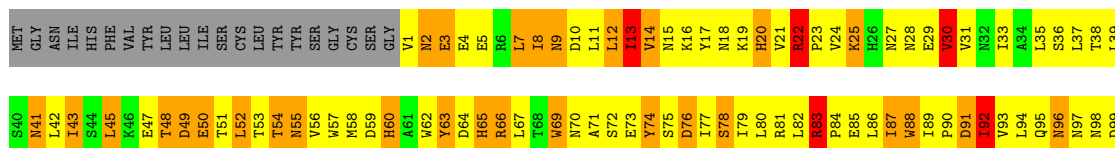
• Molecule 2: Acetylcholine receptor delta subunit

Chain M: 6% 36% 23% 5% 29%



• Molecule 2: Acetylcholine receptor delta subunit

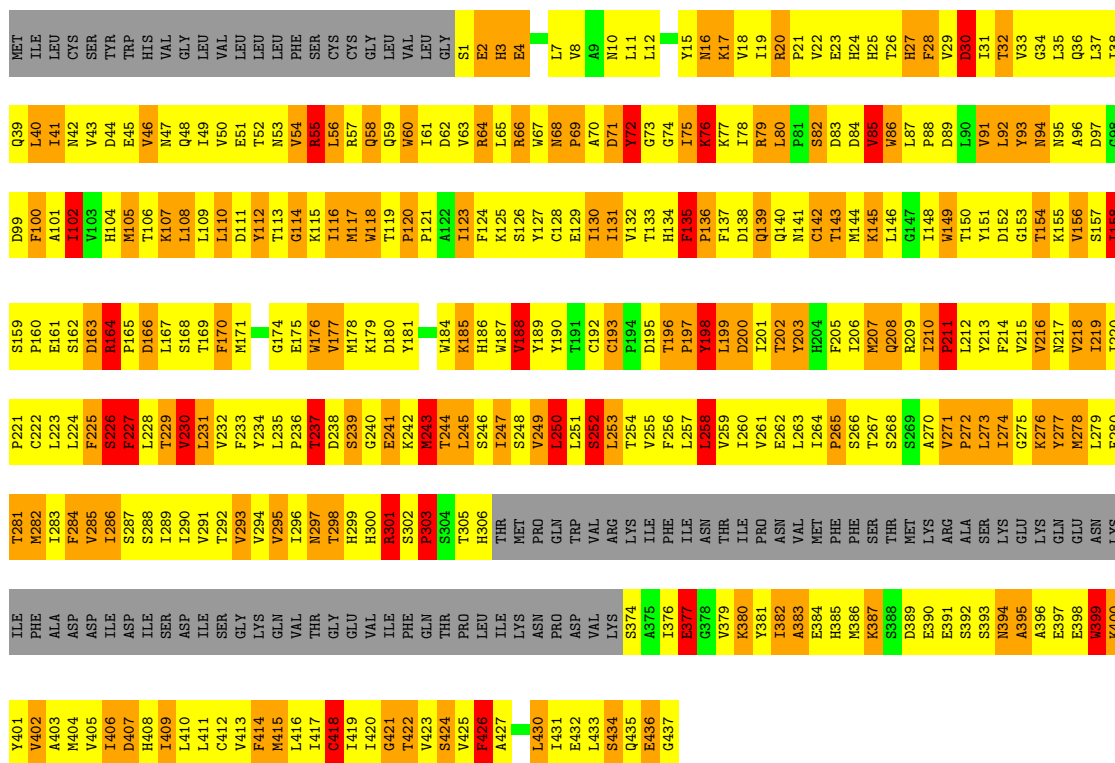
Chain R: 6% 36% 23% 5% 29%





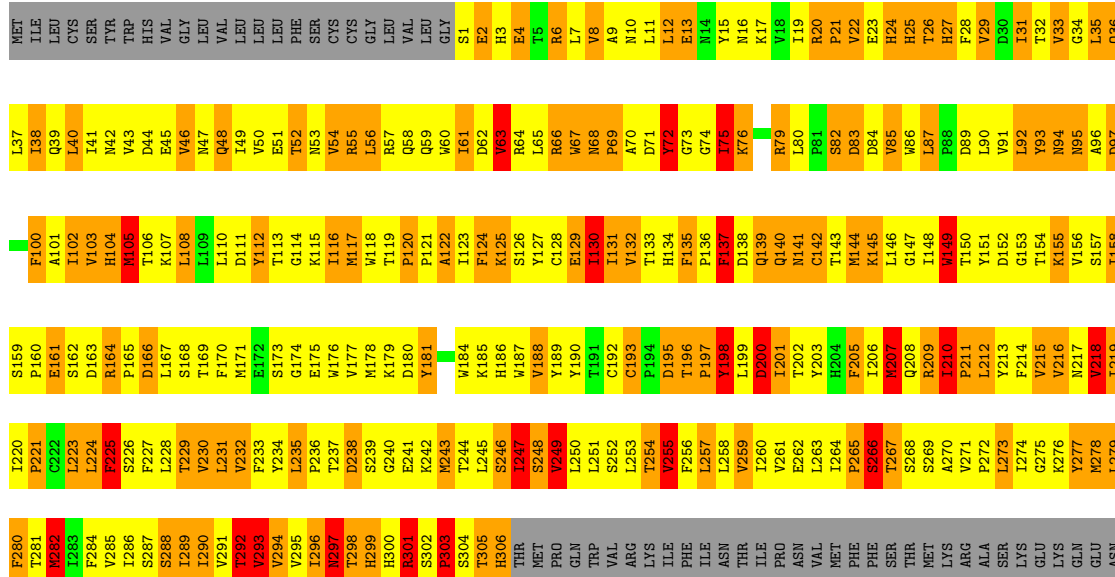
• Molecule 3: Acetylcholine receptor subunit alpha

