



Full wwPDB EM Model Validation Report ⓘ

Mar 9, 2020 – 10:22 AM EDT

PDB ID : 6VQ6
EMDB ID : EMD-21317
Title : Mammalian V-ATPase from rat brain - composite model of rotational state 1
bound to ADP and SidK (built from focused refinement models)
Authors : Abbas, Y.M.; Rubinstein, J.L.
Deposited on : 2020-02-04
Resolution : 3.90 Å(reported)

This is a Full wwPDB EM Model Validation 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:

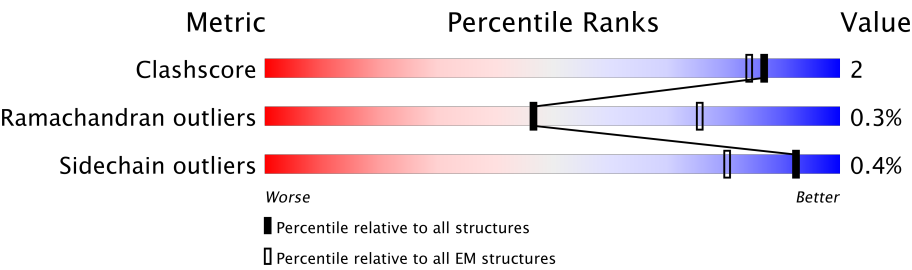
MolProbity : 4.02b-467
Mogul : 1.8.0 (224370), CSD as540be (2019)
buster-report : 1.1.7 (2018)
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (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 3.90 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.



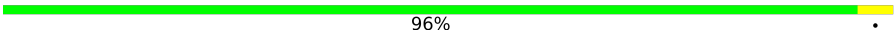
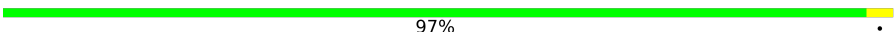

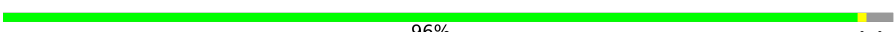








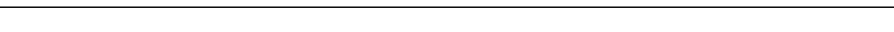

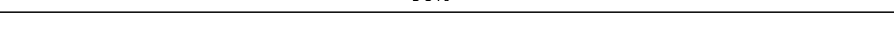

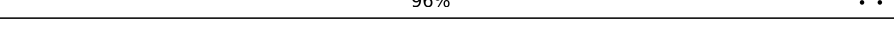
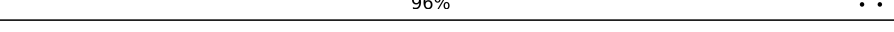
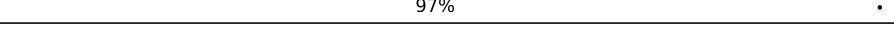
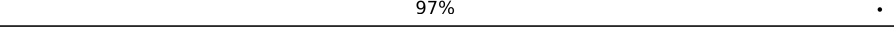
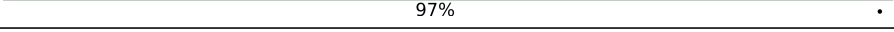
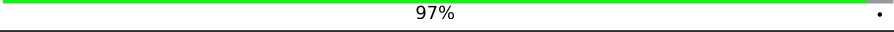
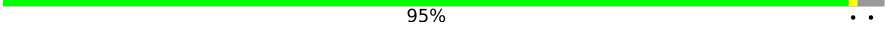
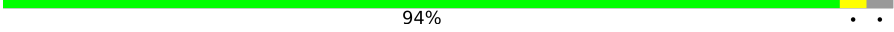
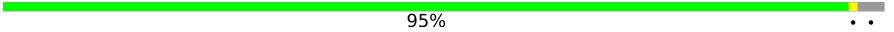
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

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	A	617	96% ..
1	B	617	95% ..
1	C	617	94% ..
2	D	511	86% . 10%
2	E	511	88% . 10%
2	F	511	85% . 10%
3	G	382	89% 5% 6%
4	H	247	76% 9% . 13%
5	I	226	92% 7%

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Mol	Chain	Length	Quality of chain
5	J	226	 96% .
5	K	226	 97% .
6	L	119	 82% 8% . 8%
7	M	118	 96% . .
7	N	118	 93% . .
7	O	118	 96% . .
8	Q	301	 71% . 26%
8	R	301	 68% . 30%
8	S	301	 76% . 23%
9	a	838	 89% 11%
10	b	205	 98% . .
11	c	463	 9% 91%
12	d	351	 99% .
13	e	81	 96% .
14	f	98	 86% 14%
15	g	155	 96% . .
15	h	155	 96% . .
15	i	155	 97% .
15	j	155	 97% .
15	k	155	 97% .
15	l	155	 97% .
15	m	155	 95% . .
15	n	155	 94% . .
15	o	155	 95% . .
16	p	350	 15% 85%

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 62385 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 A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	600	Total	C	N	O	S	0	0
			4651	2949	786	889	27		
1	B	600	Total	C	N	O	S	0	0
			4651	2949	786	889	27		
1	C	600	Total	C	N	O	S	0	0
			4651	2949	786	889	27		

- Molecule 2 is a protein called V-type proton ATPase subunit B, brain isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	459	Total	C	N	O	S	0	0
			3595	2282	613	680	20		
2	E	459	Total	C	N	O	S	0	0
			3595	2282	613	680	20		
2	F	459	Total	C	N	O	S	0	0
			3595	2282	613	680	20		

- Molecule 3 is a protein called V-type proton ATPase subunit C 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	G	360	Total	C	N	O	0	0
			1790	1070	360	360		

- Molecule 4 is a protein called ATPase H⁺-transporting V1 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	214	Total	C	N	O	S	0	0
			1726	1095	311	315	5		

