



## wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Jul 24, 2017 – 05:18 AM EDT

PDB ID : 5ARA  
EMDB ID: : EMD-3164  
Title : Bovine mitochondrial ATP synthase state 1a  
Authors : Zhou, A.; Rohou, A.; Schep, D.G.; Bason, J.V.; Montgomery, M.G.; Walker, J.E.; Grigorieff, N.; Rubinstein, J.L.  
Deposited on : unknown  
Resolution : 6.70 Å(reported)  
Based on PDB ID : 2CLY, 2XND, 2WSS

This is a wwPDB/EMDatabank EM Map/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  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

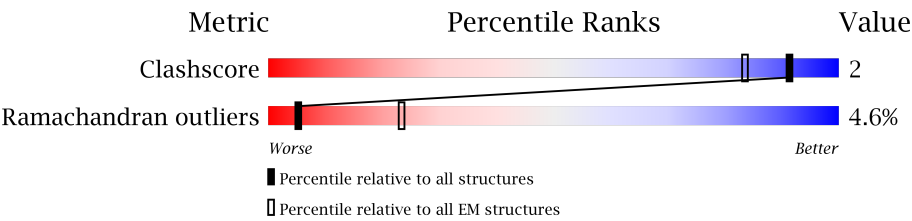
MolProbity : 4.02b-467  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029824

# 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 6.70 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	125131	1336
Ramachandran outliers	121729	1120

The table below summarises the geometric issues observed across the polymeric chains. 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. 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	510	<div><div>90%10%</div></div>
1	B	510	<div><div>85%9%6%</div></div>
1	C	510	<div><div>85%9%5%</div></div>
2	D	482	<div><div>87%9%</div></div>
2	E	482	<div><div>89%8%</div></div>
2	F	482	<div><div>85%11%</div></div>
3	G	273	<div><div>88%7%</div></div>
4	H	146	<div><div>78%12%10%</div></div>
5	I	50	<div><div>82%10%6%</div></div>
6	J	72	<div><div>97%</div></div>
6	K	72	<div><div>99%</div></div>

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
6	L	72	 100%
6	M	72	 97% .
6	N	72	 100%
6	O	72	 99% .
6	P	72	 99% .
6	Q	72	 97% .
7	S	190	 60% 25% . . 12%
8	T	174	 82% 14% .
9	U	124	 79% 15% . .
10	V	77	 74% 10% . 14%
11	W	217	 88% 11%

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 18544 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 ATP SYNTHASE SUBUNIT ALPHA, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	509	Total	C	N	O	0	0
			2035	1018	509	508		
1	B	480	Total	C	N	O	0	0
			1918	960	480	478		
1	C	487	Total	C	N	O	0	0
			1947	974	487	486		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	481	GLY	SER	conflict	UNP P19483
B	481	GLY	SER	conflict	UNP P19483
C	481	GLY	SER	conflict	UNP P19483

- Molecule 2 is a protein called ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	D	467	Total	C	N	O	0	0
			1867	934	467	466		
2	E	466	Total	C	N	O	0	0
			1863	932	466	465		
2	F	466	Total	C	N	O	0	0
			1863	932	466	465		

- Molecule 3 is a protein called ATP SYNTHASE SUBUNIT GAMMA, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	G	264	Total	C	N	O	0	0
			1053	528	264	261		

- Molecule 4 is a protein called ATP SYNTHASE SUBUNIT DELTA, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	H	131	Total	C	N	O	0	0
			523	262	131	130		

- Molecule 5 is a protein called ATP SYNTHASE SUBUNIT EPSILON, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	I	47	Total	C	N	O	0	0
			187	94	47	46		

- Molecule 6 is a protein called ATP SYNTHASE F(0) COMPLEX SUBUNIT C1, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	J	72	Total	C	N	O	0	0
			288	144	72	72		
6	K	72	Total	C	N	O	0	0
			288	144	72	72		
6	L	72	Total	C	N	O	0	0
			288	144	72	72		
6	M	72	Total	C	N	O	0	0
			288	144	72	72		
6	N	72	Total	C	N	O	0	0
			288	144	72	72		
6	O	72	Total	C	N	O	0	0
			288	144	72	72		
6	P	72	Total	C	N	O	0	0
			288	144	72	72		
6	Q	72	Total	C	N	O	0	0
			288	144	72	72		

- Molecule 7 is a protein called ATP SYNTHASE SUBUNIT O, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	S	168	Total	C	N	O	0	1
			669	334	168	167		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	129	THR	ALA	conflict	UNP P13621