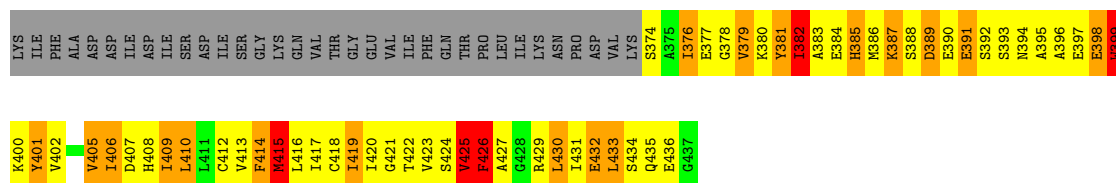
Chain D: 5% 44% 25% 6% 20%



• Molecule 3: Acetylcholine receptor subunit alpha

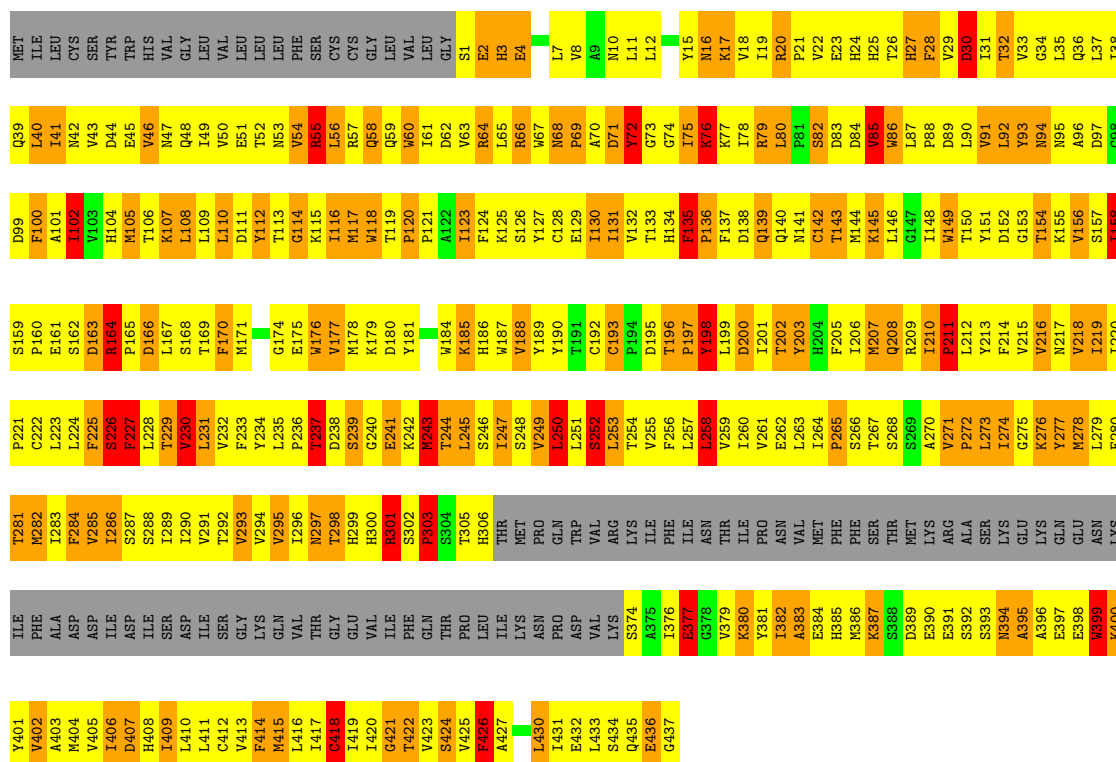
Chain F: 5% 40% 29% 6% 20%