- Molecule 5 is a protein called V-type proton ATPase subunit E 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	225	Total	C	N	O	S	0	0
			1603	1003	295	298	7		
5	J	225	Total	C	N	O	S	0	0
			1607	1005	296	299	7		
5	K	225	Total	C	N	O	S	0	0
			1607	1005	296	299	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	110	Total	C	N	O	S	0	0
			872	551	157	163	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	114	Total	C	N	O	S	0	0
			714	426	147	138	3		
7	N	114	Total	C	N	O	S	0	0
			714	426	147	138	3		
7	O	114	Total	C	N	O	S	0	0
			714	426	147	138	3		

- Molecule 8 is a protein called Effector protein SidK.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Q	224	Total	C	N	O	S	0	0
			1824	1162	306	346	10		
8	R	212	Total	C	N	O	S	0	0
			1722	1096	292	325	9		
8	S	232	Total	C	N	O	S	0	0
			1878	1197	316	354	11		

There are 69 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	0	GLY	-	expression tag	UNP Q5ZWW6
Q	279	ASP	-	expression tag	UNP Q5ZWW6
Q	280	TYR	-	expression tag	UNP Q5ZWW6
Q	281	LYS	-	expression tag	UNP Q5ZWW6
Q	282	ASP	-	expression tag	UNP Q5ZWW6
Q	283	HIS	-	expression tag	UNP Q5ZWW6
Q	284	ASP	-	expression tag	UNP Q5ZWW6

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	285	GLY	-	expression tag	UNP Q5ZWW6
Q	286	ASP	-	expression tag	UNP Q5ZWW6
Q	287	TYR	-	expression tag	UNP Q5ZWW6
Q	288	LYS	-	expression tag	UNP Q5ZWW6
Q	289	ASP	-	expression tag	UNP Q5ZWW6
Q	290	HIS	-	expression tag	UNP Q5ZWW6
Q	291	ASP	-	expression tag	UNP Q5ZWW6
Q	292	ILE	-	expression tag	UNP Q5ZWW6
Q	293	ASP	-	expression tag	UNP Q5ZWW6
Q	294	TYR	-	expression tag	UNP Q5ZWW6
Q	295	LYS	-	expression tag	UNP Q5ZWW6
Q	296	ASP	-	expression tag	UNP Q5ZWW6
Q	297	ASP	-	expression tag	UNP Q5ZWW6
Q	298	ASP	-	expression tag	UNP Q5ZWW6
Q	299	ASP	-	expression tag	UNP Q5ZWW6
Q	300	LYS	-	expression tag	UNP Q5ZWW6
R	0	GLY	-	expression tag	UNP Q5ZWW6
R	279	ASP	-	expression tag	UNP Q5ZWW6
R	280	TYR	-	expression tag	UNP Q5ZWW6
R	281	LYS	-	expression tag	UNP Q5ZWW6
R	282	ASP	-	expression tag	UNP Q5ZWW6
R	283	HIS	-	expression tag	UNP Q5ZWW6
R	284	ASP	-	expression tag	UNP Q5ZWW6
R	285	GLY	-	expression tag	UNP Q5ZWW6
R	286	ASP	-	expression tag	UNP Q5ZWW6
R	287	TYR	-	expression tag	UNP Q5ZWW6
R	288	LYS	-	expression tag	UNP Q5ZWW6
R	289	ASP	-	expression tag	UNP Q5ZWW6
R	290	HIS	-	expression tag	UNP Q5ZWW6
R	291	ASP	-	expression tag	UNP Q5ZWW6
R	292	ILE	-	expression tag	UNP Q5ZWW6
R	293	ASP	-	expression tag	UNP Q5ZWW6
R	294	TYR	-	expression tag	UNP Q5ZWW6
R	295	LYS	-	expression tag	UNP Q5ZWW6
R	296	ASP	-	expression tag	UNP Q5ZWW6
R	297	ASP	-	expression tag	UNP Q5ZWW6
R	298	ASP	-	expression tag	UNP Q5ZWW6
R	299	ASP	-	expression tag	UNP Q5ZWW6
R	300	LYS	-	expression tag	UNP Q5ZWW6
S	0	GLY	-	expression tag	UNP Q5ZWW6
S	279	ASP	-	expression tag	UNP Q5ZWW6
S	280	TYR	-	expression tag	UNP Q5ZWW6

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Chain	Residue	Modelled	Actual	Comment	Reference
S	281	LYS	-	expression tag	UNP Q5ZWW6
S	282	ASP	-	expression tag	UNP Q5ZWW6
S	283	HIS	-	expression tag	UNP Q5ZWW6
S	284	ASP	-	expression tag	UNP Q5ZWW6
S	285	GLY	-	expression tag	UNP Q5ZWW6
S	286	ASP	-	expression tag	UNP Q5ZWW6
S	287	TYR	-	expression tag	UNP Q5ZWW6
S	288	LYS	-	expression tag	UNP Q5ZWW6
S	289	ASP	-	expression tag	UNP Q5ZWW6
S	290	HIS	-	expression tag	UNP Q5ZWW6
S	291	ASP	-	expression tag	UNP Q5ZWW6
S	292	ILE	-	expression tag	UNP Q5ZWW6
S	293	ASP	-	expression tag	UNP Q5ZWW6
S	294	TYR	-	expression tag	UNP Q5ZWW6
S	295	LYS	-	expression tag	UNP Q5ZWW6
S	296	ASP	-	expression tag	UNP Q5ZWW6
S	297	ASP	-	expression tag	UNP Q5ZWW6
S	298	ASP	-	expression tag	UNP Q5ZWW6
S	299	ASP	-	expression tag	UNP Q5ZWW6
S	300	LYS	-	expression tag	UNP Q5ZWW6

- Molecule 9 is a protein called V-type proton ATPase 116 kDa subunit a isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	750	Total	C	N	O	S	0	0
			5030	3254	865	888	23		

- Molecule 10 is a protein called ATPase, H⁺ transporting, V0 subunit B (Predicted), isoform CRA_a.

