



Full wwPDB EM Model Validation Report ⓘ

Mar 9, 2020 – 09:38 AM EDT

PDB ID : 6VQC
EMDB ID : EMD-21348
Title : Mammalian V-ATPase from rat brain membrane-embedded Vo region rotational state 1 (from focused refinement)
Authors : Abbas, Y.M.; Rubinstein, J.L.
Deposited on : 2020-02-04
Resolution : 3.80 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:

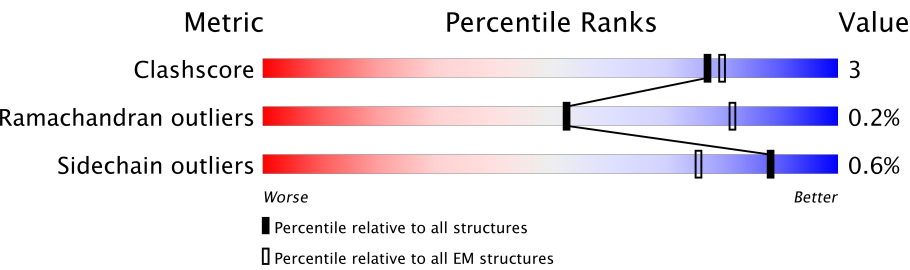
MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.8

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 3.80 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.



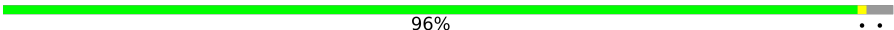
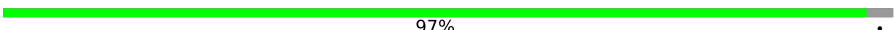
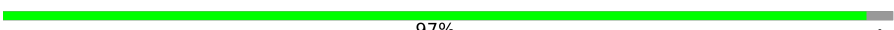
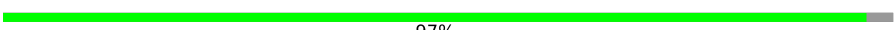
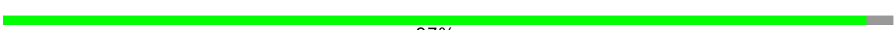




Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

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	40% . 58%
2	L	119	82% 9% . 8%
3	a	838	53% 47%
4	b	205	98% ..
5	c	463	9% 91%
6	d	351	99% .
7	e	81	96% .
8	f	98	86% 14%
9	g	155	96% ..

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Mol	Chain	Length	Quality of chain
9	h	155	 96% ..
9	i	155	 97% .
9	j	155	 97% .
9	k	155	 97% .
9	l	155	 97% .
9	m	155	 96% ..
9	n	155	 94% ..
9	o	155	 95% ..
10	p	350	 15% 85%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 20991 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
			3495	2337	556	579	23		

- 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
			621	428	98	92	3		

- Molecule 8 is a protein called Ribonuclease K.

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

- 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		

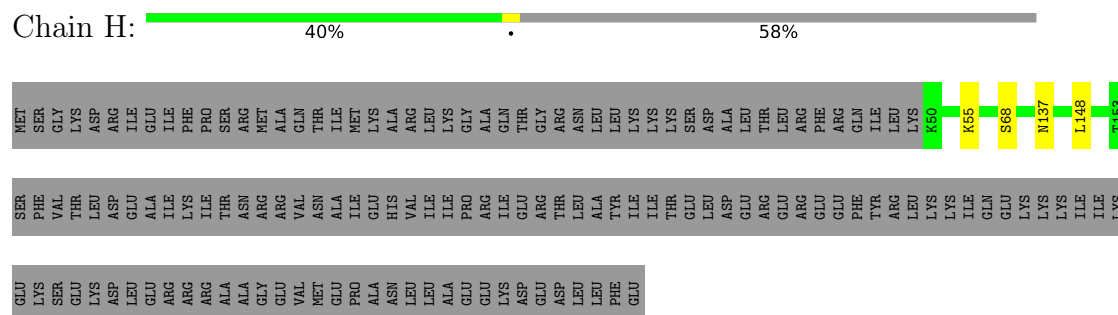
- Molecule 10 is a protein called Renin receptor.