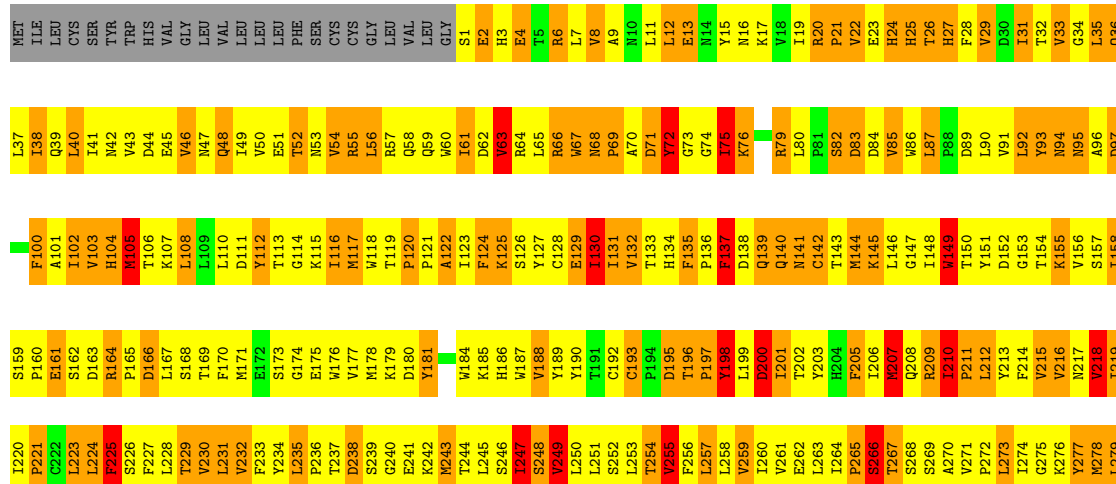
• Molecule 3: Acetylcholine receptor subunit alpha

Chain I: 5% 44% 25% 5% 20%



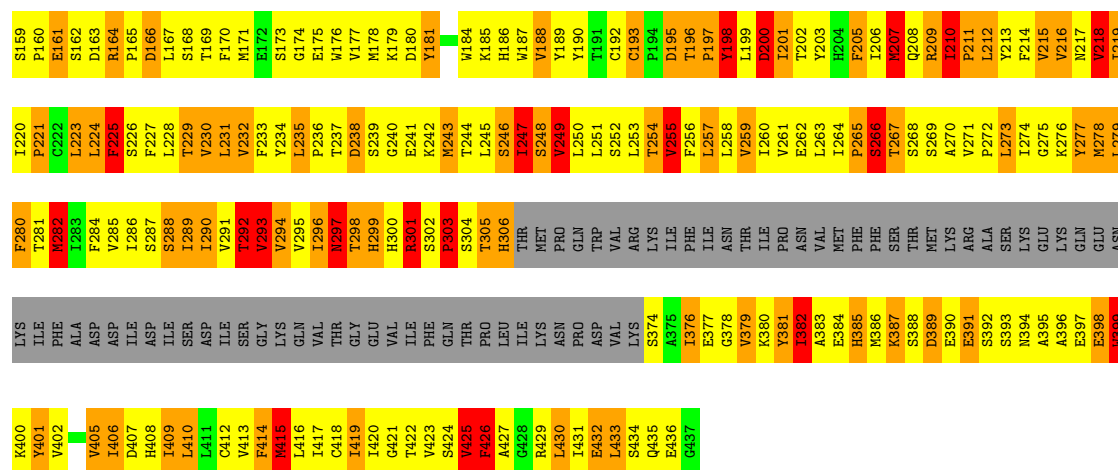
• Molecule 3: Acetylcholine receptor subunit alpha