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

- Molecule 11 is a protein called V-type proton ATPase subunit S1.

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

- Molecule 12 is a protein called V-type proton ATPase subunit.

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

- Molecule 13 is a protein called V-type proton ATPase subunit e 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	e	78	Total	C	N	O	S	0	0
			621	428	98	92	3		

- Molecule 14 is a protein called Ribonuclease K.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	f	84	Total	C	N	O	0	0
			480	309	85	86		

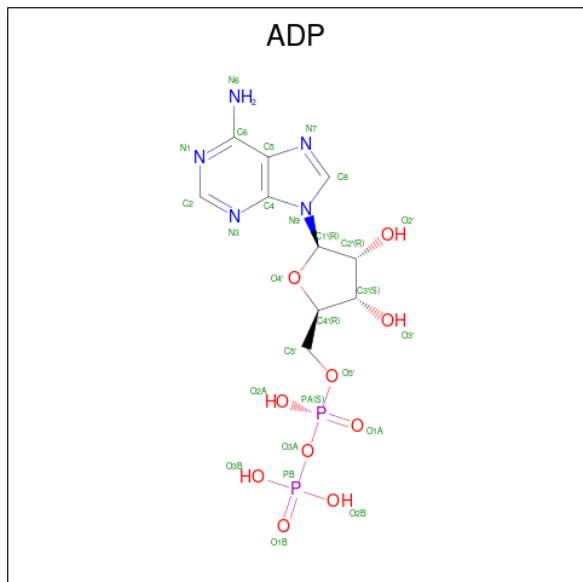
- Molecule 15 is a protein called V-type proton ATPase 16 kDa proteolipid subunit.

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

- Molecule 16 is a protein called Renin receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	52	Total	C	N	O	S	0	0
			432	290	63	76	3		

- Molecule 17 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					AltConf
17	C	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 18 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

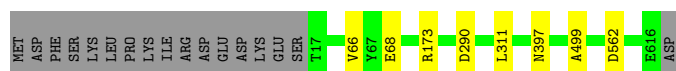
Mol	Chain	Residues	Atoms		AltConf
18	C	1	Total	Mg	0
			1	1	

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: ATPase H⁺-transporting V1 subunit A

Chain A:  96%



- Molecule 1: ATPase H⁺-transporting V1 subunit A

Chain B:  95%



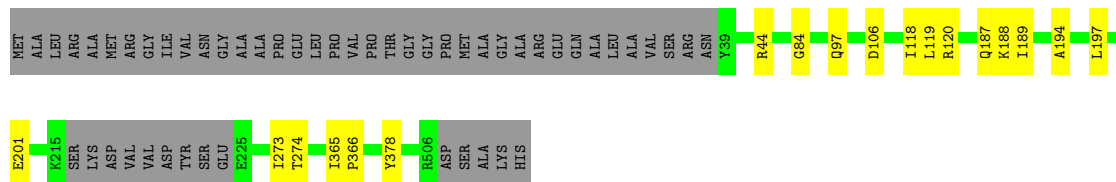
- Molecule 1: ATPase H⁺-transporting V1 subunit A

Chain C:  94%




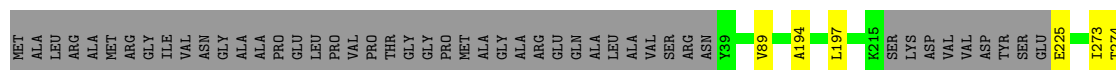
- Molecule 2: V-type proton ATPase subunit B, brain isoform

Chain D:  86% 10%



- Molecule 2: V-type proton ATPase subunit B, brain isoform

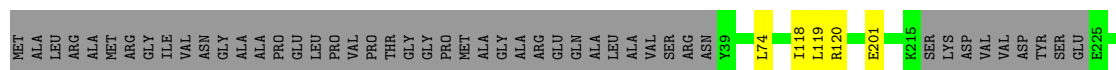
Chain E:  88% 10%





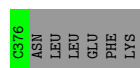
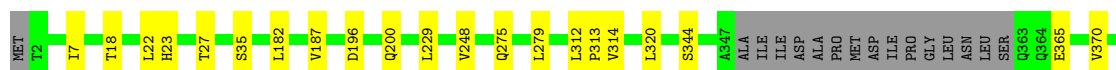
- Molecule 2: V-type proton ATPase subunit B, brain isoform

Chain F: 85% 10%



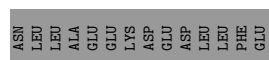
- Molecule 3: V-type proton ATPase subunit C 1

Chain G: 89% 5% 6%



- Molecule 4: ATPase H⁺-transporting V1 subunit D

Chain H: 76% 9% 13%



- Molecule 5: V-type proton ATPase subunit E 1

Chain I: 92% 7%



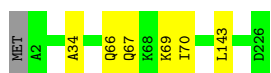
- Molecule 5: V-type proton ATPase subunit E 1

Chain J: 96% 1%



- Molecule 5: V-type proton ATPase subunit E 1

Chain K: 97% 1%



- Molecule 6: V-type proton ATPase subunit F

Chain L: 82% 8% 8%



- Molecule 7: V-type proton ATPase subunit G

Chain M: 96%



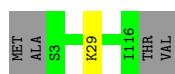
- Molecule 7: V-type proton ATPase subunit G

