



# wwPDB EM Model Validation Summary Report ⓘ

Mar 9, 2020 – 09:49 AM EDT

PDB ID : 6VQH  
EMDB ID : EMD-21350  
Title : Mammalian V-ATPase from rat brain membrane-embedded Vo region rotational state 3 (from focused refinement)  
Authors : Abbas, Y.M.; Rubinstein, J.L.  
Deposited on : 2020-02-05  
Resolution : 4.40 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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

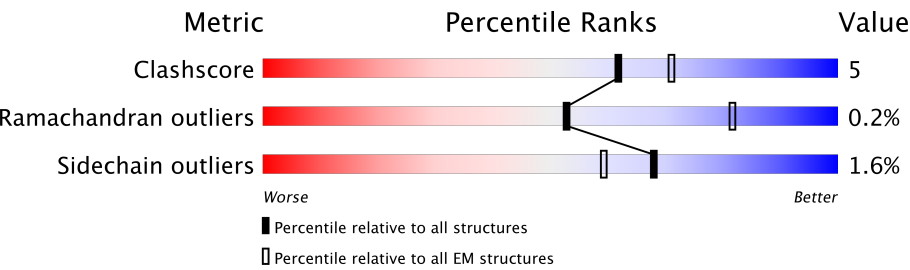
MolProbity : 4.02b-467  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.8

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.40 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	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

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 on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	H	247	<div><div>38%</div><div>58%</div></div>
2	L	119	<div><div>81%</div><div>11%</div><div>8%</div></div>
3	a	838	<div><div>53%</div><div>47%</div></div>
4	b	205	<div><div>99%</div></div>
5	c	463	<div><div>9%</div><div>91%</div></div>
6	d	351	<div><div>99%</div></div>
7	e	81	<div><div>96%</div></div>
8	f	98	<div><div>86%</div><div>14%</div></div>
9	g	155	<div><div>96%</div></div>

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Mol	Chain	Length	Quality of chain
9	h	155	<div><div></div><div>95%</div><div></div><div>..</div></div>
9	i	155	<div><div></div><div>94%</div><div></div><div>..</div></div>
9	j	155	<div><div></div><div>95%</div><div></div><div>..</div></div>
9	k	155	<div><div></div><div>95%</div><div></div><div>..</div></div>
9	l	155	<div><div></div><div>95%</div><div></div><div>..</div></div>
9	m	155	<div><div></div><div>94%</div><div></div><div>..</div></div>
9	n	155	<div><div></div><div>95%</div><div></div><div>..</div></div>
9	o	155	<div><div></div><div>94%</div><div></div><div>..</div></div>
10	p	350	<div><div></div><div>15%</div><div></div><div>85%</div></div>

## 2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 19338 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 ATPase H<sup>+</sup>-transporting V1 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	104	Total	C	N	O	S	0	0
			803	509	138	153	3		

- Molecule 2 is a protein called V-type proton ATPase subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	110	Total	C	N	O	S	0	0
			875	553	157	163	2		

- Molecule 3 is a protein called V-type proton ATPase 116 kDa subunit a isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	a	441	Total	C	N	O	0	0
			2173	1291	441	441		

- Molecule 4 is a protein called ATPase, H<sup>+</sup> transporting, V0 subunit B (Predicted), isoform CRA\_a.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	b	203	Total	C	N	O	S	0	0
			1503	996	237	259	11		

- Molecule 5 is a protein called V-type proton ATPase subunit S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	c	41	Total	C	N	O	S	0	0
			337	228	51	54	4		

- Molecule 6 is a protein called V-type proton ATPase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	d	350	Total	C	N	O	S	0	0
			2833	1829	460	530	14		

- Molecule 7 is a protein called V-type proton ATPase subunit e 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	e	78	Total	C	N	O	0	0
			384	228	78	78		

- Molecule 8 is a protein called Ribonuclease K.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	f	84	Total	C	N	O	0	0
			412	244	84	84		

- Molecule 9 is a protein called V-type proton ATPase 16 kDa proteolipid subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	g	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
9	h	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
9	i	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
9	j	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
9	k	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
9	l	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
9	m	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
9	n	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
9	o	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		

- Molecule 10 is a protein called Renin receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	p	52	Total	C	N	O	S	0	0
			406	269	61	73	3		



- Molecule 4: ATPase, H<sup>+</sup> transporting, V0 subunit B (Predicted), isoform CRA a

Chain b:  99%

- Molecule 5: V-type proton ATPase subunit S1

Chain c:  9% 91%


- Molecule 6: V-type proton ATPase subunit

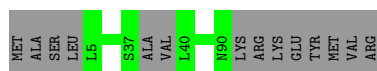
Chain d:  99%

- Molecule 7: V-type proton ATPase subunit e 2

Chain e:  96%

- Molecule 8: Ribonuclease K

Chain f:  86% 14%



- Molecule 9: V-type proton ATPase 16 kDa proteolipid subunit

Chain g:  96% ..