Chain K: 6% 40% 29% 6% 20%



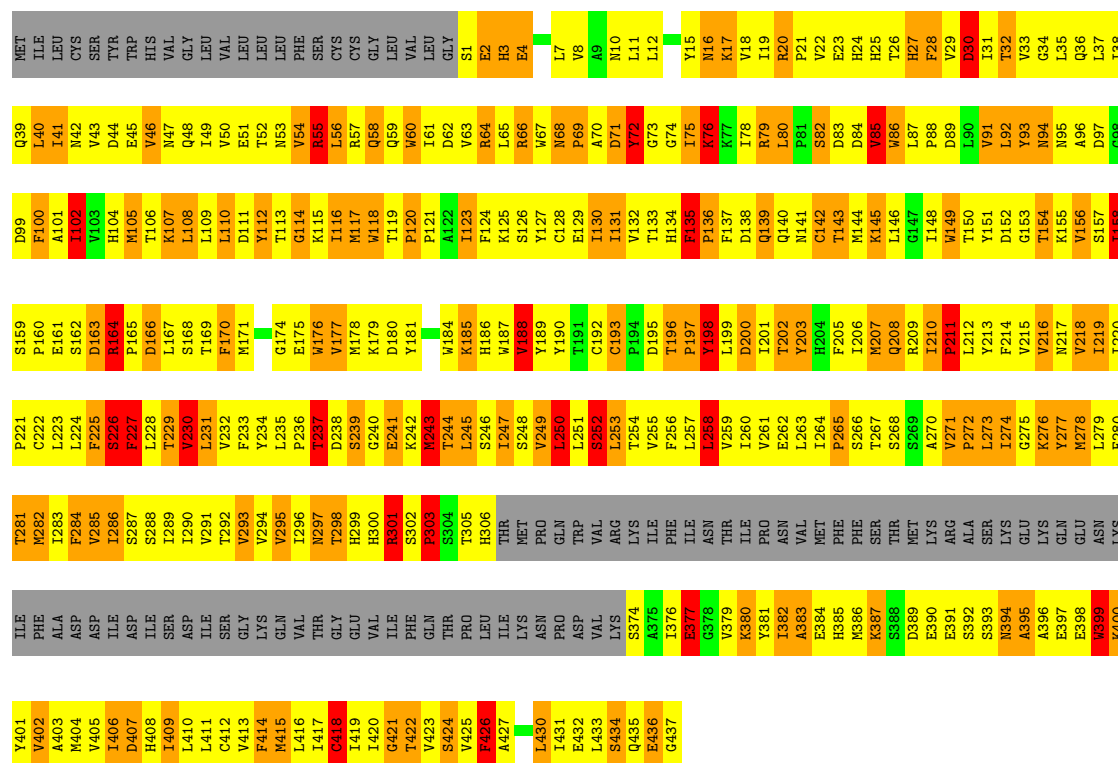


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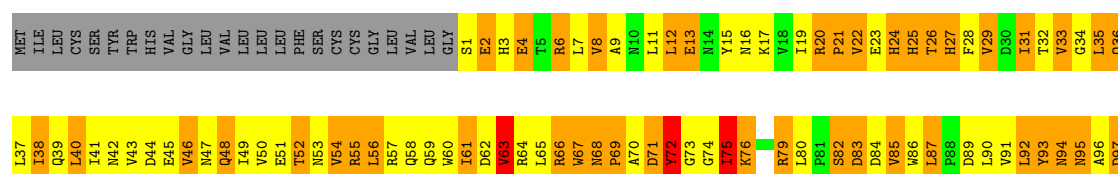
• Molecule 3: Acetylcholine receptor subunit alpha