Chain N: 93%



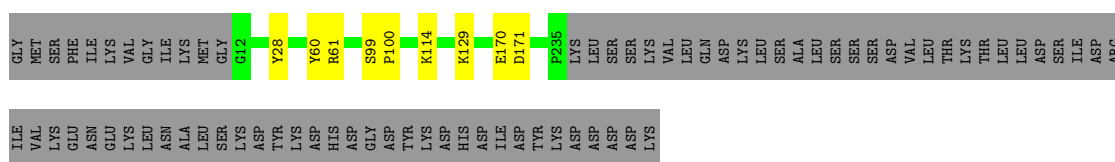
- Molecule 7: V-type proton ATPase subunit G

Chain O: 96%



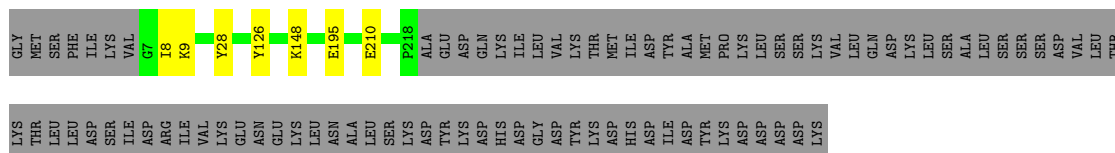
- Molecule 8: Effector protein SidK

Chain Q: 71% 26%



- Molecule 8: Effector protein SidK

Chain R: 68% 30%



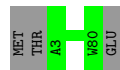
- Molecule 12: V-type proton ATPase subunit

Chain d:  99%




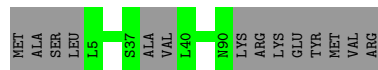
- Molecule 13: V-type proton ATPase subunit e 2

Chain e:  96%



- Molecule 14: Ribonuclease K

Chain f:  86%



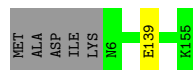
- Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain g:  96%



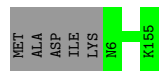
- Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain h:  96%



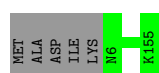
- Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain i:  97%



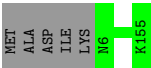
- Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain j:  97%



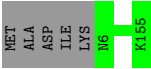
- Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain k:  97% .



- Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain l:  97% .



- Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain m:  95% ..



- Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain n:  94% ..



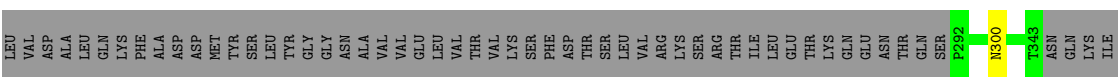
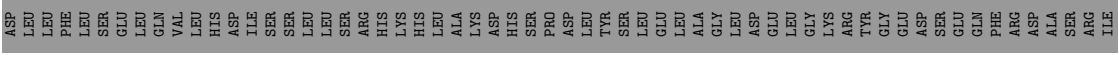
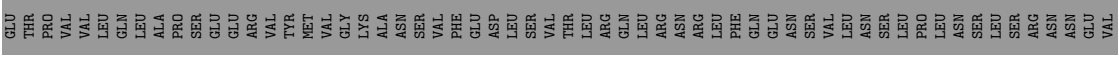
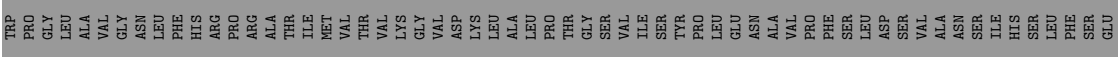
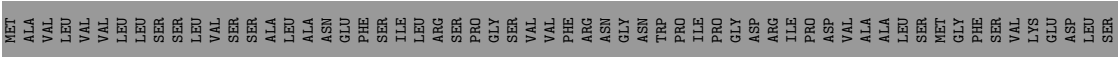
- Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain o:  95% ..



- Molecule 16: Renin receptor

Chain p:  15% 85%



ARG
MET
ASP

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	90648	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](#)

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

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	0.73	1/4746 (0.0%)	0.56	0/6425
1	B	0.72	0/4746	0.53	0/6425
1	C	0.71	0/4746	0.53	0/6425
2	D	0.68	0/3666	0.52	0/4967
2	E	0.70	0/3666	0.53	0/4967
2	F	0.70	0/3666	0.52	0/4967
3	G	0.31	0/1788	0.56	0/2494
4	H	0.81	0/1744	0.58	0/2332
5	I	0.57	0/1615	0.49	0/2187
5	J	0.57	0/1619	0.49	0/2192
5	K	0.57	0/1619	0.49	0/2192
6	L	0.80	0/886	0.74	0/1196
7	M	0.56	0/717	0.52	0/980
7	N	0.51	0/717	0.50	0/980
7	O	0.50	0/717	0.51	0/980
8	Q	0.69	0/1858	0.50	0/2505
8	R	0.69	0/1754	0.49	0/2362
8	S	0.70	0/1912	0.51	0/2575
9	a	0.48	0/5138	0.53	0/7031
10	b	0.50	0/1537	0.49	0/2088
11	c	0.48	0/347	0.54	0/466
12	d	0.73	0/2899	0.53	0/3927
13	e	0.47	0/645	0.44	0/887
14	f	0.41	0/490	0.50	0/676
15	g	0.50	0/1083	0.56	0/1466
15	h	0.47	0/1083	0.52	0/1466
15	i	0.49	0/1083	0.52	0/1466
15	j	0.47	0/1083	0.49	0/1466
15	k	0.49	0/1083	0.53	0/1466
15	l	0.48	0/1083	0.51	0/1466
15	m	0.48	0/1083	0.55	0/1466
15	n	0.47	0/1083	0.51	0/1466

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
15	o	0.49	0/1083	0.51	0/1466
16	p	0.49	0/445	0.60	0/609
All	All	0.63	1/63430 (0.0%)	0.53	0/86029

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	290	ASP	C-N	-5.24	1.22	1.34

