



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 08:08 PM UTC

PDB ID : 7ADP / pdb_00007adp
EMDB ID : EMD-11733
Title : Cryo-EM structure of human ER membrane protein complex in GDN detergent
Authors : Braeuning, B.; Prabu, J.R.; Miller-Vedam, L.E.; Weissman, J.S.; Frost, A.; Schulman, B.A.
Deposited on : 2020-09-15
Resolution : 3.60 Å(reported)

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
Mogul	:	2022.3.0, CSD as543be (2022)
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

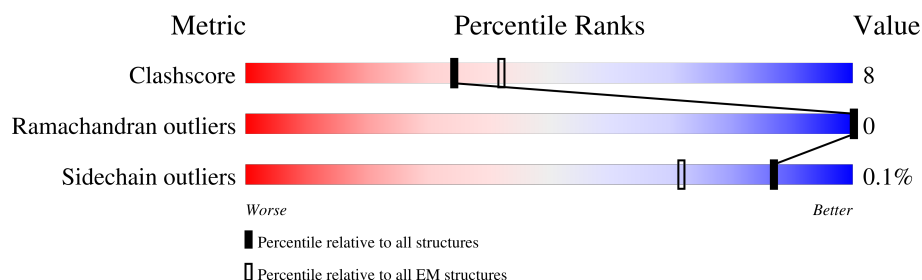
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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	A	993	70% 18% 11%
2	B	297	80% 12% 8%
3	C	261	54% 19% 27%
4	D	183	22% . 76%
5	E	139	55% 11% 34%
6	F	110	75% 16% 9%
7	H	210	62% 17% 21%
8	I	263	40% 10% 49%

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 15026 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 ER membrane protein complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	881	Total	C	N	O	S	0	0
			6983	4489	1201	1269	24		

- Molecule 2 is a protein called ER membrane protein complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	273	Total	C	N	O	S	0	0
			2249	1412	399	424	14		

- Molecule 3 is a protein called ER membrane protein complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	191	Total	C	N	O	S	0	0
			1562	1028	251	277	6		

- Molecule 4 is a protein called ER membrane protein complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	44	Total	C	N	O	S	0	0
			353	236	54	62	1		

- Molecule 5 is a protein called Membrane magnesium transporter 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	92	Total	C	N	O	S	0	0
			726	472	127	124	3		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	132	ASP	-	expression tag	UNP Q8N4V1
E	133	TYR	-	expression tag	UNP Q8N4V1
E	134	LYS	-	expression tag	UNP Q8N4V1

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Chain	Residue	Modelled	Actual	Comment	Reference
E	135	ASP	-	expression tag	UNP Q8N4V1
E	136	ASP	-	expression tag	UNP Q8N4V1
E	137	ASP	-	expression tag	UNP Q8N4V1
E	138	ASP	-	expression tag	UNP Q8N4V1
E	139	LYS	-	expression tag	UNP Q8N4V1

- Molecule 6 is a protein called ER membrane protein complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	100	Total	C	N	O	S	0	0
			781	526	127	126	2		

- Molecule 7 is a protein called ER membrane protein complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	166	Total	C	N	O	S	0	0
			1304	822	228	246	8		

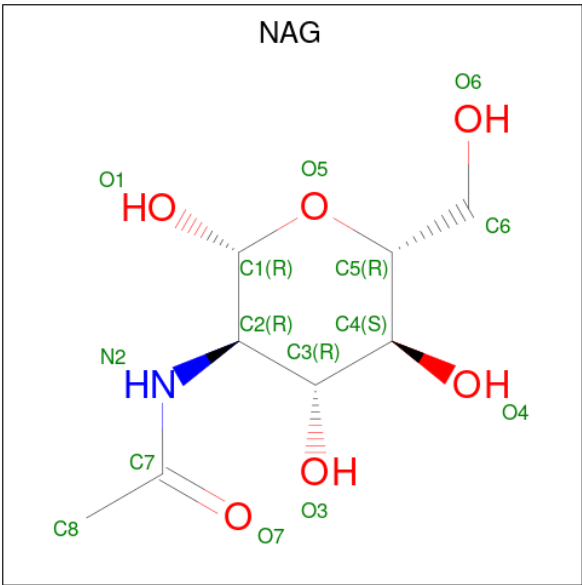
- Molecule 8 is a protein called ER membrane protein complex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	133	Total	C	N	O	S	0	0
			1026	634	190	200	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	0	MET	-	initiating methionine	UNP Q5UCC4
I	1	ALA	-	expression tag	UNP Q5UCC4

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).