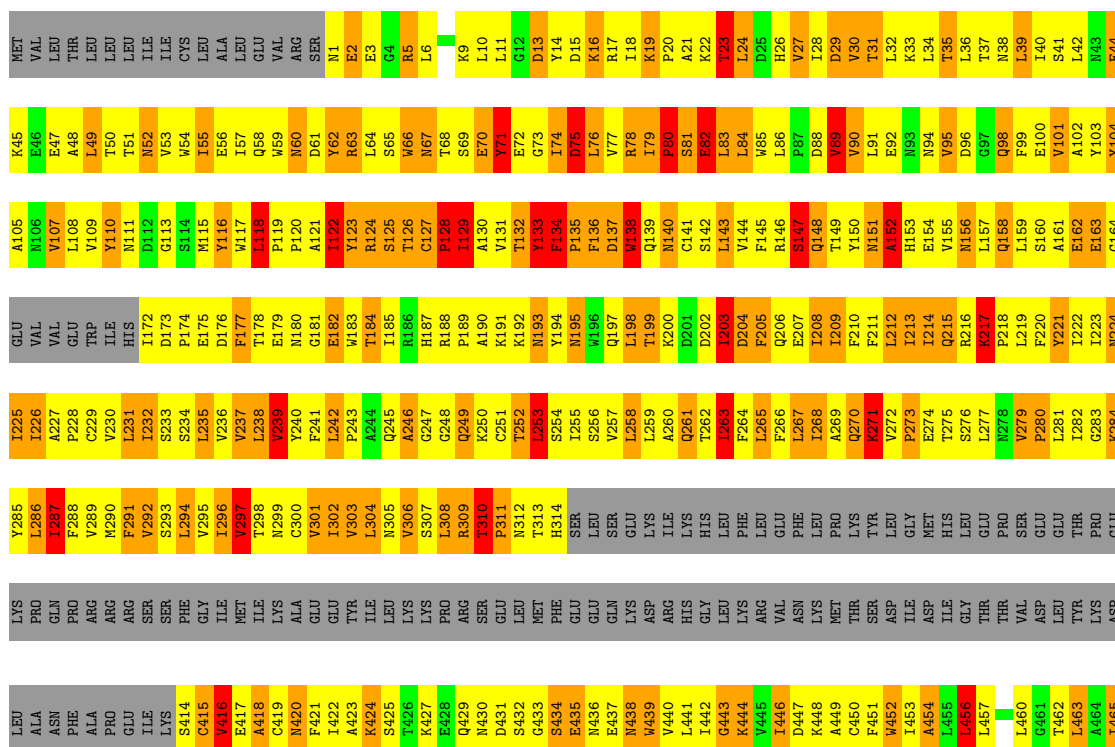
Chain X: 6% 44% 25% 6% 20%



• Molecule 3: Acetylcholine receptor subunit alpha

Chain Z: 6% 40% 29% 6% 20%

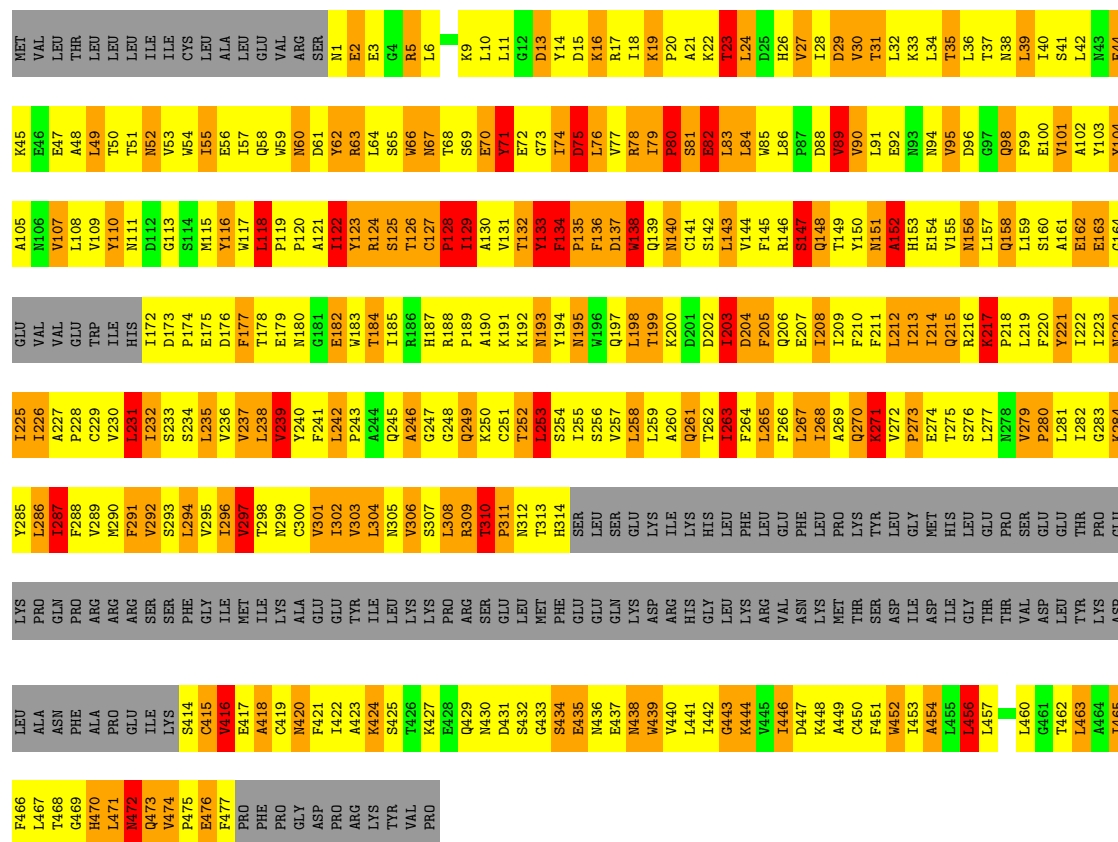




F466
L467
T468
G469
H470
L471
M472
Q473
V474
P475
E476
F477
PRO
PHE
PRO
GLY
ASP
PRO
ARG
LYS
TYR
VAL
PRO

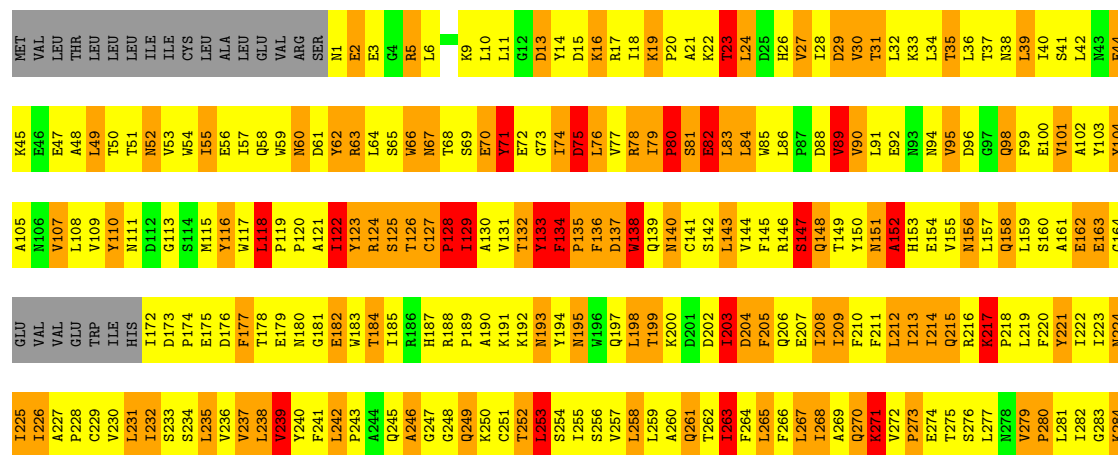
• Molecule 4: Acetylcholine receptor gamma subunit

Chain O: 5% 38% 24% 6% 27%



• Molecule 4: Acetylcholine receptor gamma subunit

Chain T: 5% 38% 25% 5% 27%



4 Experimental information

Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of tilted images used	3564	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	3000	Depositor
Maximum defocus (nm)	6000	Depositor
Magnification	80213	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	O	1.05	18/3048 (0.6%)	1.51	57/4162 (1.4%)
1	B	1.05	18/3048 (0.6%)	1.51	60/4162 (1.4%)
1	G	1.05	18/3048 (0.6%)	1.51	61/4162 (1.5%)
1	L	1.05	17/3048 (0.6%)	1.51	57/4162 (1.4%)
1	Q	1.05	18/3048 (0.6%)	1.51	59/4162 (1.4%)
1	V	1.05	18/3048 (0.6%)	1.51	60/4162 (1.4%)
2	1	0.97	13/3059 (0.4%)	1.55	72/4175 (1.7%)
2	C	0.98	13/3059 (0.4%)	1.55	72/4175 (1.7%)