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

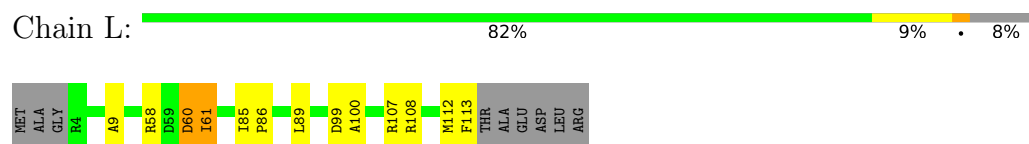
3 Residue-property plots

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.

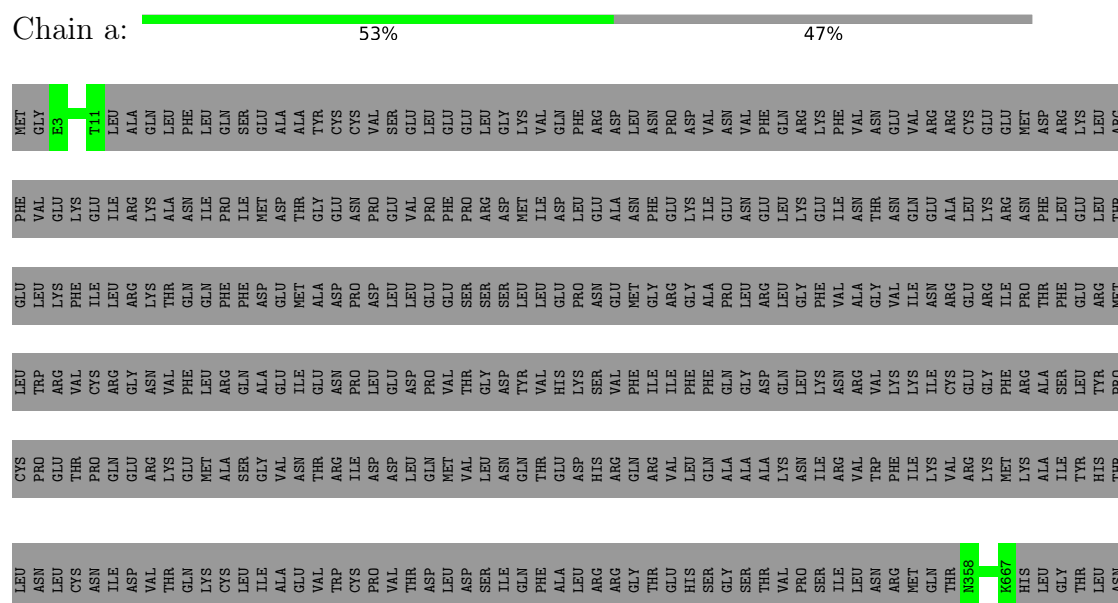
- Molecule 1: ATPase H⁺-transporting V1 subunit D



- Molecule 2: V-type proton ATPase subunit F



- Molecule 3: V-type proton ATPase 116 kDa subunit a isoform 1



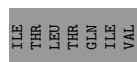
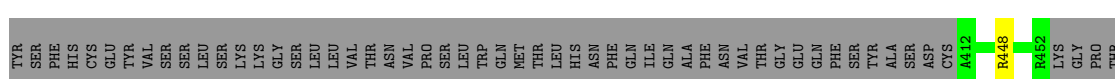
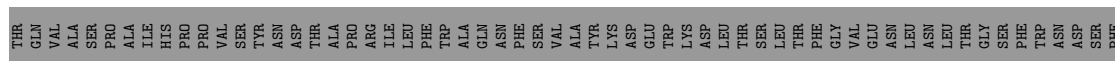
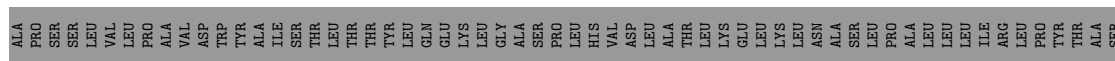
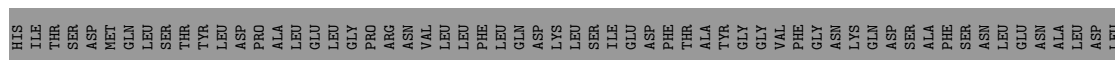
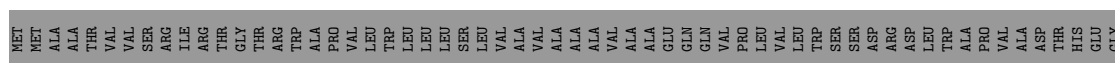
- Molecule 4: ATPase, H⁺ transporting, V0 subunit B (Predicted), isoform CRA a

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%




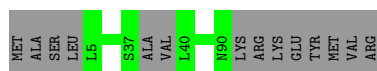
- Molecule 7: V-type proton ATPase subunit e 2

Chain e: 96% .