- Molecule 8 is a protein called ATP SYNTHASE F(0) COMPLEX SUBUNIT B1, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	T	174	Total	C	N	O	0	0
			697	348	174	175		

- Molecule 9 is a protein called ATP SYNTHASE SUBUNIT D, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	U	122	Total	C	N	O	0	1
			485	242	122	121		

- Molecule 10 is a protein called ATP SYNTHASE-COUPPLING FACTOR 6, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	V	66	Total	C	N	O	0	0
			264	132	66	66		

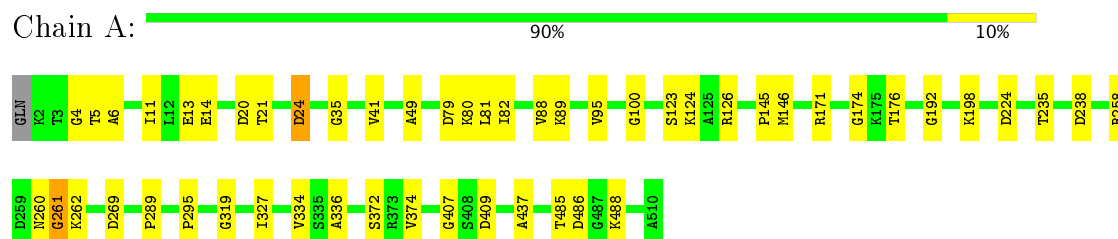
- Molecule 11 is a protein called ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	W	217	Total	C	N	O	0	0
			869	434	217	218		

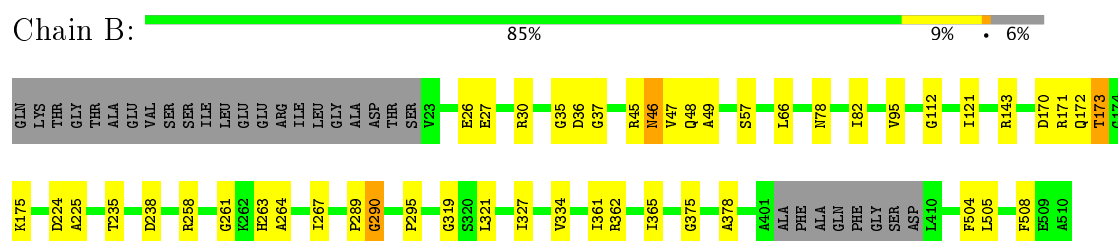
### 3 Residue-property plots

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.

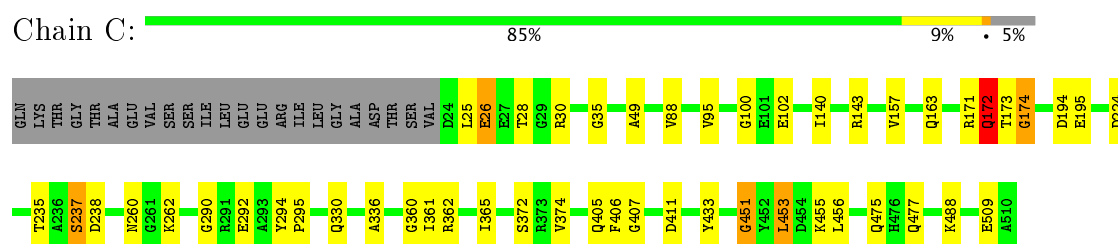
#### • Molecule 1: ATP SYNTHASE SUBUNIT ALPHA, MITOCHONDRIAL



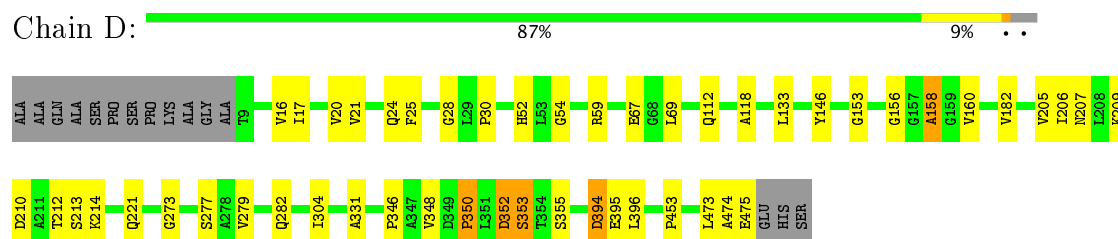
#### • Molecule 1: ATP SYNTHASE SUBUNIT ALPHA, MITOCHONDRIAL