2	H	0.97	13/3059 (0.4%)	1.55	72/4175 (1.7%)
2	M	0.97	13/3059 (0.4%)	1.55	72/4175 (1.7%)
2	R	0.97	13/3059 (0.4%)	1.55	72/4175 (1.7%)
2	W	0.97	13/3059 (0.4%)	1.55	71/4175 (1.7%)
3	2	0.98	13/3069 (0.4%)	1.49	56/4186 (1.3%)
3	A	0.96	9/3069 (0.3%)	1.55	70/4186 (1.7%)
3	D	0.98	13/3069 (0.4%)	1.49	57/4186 (1.4%)
3	F	0.96	9/3069 (0.3%)	1.55	70/4186 (1.7%)
3	I	0.98	13/3069 (0.4%)	1.49	55/4186 (1.3%)
3	K	0.96	9/3069 (0.3%)	1.55	70/4186 (1.7%)
3	N	0.98	13/3069 (0.4%)	1.49	57/4186 (1.4%)
3	P	0.96	9/3069 (0.3%)	1.55	69/4186 (1.6%)
3	S	0.98	13/3069 (0.4%)	1.49	56/4186 (1.3%)
3	U	0.96	9/3069 (0.3%)	1.55	69/4186 (1.6%)
3	X	0.98	13/3069 (0.4%)	1.49	56/4186 (1.3%)
3	Z	0.96	9/3069 (0.3%)	1.55	70/4186 (1.7%)
4	3	0.96	12/3057 (0.4%)	1.50	71/4174 (1.7%)
4	E	0.96	13/3057 (0.4%)	1.50	72/4174 (1.7%)
4	J	0.96	13/3057 (0.4%)	1.50	72/4174 (1.7%)
4	O	0.96	12/3057 (0.4%)	1.50	73/4174 (1.7%)
4	T	0.96	13/3057 (0.4%)	1.50	71/4174 (1.7%)
4	Y	0.96	13/3057 (0.4%)	1.50	72/4174 (1.7%)
All	All	0.99	393/91812 (0.4%)	1.52	1971/125298 (1.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	1	0	2
2	C	0	2
2	H	0	2
2	M	0	2
2	R	0	2
2	W	0	2
3	2	0	2
3	D	0	2
3	I	0	2
3	N	0	2
3	S	0	2
3	X	0	2
All	All	0	24