- Molecule 8: Ribonuclease K

Chain f:  86% 14%



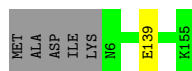
- Molecule 9: V-type proton ATPase 16 kDa proteolipid subunit

Chain g:  96% ..



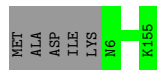
- Molecule 9: V-type proton ATPase 16 kDa proteolipid subunit

Chain h:  96% ..



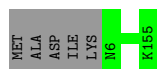
- Molecule 9: V-type proton ATPase 16 kDa proteolipid subunit

Chain i:  97% .



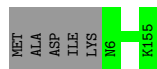
- Molecule 9: V-type proton ATPase 16 kDa proteolipid subunit

Chain j:  97% .



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

Chain k:  97% .



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

Chain l:  97% .



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

Chain m:

96%



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

Chain n:

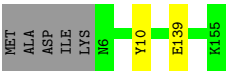
94%



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

Chain o:

95%

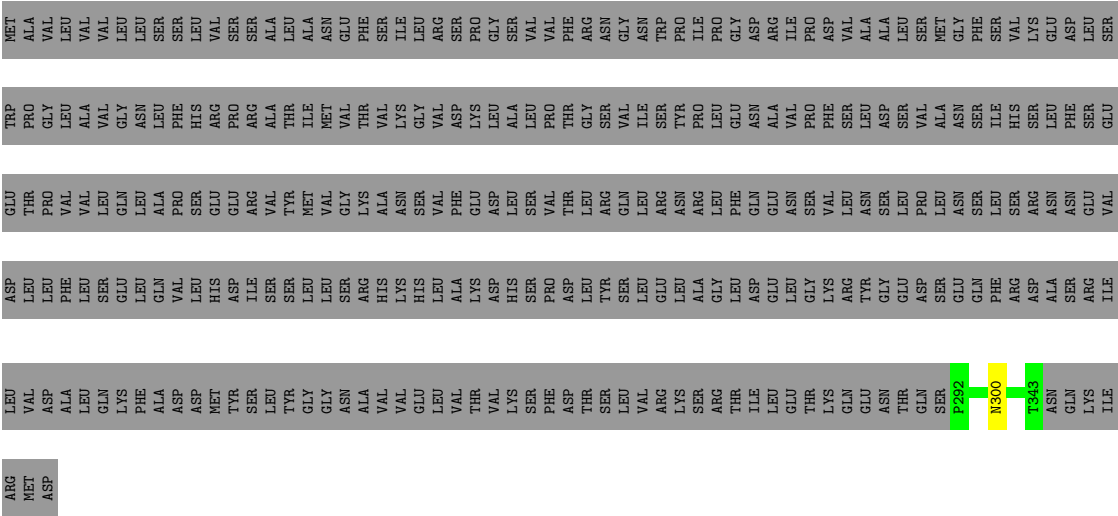


- Molecule 10: Renin receptor

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	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](#)

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	0.64	0/1091
2	L	0.80	0/889	0.74	0/1199
3	a	0.52	0/3603	0.49	0/4888
4	b	0.51	0/1537	0.49	0/2088
5	c	0.48	0/347	0.54	0/466
6	d	0.73	0/2899	0.53	0/3927
7	e	0.47	0/645	0.44	0/887
8	f	0.40	0/490	0.50	0/676
9	g	0.50	0/1083	0.56	0/1466
9	h	0.47	0/1083	0.52	0/1466
9	i	0.49	0/1083	0.52	0/1466
9	j	0.47	0/1083	0.49	0/1466
9	k	0.49	0/1083	0.53	0/1466
9	l	0.48	0/1083	0.51	0/1466
9	m	0.49	0/1083	0.55	0/1466
9	n	0.47	0/1083	0.51	0/1466
9	o	0.49	0/1083	0.51	0/1466
10	p	0.49	0/445	0.60	0/609
All	All	0.56	0/21414	0.53	0/29025

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	4	0
2	L	875	0	883	12	0
3	a	3495	0	3434	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	621	0	639	0	0
8	f	480	0	288	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	20991	0	21383	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 3.