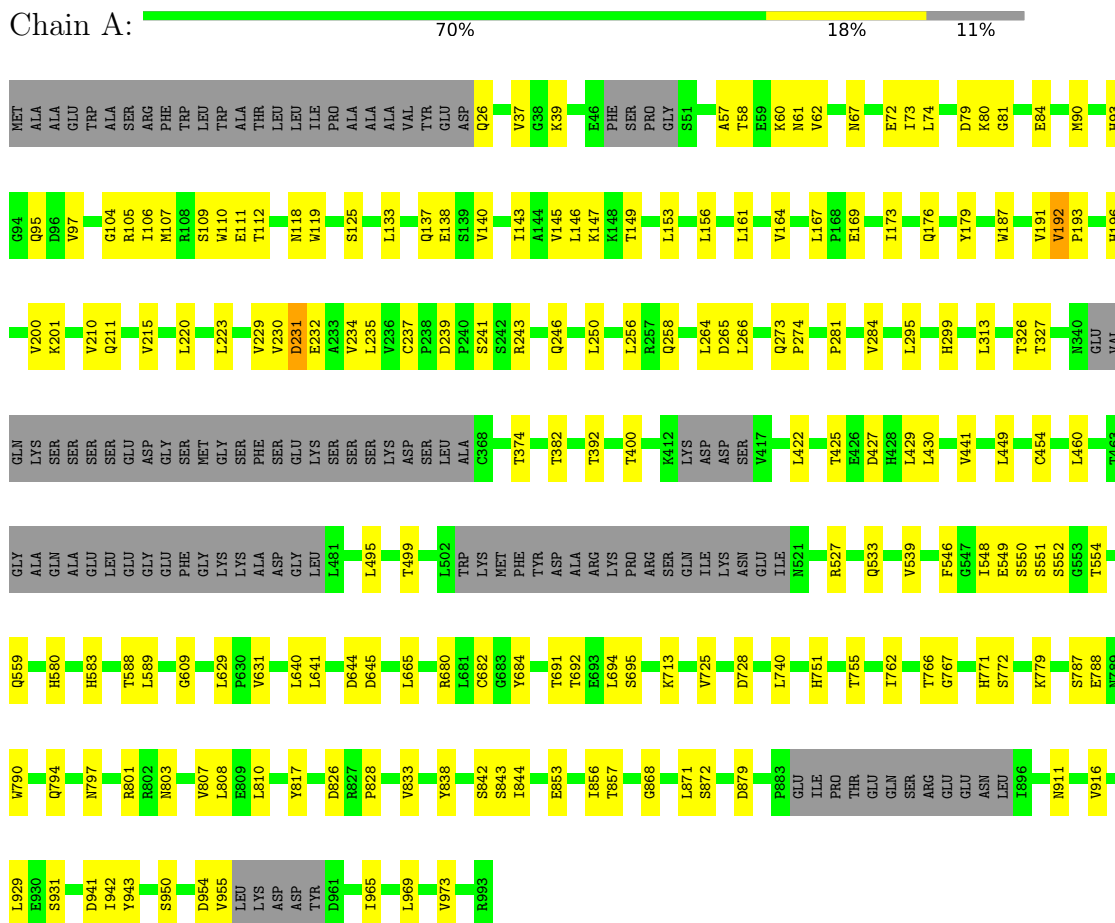


Mol	Chain	Residues	Atoms				AltConf
9	A	1	Total	C	N	O	0
			14	8	1	5	
9	A	1	Total	C	N	O	0
			14	8	1	5	
9	I	1	Total	C	N	O	0
			14	8	1	5	

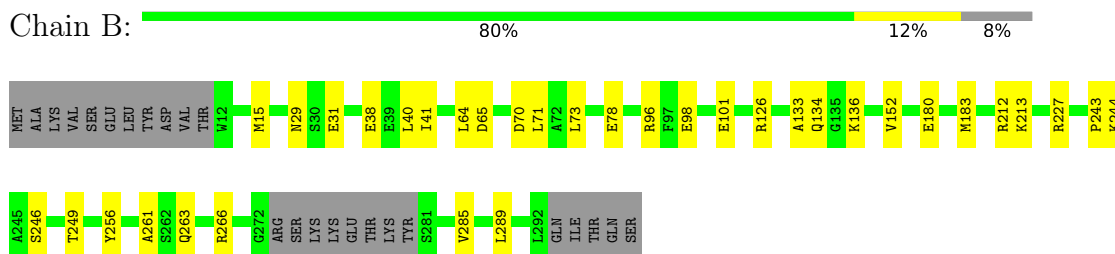
3 Residue-property plots

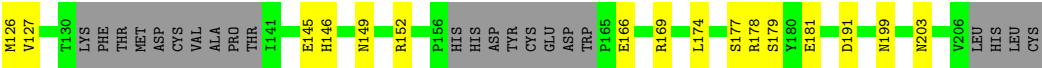
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: ER membrane protein complex subunit 1