The worst 5 of 393 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	129	THR	C-N	-18.41	1.14	1.34
1	L	129	THR	C-N	-18.41	1.14	1.34
1	V	129	THR	C-N	-18.39	1.14	1.34
1	0	129	THR	C-N	-18.38	1.14	1.34
1	G	129	THR	C-N	-18.35	1.14	1.34

The worst 5 of 1971 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	W	122	PRO	CA-C-N	13.71	134.64	119.83
2	W	122	PRO	C-N-CA	13.71	134.64	119.83
2	1	122	PRO	CA-C-N	13.68	134.60	119.83
2	1	122	PRO	C-N-CA	13.68	134.60	119.83
2	H	122	PRO	CA-C-N	13.66	134.59	119.83

There are no chirality outliers.

5 of 24 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	63	TYR	Sidechain
2	1	74	TYR	Sidechain
3	2	277	TYR	Sidechain
3	2	72	TYR	Sidechain

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Mol	Chain	Res	Type	Group
2	C	63	TYR	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	2972	0	2954	1126	0
1	B	2972	0	2954	1120	0
1	G	2972	0	2954	1120	0
1	L	2972	0	2954	1132	0
1	Q	2972	0	2954	1117	0
1	V	2972	0	2954	1110	0
2	1	2983	0	2987	1201	0
2	C	2983	0	2987	1196	0
2	H	2983	0	2987	1208	0
2	M	2983	0	2987	1194	0
2	R	2983	0	2987	1205	0
2	W	2983	0	2987	1193	0
3	2	2991	0	3006	1088	0
3	A	2991	0	3006	1100	0
3	D	2991	0	3006	1092	0
3	F	2991	0	3006	1112	0
3	I	2991	0	3006	1084	0
3	K	2991	0	3006	1097	0
3	N	2991	0	3006	1095	0
3	P	2991	0	3006	1102	0
3	S	2991	0	3006	1081	0
3	U	2991	0	3006	1096	0
3	X	2991	0	3006	1092	0
3	Z	2991	0	3006	1105	0
4	3	2987	0	2994	1109	0
4	E	2987	0	2994	1115	0
4	J	2987	0	2994	1112	0
4	O	2987	0	2994	1119	0
4	T	2987	0	2994	1108	0
4	Y	2987	0	2994	1113	0
All	All	89544	0	89682	32137	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 179.

The worst 5 of 32137 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Y:183:TRP:CB	4:Y:216:ARG:HG2	1.33	1.59
4:3:183:TRP:CB	4:3:216:ARG:HG2	1.33	1.56
4:E:183:TRP:CB	4:E:216:ARG:HG2	1.33	1.55
4:J:183:TRP:CB	4:J:216:ARG:HG2	1.33	1.53
1:G:134:TYR:CE1	1:G:213:ILE:HG13	1.44	1.52

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	364/493 (74%)	274 (75%)	58 (16%)	32 (9%)	0	8
1	B	364/493 (74%)	274 (75%)	58 (16%)	32 (9%)	0	8
1	G	364/493 (74%)	273 (75%)	59 (16%)	32 (9%)	0	8
1	L	364/493 (74%)	273 (75%)	59 (16%)	32 (9%)	0	8
1	Q	364/493 (74%)	274 (75%)	58 (16%)	32 (9%)	0	8
1	V	364/493 (74%)	274 (75%)	58 (16%)	32 (9%)	0	8
2	1	364/522 (70%)	289 (79%)	57 (16%)	18 (5%)	1	16
2	C	364/522 (70%)	289 (79%)	57 (16%)	18 (5%)	1	16
2	H	364/522 (70%)	288 (79%)	58 (16%)	18 (5%)	1	16
2	M	364/522 (70%)	288 (79%)	58 (16%)	18 (5%)	1	16
2	R	364/522 (70%)	288 (79%)	58 (16%)	18 (5%)	1	16
2	W	364/522 (70%)	289 (79%)	57 (16%)	18 (5%)	1	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	2	366/461 (79%)	294 (80%)	41 (11%)	31 (8%)	0	9
3	A	366/461 (79%)	288 (79%)	50 (14%)	28 (8%)	1	10
3	D	366/461 (79%)	294 (80%)	41 (11%)	31 (8%)	0	9
3	F	366/461 (79%)	288 (79%)	50 (14%)	28 (8%)	1	10
3	I	366/461 (79%)	294 (80%)	41 (11%)	31 (8%)	0	9
3	K	366/461 (79%)	289 (79%)	48 (13%)	29 (8%)	1	10
3	N	366/461 (79%)	293 (80%)	42 (12%)	31 (8%)	0	9
3	P	366/461 (79%)	289 (79%)	49 (13%)	28 (8%)	1	10
3	S	366/461 (79%)	294 (80%)	41 (11%)	31 (8%)	0	9
3	U	366/461 (79%)	288 (79%)	50 (14%)	28 (8%)	1	10
3	X	366/461 (79%)	294 (80%)	41 (11%)	31 (8%)	0	9
3	Z	366/461 (79%)	289 (79%)	48 (13%)	29 (8%)	1	10
4	3	365/505 (72%)	281 (77%)	58 (16%)	26 (7%)	1	11
4	E	365/505 (72%)	281 (77%)	58 (16%)	26 (7%)	1	11
4	J	365/505 (72%)	281 (77%)	58 (16%)	26 (7%)	1	11
4	O	365/505 (72%)	281 (77%)	58 (16%)	26 (7%)	1	11
4	T	365/505 (72%)	281 (77%)	58 (16%)	26 (7%)	1	11
4	Y	365/505 (72%)	281 (77%)	58 (16%)	26 (7%)	1	11
All	All	10950/14652 (75%)	8553 (78%)	1585 (14%)	812 (7%)	1	10