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	A	4651	0	4643	5	0
1	B	4651	0	4644	10	0
1	C	4651	0	4643	20	0
2	D	3595	0	3602	10	0
2	E	3595	0	3602	8	0
2	F	3595	0	3602	21	0
3	G	1790	0	794	9	0
4	H	1726	0	1835	24	0
5	I	1603	0	1510	17	0
5	J	1607	0	1516	6	0
5	K	1607	0	1516	7	0
6	L	872	0	876	11	0
7	M	714	0	551	7	0
7	N	714	0	551	2	0
7	O	714	0	551	1	0
8	Q	1824	0	1835	5	0
8	R	1722	0	1733	7	0
8	S	1878	0	1898	2	0
9	a	5030	0	4097	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	b	1503	0	1551	0	0
11	c	337	0	338	0	0
12	d	2833	0	2770	0	0
13	e	621	0	639	0	0
14	f	480	0	288	0	0
15	g	1068	0	1136	0	0
15	h	1068	0	1136	0	0
15	i	1068	0	1136	0	0
15	j	1068	0	1136	0	0
15	k	1068	0	1136	0	0
15	l	1068	0	1136	0	0
15	m	1068	0	1136	0	0
15	n	1068	0	1136	0	0
15	o	1068	0	1136	0	0
16	p	432	0	428	0	0
17	C	27	0	12	1	0
18	C	1	0	0	0	0
All	All	62385	0	60249	138	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 2.