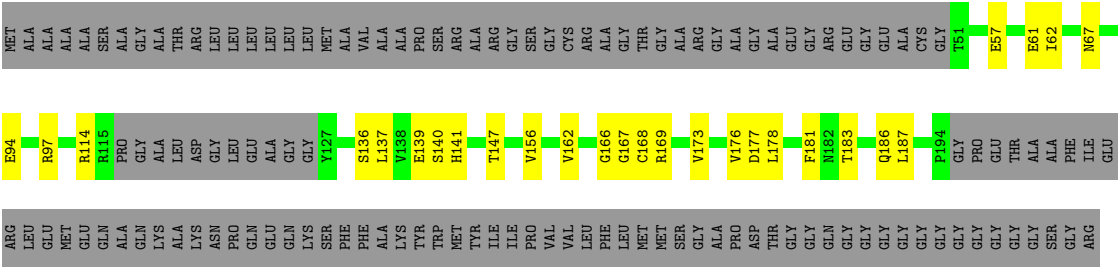
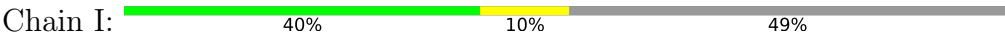


• Molecule 2: ER membrane protein complex subunit 2





● Molecule 8: ER membrane protein complex subunit 10



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	144222	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	62	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

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	A	0.30	0/7137	0.48	0/9695
2	B	0.23	0/2290	0.41	0/3077
3	C	0.22	0/1600	0.44	0/2168
4	D	0.23	0/364	0.47	0/492
5	E	0.21	0/743	0.35	0/1004
6	F	0.25	0/803	0.50	0/1089
7	H	0.19	0/1332	0.43	0/1812
8	I	0.29	0/1042	0.54	0/1415
All	All	0.26	0/15311	0.46	0/20752

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
1	A	0	2
4	D	0	1
7	H	0	1
All	All	0	4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	231	ASP	Peptide
1	A	232	GLU	Peptide

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Mol	Chain	Res	Type	Group
4	D	44	PRO	Peptide
7	H	59	PRO	Peptide

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	A	6983	0	7063	128	0
2	B	2249	0	2194	28	0
3	C	1562	0	1556	43	0
4	D	353	0	335	3	0
5	E	726	0	730	11	0
6	F	781	0	810	13	0
7	H	1304	0	1248	27	0
8	I	1026	0	1005	18	0
9	A	28	0	26	0	0
9	I	14	0	13	0	0
All	All	15026	0	14980	243	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 8.

The worst 5 of 243 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)
1:A:374:THR:HG22	1:A:392:THR:HG22	1.41	1.00
1:A:533:GLN:O	1:A:550:SER:OG	1.92	0.87
1:A:97:VAL:HG23	1:A:112:THR:HG22	1.62	0.82
1:A:751:HIS:O	1:A:755:THR:OG1	1.99	0.80
1:A:559:GLN:NE2	1:A:609:GLY:O	2.14	0.79

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	A	865/993 (87%)	847 (98%)	18 (2%)	0	100	100
2	B	269/297 (91%)	267 (99%)	2 (1%)	0	100	100
3	C	185/261 (71%)	179 (97%)	6 (3%)	0	100	100
4	D	38/183 (21%)	38 (100%)	0	0	100	100
5	E	88/139 (63%)	88 (100%)	0	0	100	100
6	F	98/110 (89%)	95 (97%)	3 (3%)	0	100	100
7	H	158/210 (75%)	157 (99%)	1 (1%)	0	100	100
8	I	129/263 (49%)	126 (98%)	3 (2%)	0	100	100
All	All	1830/2456 (74%)	1797 (98%)	33 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	A	695/872 (80%)	694 (100%)	1 (0%)	88	87
2	B	213/255 (84%)	213 (100%)	0	100	100
3	C	159/235 (68%)	159 (100%)	0	100	100
4	D	36/149 (24%)	36 (100%)	0	100	100
5	E	76/120 (63%)	76 (100%)	0	100	100
6	F	79/85 (93%)	79 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	H	134/182 (74%)	134 (100%)	0	100	100
8	I	116/194 (60%)	116 (100%)	0	100	100
All	All	1508/2092 (72%)	1507 (100%)	1 (0%)	87	87

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	192	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	62	HIS
7	H	149	ASN
8	I	188	GLN
1	A	905	HIS
1	A	989	ASN

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](#)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
9	NAG	I	301	8	14,14,15	0.28	0	17,19,21	0.44	0
9	NAG	A	1002	1	14,14,15	0.23	0	17,19,21	0.44	0
9	NAG	A	1001	1	14,14,15	0.22	0	17,19,21	0.52	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	I	301	8	-	3/6/23/26	0/1/1/1
9	NAG	A	1002	1	-	1/6/23/26	0/1/1/1
9	NAG	A	1001	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	1001	NAG	O5-C5-C6-O6
9	A	1001	NAG	C4-C5-C6-O6
9	A	1002	NAG	O5-C5-C6-O6
9	I	301	NAG	O5-C5-C6-O6
9	I	301	NAG	C1-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-11733. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.