- Molecule 9: V-type proton ATPase 16 kDa proteolipid subunit

Chain h:  95% ..



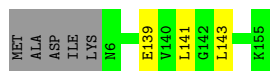
- Molecule 9: V-type proton ATPase 16 kDa proteolipid subunit

Chain i:  94% ..



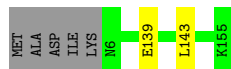
- Molecule 9: V-type proton ATPase 16 kDa proteolipid subunit

Chain j:  95% ..



- Molecule 9: V-type proton ATPase 16 kDa proteolipid subunit

Chain k:  95% ..



- Molecule 9: V-type proton ATPase 16 kDa proteolipid subunit

Chain l:  95% ..



- Molecule 9: V-type proton ATPase 16 kDa proteolipid subunit



Chain m: 

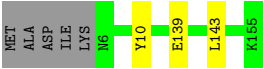
94%



- Molecule 9: V-type proton ATPase 16 kDa proteolipid subunit

Chain n: 

95%



- Molecule 9: V-type proton ATPase 16 kDa proteolipid subunit

Chain o: 

94%

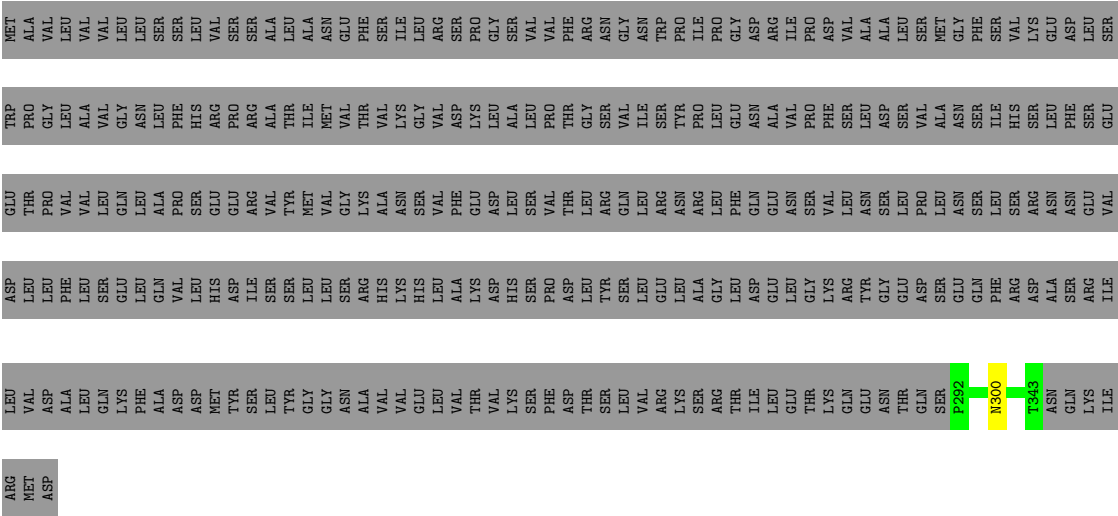


- Molecule 10: Renin receptor

Chain p: 

15%

85%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	79654	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 ( $e^-/\text{\AA}^2$ )	43	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	H	0.83	0/812	0.63	0/1091
2	L	0.81	0/889	0.75	0/1199
3	a	0.30	0/2170	0.46	0/3014
4	b	0.52	0/1537	0.51	0/2088
5	c	0.53	0/347	0.56	0/466
6	d	0.73	0/2899	0.54	0/3927
7	e	0.28	0/383	0.45	0/531
8	f	0.35	0/410	0.48	0/566
9	g	0.50	0/1083	0.54	0/1466
9	h	0.49	0/1083	0.52	0/1466
9	i	0.49	0/1083	0.51	0/1466
9	j	0.47	0/1083	0.50	0/1466
9	k	0.49	0/1083	0.52	0/1466
9	l	0.48	0/1083	0.51	0/1466
9	m	0.51	0/1083	0.57	0/1466
9	n	0.47	0/1083	0.50	0/1466
9	o	0.49	0/1083	0.51	0/1466
10	p	0.50	0/416	0.57	0/571
All	All	0.55	0/19610	0.53	0/26647