All (138) 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)
5:I:68:LYS:CE	7:M:62:ALA:HB1	1.78	1.12
5:I:68:LYS:HE2	7:M:62:ALA:HB1	1.48	0.96
1:C:525:TYR:CE2	2:F:403:LYS:HD2	2.00	0.95
4:H:109:PHE:HE1	4:H:153:THR:HG1	0.93	0.90
2:F:374:GLU:HA	2:F:400:ARG:HD2	1.57	0.86
5:I:68:LYS:CE	7:M:62:ALA:CB	2.56	0.84
1:C:525:TYR:CE2	2:F:403:LYS:CD	2.62	0.83
5:I:68:LYS:HE3	7:M:62:ALA:HB1	1.61	0.83
1:C:525:TYR:CD2	2:F:403:LYS:HD2	2.16	0.79
1:C:525:TYR:CE2	2:F:403:LYS:HE3	2.22	0.75
5:K:67:GLN:HA	5:K:70:ILE:HG22	1.68	0.74
7:N:66:GLN:O	7:N:70:SER:N	2.21	0.74
4:H:106:LEU:HD11	4:H:158:LEU:HD21	1.70	0.72
4:H:109:PHE:HE1	4:H:153:THR:OG1	1.70	0.71
1:B:94:ILE:N	1:B:94:ILE:HD12	3.98	0.71
5:I:143:LEU:HD12	5:I:143:LEU:O	5.86	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:525:TYR:CE2	2:F:403:LYS:CE	2.77	0.68
1:A:499:ALA:HB1	4:H:103:GLY:HA2	1.77	0.67
5:I:61:GLU:O	5:I:65:GLU:N	2.29	0.66
4:H:106:LEU:HD22	4:H:157:THR:OG1	1.97	0.65
5:I:68:LYS:HZ1	7:M:62:ALA:HB2	1.60	0.65
1:A:499:ALA:CB	4:H:103:GLY:HA2	2.26	0.65
1:C:525:TYR:CZ	2:F:403:LYS:CD	2.80	0.64
5:J:59:LYS:O	5:J:63:GLN:N	2.23	0.64
5:I:68:LYS:NZ	7:M:62:ALA:CB	2.62	0.61
1:B:94:ILE:H	1:B:94:ILE:HD12	4.35	0.61
4:H:159:ASP:HB3	6:L:108:ARG:HH11	1.66	0.60
1:C:525:TYR:CZ	2:F:403:LYS:HE3	2.38	0.58
6:L:85:ILE:N	6:L:86:PRO:CD	2.67	0.58
1:C:397:ASN:N	1:C:398:PRO:CD	2.67	0.58
4:H:51:ILE:HD11	4:H:152:GLN:HG2	1.85	0.58
1:B:397:ASN:N	1:B:398:PRO:CD	2.68	0.57
4:H:149:ALA:O	4:H:153:THR:N	2.28	0.57
4:H:150:SER:O	4:H:154:SER:HB2	2.04	0.57
2:F:298:THR:O	2:F:299:ASP:C	2.44	0.56
3:G:196:ASP:O	3:G:200:GLN:N	2.34	0.56
3:G:275:GLN:O	3:G:279:LEU:N	2.39	0.56
3:G:23:HIS:O	3:G:27:THR:N	2.37	0.55
5:I:135:ARG:NE	5:I:171:ALA:O	2.39	0.55
3:G:35:SER:HA	3:G:320:LEU:O	2.06	0.55
2:E:360:ASP:OD2	4:H:20:LYS:NZ	2.41	0.54
5:K:67:GLN:CA	5:K:70:ILE:HG22	2.38	0.54
6:L:85:ILE:N	6:L:86:PRO:HD2	2.23	0.54
4:H:48:LEU:O	4:H:51:ILE:HG22	2.08	0.54
1:C:436:ASP:OD2	4:H:4:LYS:NZ	2.41	0.54
3:G:7:ILE:HA	3:G:370:VAL:O	2.07	0.54
5:K:67:GLN:HA	5:K:70:ILE:CG2	2.37	0.53
4:H:68:SER:OG	4:H:137:ASN:ND2	2.41	0.53
5:J:129:GLU:H	5:J:132:MET:CE	2.22	0.53
2:D:189:ILE:O	2:D:189:ILE:HG23	2.09	0.52
5:K:143:LEU:HD12	5:K:143:LEU:O	5.78	0.52
4:H:55:LYS:NZ	6:L:99:ASP:OD2	2.32	0.52
8:Q:114:LYS:NZ	8:Q:170:GLU:OE2	2.43	0.52
1:B:299:ASP:O	8:R:148:LYS:NZ	2.42	0.52
3:G:18:THR:O	3:G:22:LEU:N	2.43	0.51
5:K:66:GLN:HA	5:K:69:LYS:HE3	1.91	0.51
2:F:266:ASP:OD1	8:R:9:LYS:NZ	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:64:ILE:O	5:I:67:GLN:HB3	2.11	0.51
4:H:151:LEU:O	4:H:155:PHE:HB2	2.11	0.50
8:Q:99:SER:N	8:Q:100:PRO:HD2	2.27	0.50
6:L:61:ILE:HG22	6:L:62:GLY:N	2.28	0.49
2:D:118:ILE:O	2:D:120:ARG:N	2.46	0.49
4:H:43:ARG:O	4:H:47:ILE:HG12	2.12	0.49
5:I:68:LYS:HE2	7:M:62:ALA:CB	2.31	0.49
1:A:66:VAL:HG12	1:A:68:GLU:H	1.78	0.48
1:B:94:ILE:CD1	1:B:94:ILE:N	4.33	0.48
5:J:119:LEU:O	5:J:194:ASN:ND2	2.46	0.48
1:B:436:ASP:OD1	1:B:437:LYS:N	2.46	0.48
1:C:449:ASN:O	1:C:450:TRP:CG	2.67	0.48
5:K:66:GLN:O	5:K:69:LYS:HG2	2.14	0.48
4:H:210:LYS:NZ	4:H:214:GLU:OE2	2.46	0.47
4:H:148:LEU:HG	6:L:89:LEU:HD22	1.95	0.47
5:I:137:ARG:NH1	5:I:177:ILE:O	2.47	0.47
7:N:71:ALA:O	7:N:75:GLN:N	2.36	0.47
5:J:63:GLN:O	5:J:67:GLN:HG2	2.15	0.47
1:B:100:ASP:OD1	1:B:101:GLY:N	2.46	0.47
4:H:51:ILE:HA	4:H:151:LEU:HD13	1.97	0.47
5:K:34:ALA:HB1	7:O:29:LYS:HA	1.97	0.47
5:J:137:ARG:NH1	5:J:177:ILE:O	2.48	0.46
8:Q:60:TYR:O	8:Q:61:ARG:HB2	2.16	0.46
1:B:94:ILE:CD1	1:B:94:ILE:H	4.55	0.45
1:C:391:ARG:NH1	1:C:401:GLU:OE2	2.49	0.45
1:C:525:TYR:CZ	2:F:403:LYS:HD3	2.51	0.45
2:F:365:ILE:HB	2:F:366:PRO:CD	2.47	0.45
1:C:280:ARG:NH1	2:F:372:ILE:O	2.49	0.45
5:I:64:ILE:HA	5:I:67:GLN:HB3	1.99	0.45
5:I:129:GLU:H	5:I:132:MET:HE2	1.81	0.45
2:E:395:LEU:N	2:E:396:PRO:HD2	2.32	0.44
3:G:312:LEU:HA	3:G:313:PRO:C	2.37	0.44
1:C:100:ASP:OD1	1:C:100:ASP:C	2.55	0.44
4:H:154:SER:O	4:H:158:LEU:HG	2.17	0.44
2:D:106:ASP:C	2:D:106:ASP:OD1	2.56	0.44
1:B:397:ASN:N	1:B:398:PRO:HD3	2.33	0.44
1:C:525:TYR:CZ	2:F:403:LYS:CE	3.00	0.44
8:Q:129:LYS:NZ	8:Q:171:ASP:OD1	2.49	0.44
1:C:397:ASN:HB3	8:S:28:TYR:CG	2.53	0.43
1:C:525:TYR:OH	2:F:403:LYS:HE3	2.18	0.43
6:L:112:MET:O	6:L:113:PHE:C	2.55	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:89:VAL:O	2:E:89:VAL:HG23	2.18	0.43
2:D:365:ILE:HB	2:D:366:PRO:CD	2.49	0.43
2:D:187:GLN:CG	2:D:188:LYS:N	2.82	0.43
1:C:163:LYS:NZ	8:S:138:ASP:OD2	2.50	0.43
1:A:562:ASP:OD1	1:A:562:ASP:N	2.52	0.43
5:I:152:ILE:N	5:I:153:PRO:HD2	2.34	0.43
8:R:210:GLU:OE1	8:R:210:GLU:N	2.52	0.43
1:C:255:GLY:HA2	17:C:701:ADP:O5'	2.18	0.43
2:E:505:PRO:O	2:E:506:ARG:HB2	2.19	0.43
5:I:185:ASN:ND2	5:I:187:ASP:OD1	2.53	0.42
2:F:118:ILE:O	2:F:120:ARG:N	2.53	0.42
6:L:58:ARG:HG2	6:L:60:ASP:H	1.84	0.42
3:G:182:LEU:HA	3:G:229:LEU:O	2.19	0.42
2:F:504:TYR:N	2:F:505:PRO:CD	2.83	0.42
4:H:106:LEU:HD11	4:H:158:LEU:CD2	2.45	0.42
2:F:201:GLU:OE1	2:F:201:GLU:N	2.49	0.41
3:G:187:VAL:HA	3:G:248:VAL:HA	2.02	0.41
8:R:195:GLU:N	8:R:195:GLU:OE1	2.50	0.41
1:B:397:ASN:HB2	8:R:28:TYR:CG	2.55	0.41
6:L:85:ILE:HB	6:L:86:PRO:HD3	2.01	0.41
1:A:397:ASN:HB3	8:Q:28:TYR:CG	2.56	0.41
2:D:84:GLY:CA	2:D:97:GLN:O	2.69	0.41
2:E:194:ALA:H	2:E:197:LEU:HD12	1.85	0.41
2:E:225:GLU:N	2:E:225:GLU:OE1	2.54	0.41
2:D:194:ALA:H	2:D:197:LEU:HD22	1.84	0.41
2:E:273:ILE:O	2:E:274:THR:C	2.59	0.41
8:R:8:ILE:O	8:R:9:LYS:C	2.59	0.41
2:D:187:GLN:CG	2:D:188:LYS:H	2.34	0.41
2:D:273:ILE:O	2:D:274:THR:C	2.59	0.41
5:J:129:GLU:H	5:J:132:MET:HE2	1.85	0.41
1:C:233:VAL:O	1:C:234:LEU:HB2	2.21	0.41
2:D:201:GLU:OE1	2:D:201:GLU:N	2.52	0.40
2:F:389:TYR:CD2	2:F:389:TYR:C	2.94	0.40
4:H:156:VAL:HG12	6:L:108:ARG:HG2	2.03	0.40
2:E:395:LEU:HB2	2:E:396:PRO:HD3	2.03	0.40
2:F:287:TYR:O	2:F:344:ARG:NH1	2.52	0.40
8:R:126:TYR:N	8:R:126:TYR:CD1	2.89	0.40
2:F:380:ASP:OD1	2:F:380:ASP:C	2.60	0.40
4:H:159:ASP:HB3	6:L:108:ARG:NH1	2.34	0.40
5:I:143:LEU:HD12	5:I:143:LEU:C	5.01	0.40

