



wwPDB EM Model Validation Summary Report ⓘ

Mar 9, 2020 – 10:42 AM EDT

PDB ID : 6VQG
EMDB ID : EMD-21349
Title : Mammalian V-ATPase from rat brain membrane-embedded Vo region rotational state 2 (from focused refinement)
Authors : Abbas, Y.M.; Rubinstein, J.L.
Deposited on : 2020-02-05
Resolution : 4.20 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

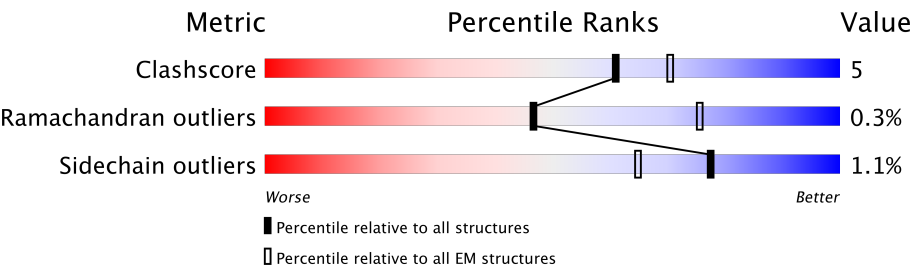
MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.8

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 4.20 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 ≥ 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>39%</div><div>58%</div></div>
2	L	119	<div><div>82%</div><div>9%</div><div>8%</div></div>
3	a	838	<div><div>53%</div><div>47%</div></div>
4	b	205	<div><div>98%</div><div>..</div></div>
5	c	463	<div><div>9%</div><div>91%</div></div>
6	d	351	<div><div>99%</div><div>.</div></div>
7	e	81	<div><div>96%</div><div>.</div></div>
8	f	98	<div><div>86%</div><div>14%</div></div>
9	g	155	<div><div>95%</div><div>..</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>93%</div><div></div><div>. .</div></div>
9	j	155	<div><div></div><div>94%</div><div></div><div>. .</div></div>
9	k	155	<div><div></div><div>96%</div><div></div><div>. .</div></div>
9	l	155	<div><div></div><div>96%</div><div></div><div>. .</div></div>
9	m	155	<div><div></div><div>97%</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>95%</div><div></div><div>. .</div></div>
10	p	350	<div><div></div><div>15%</div><div></div><div>85%</div></div>

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 20946 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⁺-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	S	0	0
			3477	2326	555	574	22		

- Molecule 4 is a protein called ATPase, H⁺ 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	S	0	0
			622	428	98	93	3		

- Molecule 8 is a protein called Ribonuclease K.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	f	84	Total	C	N	O	0	0
			452	282	85	85		

- 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
			432	290	63	76	3		

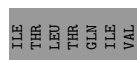
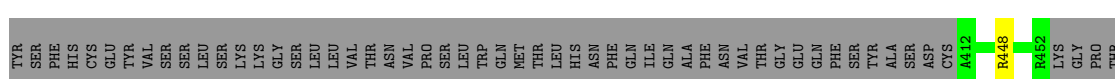
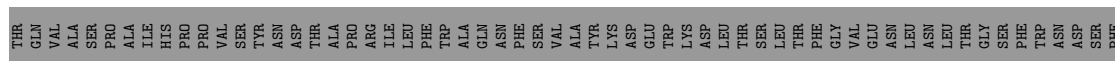
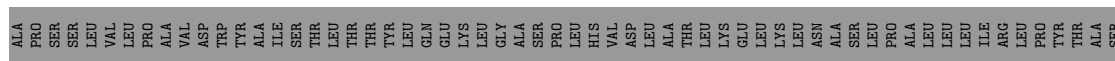
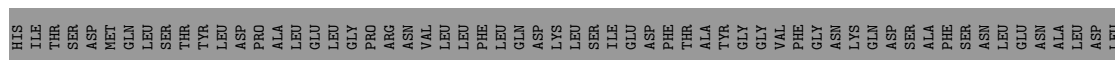
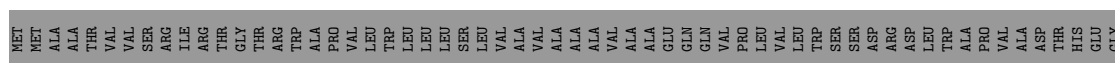
- Molecule 4: ATPase, H⁺ transporting, V0 subunit B (Predicted), isoform CRA a