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	H	803	0	828	5	0
2	L	875	0	883	11	0
3	a	2173	0	962	0	0
4	b	1503	0	1551	0	0
5	c	337	0	338	0	0
6	d	2833	0	2770	0	0
7	e	384	0	176	0	0
8	f	412	0	186	0	0
9	g	1068	0	1136	0	0
9	h	1068	0	1136	0	0
9	i	1068	0	1136	0	0
9	j	1068	0	1136	0	0
9	k	1068	0	1136	0	0
9	l	1068	0	1136	0	0
9	m	1068	0	1136	0	0
9	n	1068	0	1136	0	0
9	o	1068	0	1136	0	0
10	p	406	0	384	0	0
All	All	19338	0	18302	15	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 5.

The worst 5 of 15 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)
2:L:62:GLY:O	2:L:86:PRO:HA	1.99	0.61
2:L:85:ILE:N	2:L:86:PRO:HD2	2.17	0.59
2:L:85:ILE:N	2:L:86:PRO:CD	2.66	0.58
1:H:107:PRO:HG2	1:H:153:THR:HG21	1.85	0.57
2:L:96:HIS:CG	2:L:97:PRO:HD2	2.46	0.51

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	H	102/247 (41%)	97 (95%)	5 (5%)	0	100	100
2	L	108/119 (91%)	101 (94%)	5 (5%)	2 (2%)	9	46
3	a	435/838 (52%)	426 (98%)	9 (2%)	0	100	100
4	b	201/205 (98%)	198 (98%)	3 (2%)	0	100	100
5	c	39/463 (8%)	39 (100%)	0	0	100	100
6	d	348/351 (99%)	329 (94%)	18 (5%)	1 (0%)	43	80
7	e	76/81 (94%)	75 (99%)	1 (1%)	0	100	100
8	f	80/98 (82%)	77 (96%)	3 (4%)	0	100	100
9	g	148/155 (96%)	146 (99%)	2 (1%)	0	100	100
9	h	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
9	i	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
9	j	148/155 (96%)	146 (99%)	2 (1%)	0	100	100
9	k	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
9	l	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
9	m	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
9	n	148/155 (96%)	145 (98%)	2 (1%)	1 (1%)	24	66
9	o	148/155 (96%)	143 (97%)	4 (3%)	1 (1%)	24	66
10	p	50/350 (14%)	46 (92%)	3 (6%)	1 (2%)	8	45
All	All	2771/4147 (67%)	2693 (97%)	72 (3%)	6 (0%)	53	84

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	p	300	ASN
9	n	10	TYR
9	o	10	TYR
2	L	100	ALA
6	d	119	GLN

### 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	H	84/212 (40%)	84 (100%)	0	100	100
2	L	94/100 (94%)	94 (100%)	0	100	100
4	b	156/158 (99%)	156 (100%)	0	100	100
5	c	36/395 (9%)	35 (97%)	1 (3%)	47	71
6	d	305/306 (100%)	305 (100%)	0	100	100
9	g	109/113 (96%)	108 (99%)	1 (1%)	81	90
9	h	109/113 (96%)	107 (98%)	2 (2%)	62	82
9	i	109/113 (96%)	104 (95%)	5 (5%)	29	61
9	j	109/113 (96%)	106 (97%)	3 (3%)	47	71
9	k	109/113 (96%)	107 (98%)	2 (2%)	62	82
9	l	109/113 (96%)	106 (97%)	3 (3%)	47	71
9	m	109/113 (96%)	105 (96%)	4 (4%)	37	66
9	n	109/113 (96%)	107 (98%)	2 (2%)	62	82
9	o	109/113 (96%)	105 (96%)	4 (4%)	37	66
10	p	41/313 (13%)	41 (100%)	0	100	100
All	All	1697/2501 (68%)	1670 (98%)	27 (2%)	68	83

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	k	139	GLU
9	l	141	LEU
9	o	139	GLU
9	k	143	LEU
9	i	61	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	137	ASN
6	d	297	HIS

### 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 carbohydrates 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 [i](#)

There are no chain breaks in this entry.