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	598/617 (97%)	578 (97%)	20 (3%)	0	100	100
1	B	598/617 (97%)	575 (96%)	22 (4%)	1 (0%)	49	83
1	C	598/617 (97%)	572 (96%)	25 (4%)	1 (0%)	49	83
2	D	455/511 (89%)	442 (97%)	11 (2%)	2 (0%)	36	74
2	E	455/511 (89%)	443 (97%)	12 (3%)	0	100	100
2	F	455/511 (89%)	443 (97%)	9 (2%)	3 (1%)	24	64
3	G	356/382 (93%)	346 (97%)	7 (2%)	3 (1%)	21	62
4	H	212/247 (86%)	203 (96%)	7 (3%)	2 (1%)	19	59
5	I	223/226 (99%)	223 (100%)	0	0	100	100
5	J	223/226 (99%)	221 (99%)	2 (1%)	0	100	100
5	K	223/226 (99%)	223 (100%)	0	0	100	100
6	L	108/119 (91%)	101 (94%)	5 (5%)	2 (2%)	9	46
7	M	112/118 (95%)	109 (97%)	3 (3%)	0	100	100
7	N	112/118 (95%)	111 (99%)	1 (1%)	0	100	100
7	O	112/118 (95%)	111 (99%)	1 (1%)	0	100	100
8	Q	222/301 (74%)	215 (97%)	7 (3%)	0	100	100
8	R	210/301 (70%)	204 (97%)	6 (3%)	0	100	100
8	S	230/301 (76%)	223 (97%)	6 (3%)	1 (0%)	36	74
9	a	744/838 (89%)	722 (97%)	19 (3%)	3 (0%)	36	74
10	b	201/205 (98%)	197 (98%)	4 (2%)	0	100	100
11	c	39/463 (8%)	39 (100%)	0	0	100	100
12	d	348/351 (99%)	328 (94%)	19 (6%)	1 (0%)	43	79
13	e	76/81 (94%)	75 (99%)	1 (1%)	0	100	100
14	f	80/98 (82%)	77 (96%)	3 (4%)	0	100	100
15	g	148/155 (96%)	146 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	h	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
15	i	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
15	j	148/155 (96%)	146 (99%)	2 (1%)	0	100	100
15	k	148/155 (96%)	146 (99%)	2 (1%)	0	100	100
15	l	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
15	m	148/155 (96%)	145 (98%)	2 (1%)	1 (1%)	24	64
15	n	148/155 (96%)	145 (98%)	2 (1%)	1 (1%)	24	64
15	o	148/155 (96%)	143 (97%)	4 (3%)	1 (1%)	24	64
16	p	50/350 (14%)	47 (94%)	2 (4%)	1 (2%)	8	45
All	All	8372/9848 (85%)	8134 (97%)	215 (3%)	23 (0%)	47	79

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	H	154	SER
9	a	245	TYR
9	a	356	GLN
12	d	119	GLN
15	o	10	TYR
2	D	119	LEU
2	F	299	ASP
3	G	365	GLU
6	L	61	ILE
16	p	300	ASN
1	C	350	SER
2	F	119	LEU
3	G	344	SER
6	L	100	ALA
8	S	12	GLY
15	m	10	TYR
15	n	10	TYR
1	B	278	GLY
2	D	378	TYR
2	F	378	TYR
4	H	151	LEU
3	G	314	VAL
9	a	79	ILE