Chain b: 98%



- Molecule 5: V-type proton ATPase subunit S1

Chain c: 9% 91%



- Molecule 6: V-type proton ATPase subunit

Chain d:  99%




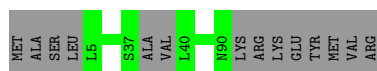
- Molecule 7: V-type proton ATPase subunit e 2

Chain e: 96%



- Molecule 8: Ribonuclease K

Chain f:  86% 14%



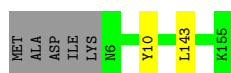
- Molecule 9: V-type proton ATPase 16 kDa proteolipid subunit

Chain g:  95%



- 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:  93%



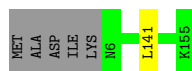
- Molecule 9: V-type proton ATPase 16 kDa proteolipid subunit

Chain j:  94%



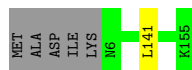
- Molecule 9: V-type proton ATPase 16 kDa proteolipid subunit

Chain k:  96%



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

Chain l:  96%



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

MET
ALA
ASP
ILE
LYS
N6
K155

- Chain n: 95% ...

MET
ALA
ASP
ILE
LYS
N6
Y10
I65
K155

- Chain 0: 95% ..

MET
 ALA
 ASP
 ILE
 LYS
 N6
 Y10
 E139
 V140
 K155

- Chain p: 15% 85%

ARG	LEU	ASP	GLU	TRP	MET
	VAL	LEU	THR	PRO	ALA
MET	ASP	LEU	PRO	GLY	VAL
ASP	ALA	PHE	VAL	LEU	VAL
	LEU	SER	VAL	VAL	VAL
	GLN	SER	LEU	GLY	VAL
	LYS	GLU	GLN	ASN	LEU
	PHE	LEU	ALA	LEU	SER
	ALA	GLN	ALA	LEU	SER
	ASP	VAL	PRO	PHE	SER
	ASP	LEU	SER	HIS	LEU
	MET	HIS	GLU	ARG	VAL
	TYR	ASP	GLU	PRO	SER
	SER	ILE	ARG	ARG	SER
	LEU	SER	VAL	ALA	ALA
	TYR	SER	TYR	THR	LEU
	GLY	LEU	MET	ILE	ALA
	GLY	LEU	VAL	MET	ASN
	ASN	SER	GLY	VAL	ASN
	ALA	ARG	LYS	THR	PHE
	VAL	HIS	ALA	VAL	SER
	VAL	LYS	ASN	LYS	ILE
	GLU	HIS	SER	GLY	LEU
	LEU	LEU	SER	VAL	ARG
	VAL	ALA	PHE	ASP	SER
	THR	GLY	GLY	LEU	PRO
	VAL	ASP	ASP	LYS	GLY
	LYS	HIS	LEU	ALA	SER
	SER	SER	SER	LEU	VAL
	PHE	PRO	VAL	LEU	VAL
	ASP	ASP	THR	THR	VAL
	THR	TYR	LEU	GLY	PHE
	SER	SER	ARG	SER	ASN
	LEU	SER	GLN	VAL	GLY
	VAL	LEU	LEU	ILE	ASN
	ARG	GLU	ARG	ASN	ASP
	LEU	ASP	GLU	ALA	ARG
	GLU	LEU	ASN	VAL	ILE
	THR	GLY	SER	PRO	PRO
	LYS	LYS	VAL	PHE	ASP
	GLN	ARG	LEU	SER	VAL
	GLU	TYR	ASN	LEU	ALA
	ASN	GLY	SER	ASP	ALA
	GLN	ASP	LEU	VAL	SER
	SER	SER	LEU	ALA	MET
	P292	GLU	ASN	ASN	GLY
	N300	PHE	SER	ILE	PHE
	T343	ARG	SER	HIS	VAL
	ASN	ASP	ARG	LYS	LYS
	GLN	ALA	ASN	LEU	GLU
	LYS	SER	ASN	PHE	ASP
		ARG	GLU	SER	LEU

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	74789	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