5 of 812 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	2	VAL
1	0	68	ASP
1	0	82	SER
1	0	95	ASN
1	0	131	LYS

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	340/449 (76%)	261 (77%)	79 (23%)	1	5
1	B	340/449 (76%)	261 (77%)	79 (23%)	1	5
1	G	340/449 (76%)	261 (77%)	79 (23%)	1	5
1	L	340/449 (76%)	261 (77%)	79 (23%)	1	5
1	Q	340/449 (76%)	261 (77%)	79 (23%)	1	5
1	V	340/449 (76%)	261 (77%)	79 (23%)	1	5
2	1	335/475 (70%)	240 (72%)	95 (28%)	0	2
2	C	335/475 (70%)	240 (72%)	95 (28%)	0	2
2	H	335/475 (70%)	240 (72%)	95 (28%)	0	2
2	M	335/475 (70%)	240 (72%)	95 (28%)	0	2
2	R	335/475 (70%)	240 (72%)	95 (28%)	0	2
2	W	335/475 (70%)	240 (72%)	95 (28%)	0	2
3	2	343/427 (80%)	248 (72%)	95 (28%)	0	3
3	A	343/427 (80%)	236 (69%)	107 (31%)	0	2
3	D	343/427 (80%)	247 (72%)	96 (28%)	0	3
3	F	343/427 (80%)	236 (69%)	107 (31%)	0	2
3	I	343/427 (80%)	247 (72%)	96 (28%)	0	3
3	K	343/427 (80%)	236 (69%)	107 (31%)	0	2
3	N	343/427 (80%)	247 (72%)	96 (28%)	0	3
3	P	343/427 (80%)	236 (69%)	107 (31%)	0	2
3	S	343/427 (80%)	247 (72%)	96 (28%)	0	3
3	U	343/427 (80%)	236 (69%)	107 (31%)	0	2
3	X	343/427 (80%)	247 (72%)	96 (28%)	0	3
3	Z	343/427 (80%)	236 (69%)	107 (31%)	0	2
4	3	337/463 (73%)	238 (71%)	99 (29%)	0	2
4	E	337/463 (73%)	237 (70%)	100 (30%)	0	2
4	J	337/463 (73%)	238 (71%)	99 (29%)	0	2
4	O	337/463 (73%)	238 (71%)	99 (29%)	0	2
4	T	337/463 (73%)	238 (71%)	99 (29%)	0	2
4	Y	337/463 (73%)	238 (71%)	99 (29%)	0	2
All	All	10188/13446 (76%)	7332 (72%)	2856 (28%)	1	3

5 of 2856 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	P	207	MET
3	U	72	TYR
1	Q	19	VAL
3	P	200	ASP
3	S	17	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 423 such sidechains are listed below:

Mol	Chain	Res	Type
2	M	70	ASN
1	Q	111	GLN
4	Y	98	GLN
2	M	267	GLN
4	O	98	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	0	1
1	B	1
1	G	1
1	L	1
1	Q	1
1	V	1

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	0	129:THR	C	130:ILE	N	1.14
1	B	129:THR	C	130:ILE	N	1.14
1	G	129:THR	C	130:ILE	N	1.14
1	L	129:THR	C	130:ILE	N	1.14
1	Q	129:THR	C	130:ILE	N	1.14

6 Tomogram visualisation

This section contains visualisations of the EMDB entry EMD-2376. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Tomogram analysis

This section contains the results of statistical analysis of the tomogram.

7.1 Map-value distribution

This section was not generated.

8 Map-model fit

This section was not generated.