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	507/524 (97%)	505 (100%)	2 (0%)	92	96
1	B	507/524 (97%)	505 (100%)	2 (0%)	92	96
1	C	507/524 (97%)	504 (99%)	3 (1%)	87	94
2	D	393/431 (91%)	392 (100%)	1 (0%)	93	96
2	E	393/431 (91%)	393 (100%)	0	100	100
2	F	393/431 (91%)	390 (99%)	3 (1%)	83	91
4	H	185/212 (87%)	183 (99%)	2 (1%)	76	88
5	I	140/198 (71%)	140 (100%)	0	100	100
5	J	141/198 (71%)	141 (100%)	0	100	100
5	K	141/198 (71%)	141 (100%)	0	100	100
6	L	93/100 (93%)	92 (99%)	1 (1%)	76	88
7	M	43/100 (43%)	43 (100%)	0	100	100
7	N	43/100 (43%)	43 (100%)	0	100	100
7	O	43/100 (43%)	43 (100%)	0	100	100
8	Q	203/274 (74%)	203 (100%)	0	100	100
8	R	191/274 (70%)	191 (100%)	0	100	100
8	S	208/274 (76%)	208 (100%)	0	100	100
9	a	362/743 (49%)	362 (100%)	0	100	100
10	b	156/158 (99%)	154 (99%)	2 (1%)	71	86
11	c	36/395 (9%)	35 (97%)	1 (3%)	47	73
12	d	305/306 (100%)	304 (100%)	1 (0%)	93	96
13	e	64/68 (94%)	64 (100%)	0	100	100
14	f	14/83 (17%)	14 (100%)	0	100	100
15	g	109/113 (96%)	108 (99%)	1 (1%)	81	90
15	h	109/113 (96%)	108 (99%)	1 (1%)	81	90
15	i	109/113 (96%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	j	109/113 (96%)	109 (100%)	0	100	100
15	k	109/113 (96%)	109 (100%)	0	100	100
15	l	109/113 (96%)	109 (100%)	0	100	100
15	m	109/113 (96%)	108 (99%)	1 (1%)	81	90
15	n	109/113 (96%)	106 (97%)	3 (3%)	47	73
15	o	109/113 (96%)	108 (99%)	1 (1%)	81	90
16	p	47/313 (15%)	47 (100%)	0	100	100
All	All	6096/7976 (76%)	6071 (100%)	25 (0%)	92	96

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	173	ARG
1	A	311	LEU
1	B	173	ARG
1	B	296	MET
1	C	173	ARG
1	C	400	ARG
1	C	571	ARG
2	D	44	ARG
2	F	74	LEU
2	F	402	MET
2	F	406	ILE
4	H	153	THR
4	H	155	PHE
6	L	60	ASP
10	b	58	ILE
10	b	70	TYR
11	c	448	ARG
12	d	24	LYS
15	g	141	LEU
15	h	139	GLU
15	m	61	MET
15	n	139	GLU
15	n	141	LEU
15	n	143	LEU
15	o	139	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
2	E	181	ASN
4	H	137	ASN
5	K	67	GLN
12	d	297	HIS
12	d	340	HIS
15	m	123	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
17	ADP	C	701	18	24,29,29	0.68	0	25,45,45	0.72	1 (4%)

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
17	ADP	C	701	18	-	4/12/32/32	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	C	701	ADP	C5-C6-N6	2.09	123.67	120.38

There are no chirality outliers.

All (4) torsion outliers are listed below:

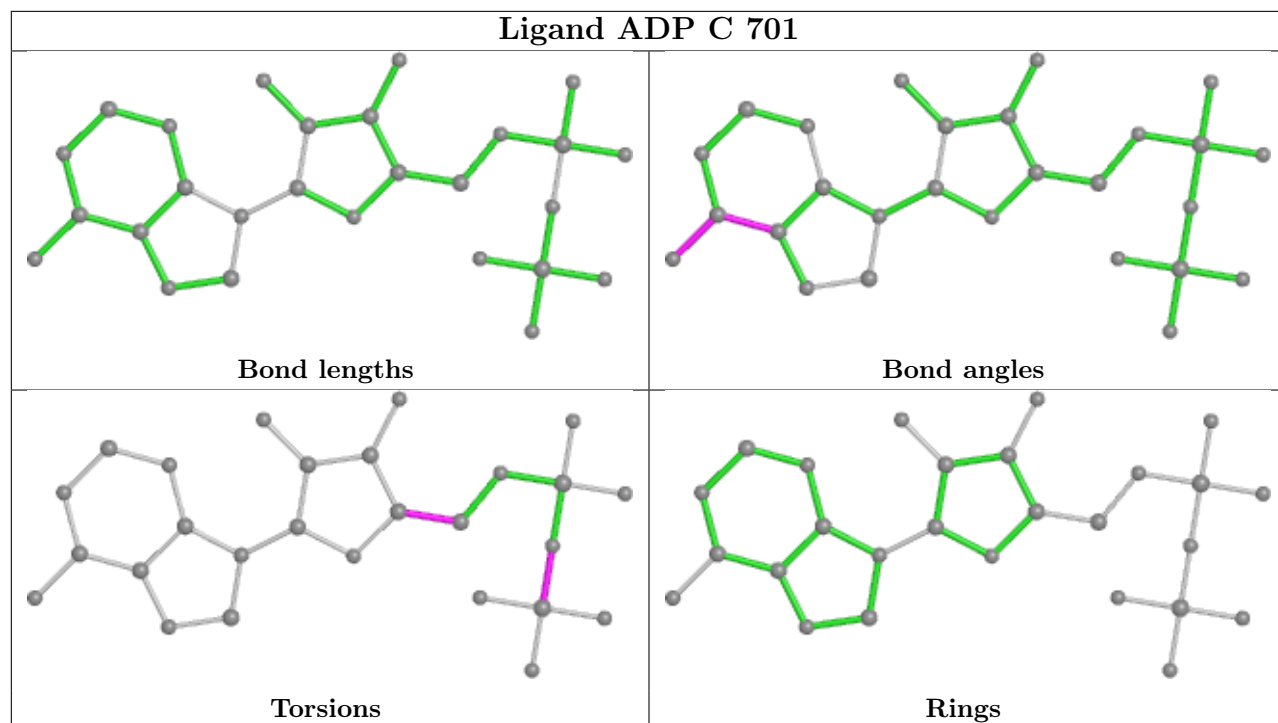
Mol	Chain	Res	Type	Atoms
17	C	701	ADP	O4'-C4'-C5'-O5'
17	C	701	ADP	C3'-C4'-C5'-O5'
17	C	701	ADP	PA-O3A-PB-O1B
17	C	701	ADP	PA-O3A-PB-O2B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	C	701	ADP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.