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	H	0.84	0/812	0.63	0/1091
2	L	0.80	0/889	0.75	0/1199
3	a	0.53	0/3585	0.49	0/4868
4	b	0.51	0/1537	0.49	0/2088
5	c	0.53	0/347	0.56	0/466
6	d	0.73	0/2899	0.53	0/3927
7	e	0.46	0/646	0.46	0/889
8	f	0.40	0/459	0.49	0/635
9	g	0.50	0/1083	0.53	0/1466
9	h	0.47	0/1083	0.53	0/1466
9	i	0.49	0/1083	0.52	0/1466
9	j	0.48	0/1083	0.50	0/1466
9	k	0.49	0/1083	0.53	0/1466
9	l	0.48	0/1083	0.52	0/1466
9	m	0.53	0/1083	0.60	0/1466
9	n	0.47	0/1083	0.51	0/1466
9	o	0.49	0/1083	0.51	0/1466
10	p	0.50	0/445	0.60	0/609
All	All	0.57	0/21366	0.53	0/28966

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

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	9	0
3	a	3477	0	3399	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	622	0	639	0	0
8	f	452	0	240	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	432	0	428	0	0
All	All	20946	0	21300	13	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 13 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:HA2	2:L:85:ILE:HG22	1.85	0.59
2:L:85:ILE:N	2:L:86:PRO:CD	2.68	0.56
2:L:85:ILE:N	2:L:86:PRO:HD2	2.21	0.55
2:L:112:MET:O	2:L:113:PHE:C	2.48	0.52
1:H:88:ASN:N	1:H:119:TYR:HH	2.15	0.45

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	H	102/247 (41%)	98 (96%)	4 (4%)	0	100	100
2	L	108/119 (91%)	101 (94%)	5 (5%)	2 (2%)	9	46
3	a	435/838 (52%)	424 (98%)	11 (2%)	0	100	100
4	b	201/205 (98%)	199 (99%)	2 (1%)	0	100	100
5	c	39/463 (8%)	39 (100%)	0	0	100	100
6	d	348/351 (99%)	330 (95%)	17 (5%)	1 (0%)	43	80
7	e	76/81 (94%)	74 (97%)	2 (3%)	0	100	100
8	f	80/98 (82%)	77 (96%)	3 (4%)	0	100	100
9	g	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
9	h	148/155 (96%)	145 (98%)	2 (1%)	1 (1%)	24	66
9	i	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
9	j	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
9	k	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
9	l	148/155 (96%)	146 (99%)	2 (1%)	0	100	100
9	m	148/155 (96%)	146 (99%)	2 (1%)	0	100	100
9	n	148/155 (96%)	144 (97%)	3 (2%)	1 (1%)	24	66
9	o	148/155 (96%)	143 (97%)	4 (3%)	1 (1%)	24	66
10	p	50/350 (14%)	47 (94%)	2 (4%)	1 (2%)	8	45
All	All	2771/4147 (67%)	2693 (97%)	71 (3%)	7 (0%)	47	80

5 of 7 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
3	a	355/743 (48%)	355 (100%)	0	100	100
4	b	156/158 (99%)	154 (99%)	2 (1%)	71	86
5	c	36/395 (9%)	35 (97%)	1 (3%)	47	71
6	d	305/306 (100%)	304 (100%)	1 (0%)	93	95
7	e	64/68 (94%)	64 (100%)	0	100	100
8	f	8/83 (10%)	8 (100%)	0	100	100
9	g	109/113 (96%)	106 (97%)	3 (3%)	47	71
9	h	109/113 (96%)	108 (99%)	1 (1%)	81	90
9	i	109/113 (96%)	103 (94%)	6 (6%)	24	57
9	j	109/113 (96%)	105 (96%)	4 (4%)	37	66
9	k	109/113 (96%)	108 (99%)	1 (1%)	81	90
9	l	109/113 (96%)	108 (99%)	1 (1%)	81	90
9	m	109/113 (96%)	109 (100%)	0	100	100
9	n	109/113 (96%)	108 (99%)	1 (1%)	81	90
9	o	109/113 (96%)	107 (98%)	2 (2%)	62	82
10	p	47/313 (15%)	47 (100%)	0	100	100
All	All	2130/3395 (63%)	2107 (99%)	23 (1%)	77	87

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	i	139	GLU
9	i	141	LEU
9	o	139	GLU
9	i	140	VAL
9	i	143	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	137	ASN

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Mol	Chain	Res	Type
3	a	548	HIS
3	a	762	HIS
6	d	297	HIS
9	m	78	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 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.