All (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:58:ARG:HG2	2:L:60:ASP:H	1.65	0.61
2:L:85:ILE:N	2:L:86:PRO:CD	2.67	0.58
2:L:85:ILE:N	2:L:86:PRO:HD2	2.23	0.54
1:H:68:SER:OG	1:H:137:ASN:ND2	2.41	0.53
1:H:55:LYS:NZ	2:L:99:ASP:OD2	2.32	0.53
2:L:112:MET:O	2:L:113:PHE:C	2.55	0.43
2:L:60:ASP:OD1	2:L:60:ASP:N	2.52	0.42
1:H:148:LEU:HG	2:L:89:LEU:HD22	2.01	0.42
2:L:9:ALA:CB	2:L:61:ILE:HG21	2.51	0.41
2:L:85:ILE:HB	2:L:86:PRO:HD3	2.01	0.41
1:H:148:LEU:HD23	2:L:89:LEU:HD13	2.02	0.41
2:L:107:ARG:O	2:L:108:ARG:C	2.58	0.40
2:L:9:ALA:HB2	2:L:61:ILE:HG21	2.02	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	H	102/247 (41%)	97 (95%)	5 (5%)	0	100	100
2	L	108/119 (91%)	101 (94%)	5 (5%)	2 (2%)	9	48
3	a	435/838 (52%)	424 (98%)	11 (2%)	0	100	100
4	b	201/205 (98%)	197 (98%)	4 (2%)	0	100	100
5	c	39/463 (8%)	39 (100%)	0	0	100	100
6	d	348/351 (99%)	328 (94%)	19 (6%)	1 (0%)	43	79
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%)	146 (99%)	2 (1%)	0	100	100
9	l	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
9	m	148/155 (96%)	146 (99%)	2 (1%)	0	100	100
9	n	148/155 (96%)	145 (98%)	2 (1%)	1 (1%)	24	65
9	o	148/155 (96%)	143 (97%)	4 (3%)	1 (1%)	24	65
10	p	50/350 (14%)	47 (94%)	2 (4%)	1 (2%)	8	47
All	All	2771/4147 (67%)	2692 (97%)	73 (3%)	6 (0%)	53	83

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	61	ILE
6	d	119	GLN
9	o	10	TYR
10	p	300	ASN

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Mol	Chain	Res	Type
2	L	100	ALA
9	n	10	TYR

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%)	93 (99%)	1 (1%)	76	88
3	a	362/743 (49%)	362 (100%)	0	100	100
4	b	156/158 (99%)	154 (99%)	2 (1%)	71	87
5	c	36/395 (9%)	35 (97%)	1 (3%)	47	74
6	d	305/306 (100%)	304 (100%)	1 (0%)	93	97
7	e	64/68 (94%)	64 (100%)	0	100	100
8	f	14/83 (17%)	14 (100%)	0	100	100
9	g	109/113 (96%)	108 (99%)	1 (1%)	81	91
9	h	109/113 (96%)	108 (99%)	1 (1%)	81	91
9	i	109/113 (96%)	109 (100%)	0	100	100
9	j	109/113 (96%)	109 (100%)	0	100	100
9	k	109/113 (96%)	109 (100%)	0	100	100
9	l	109/113 (96%)	109 (100%)	0	100	100
9	m	109/113 (96%)	108 (99%)	1 (1%)	81	91
9	n	109/113 (96%)	106 (97%)	3 (3%)	47	74
9	o	109/113 (96%)	108 (99%)	1 (1%)	81	91
10	p	47/313 (15%)	47 (100%)	0	100	100
All	All	2143/3395 (63%)	2131 (99%)	12 (1%)	88	94

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	60	ASP
4	b	58	ILE
4	b	70	TYR
5	c	448	ARG
6	d	24	LYS
9	g	141	LEU
9	h	139	GLU
9	m	61	MET
9	n	139	GLU
9	n	141	LEU
9	n	143	LEU
9	o	139	GLU

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
3	a	751	GLN
6	d	297	HIS
6	d	340	HIS
9	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](#)

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.