#### • Molecule 1: ATP SYNTHASE SUBUNIT ALPHA, MITOCHONDRIAL

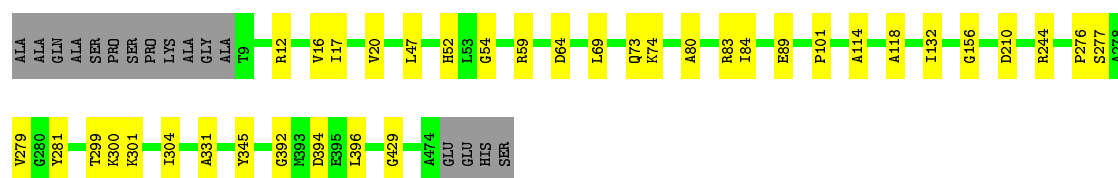


#### • Molecule 2: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL




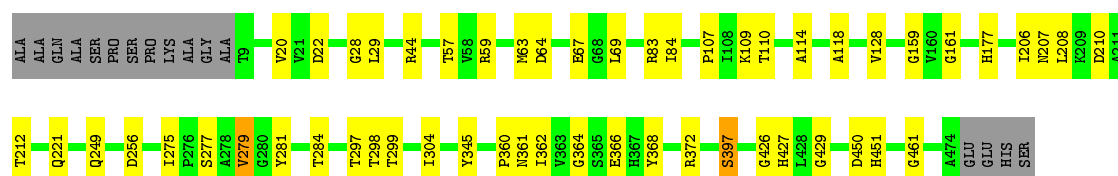
#### • Molecule 2: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL

Chain E:  89% 8% .




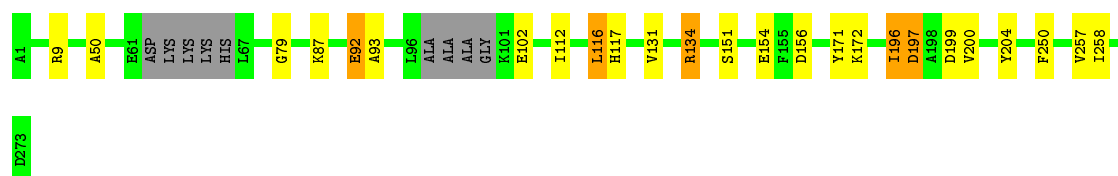
- Molecule 2: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL

Chain F:  85% 11% .




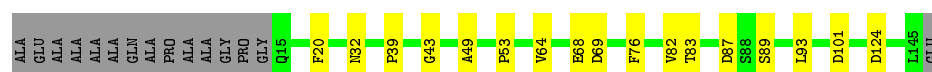
- Molecule 3: ATP SYNTHASE SUBUNIT GAMMA, MITOCHONDRIAL

Chain G:  88% 7% . .




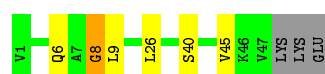
- Molecule 4: ATP SYNTHASE SUBUNIT DELTA, MITOCHONDRIAL

Chain H:  78% 12% 10%



- Molecule 5: ATP SYNTHASE SUBUNIT EPSILON, MITOCHONDRIAL

Chain I:  82% 10% 6%



- Molecule 6: ATP SYNTHASE F(0) COMPLEX SUBUNIT C1, MITOCHONDRIAL

Chain J:  97% .



- Molecule 6: ATP SYNTHASE F(0) COMPLEX SUBUNIT C1, MITOCHONDRIAL



Chain K:  99%



- Molecule 6: ATP SYNTHASE F(0) COMPLEX SUBUNIT C1, MITOCHONDRIAL

Chain L:  100%

There are no outlier residues recorded for this chain.

- Molecule 6: ATP SYNTHASE F(0) COMPLEX SUBUNIT C1, MITOCHONDRIAL

Chain M:  97%



- Molecule 6: ATP SYNTHASE F(0) COMPLEX SUBUNIT C1, MITOCHONDRIAL

Chain N:  100%

There are no outlier residues recorded for this chain.

- Molecule 6: ATP SYNTHASE F(0) COMPLEX SUBUNIT C1, MITOCHONDRIAL

Chain O:  99%



- Molecule 6: ATP SYNTHASE F(0) COMPLEX SUBUNIT C1, MITOCHONDRIAL

Chain P:  99%



- Molecule 6: ATP SYNTHASE F(0) COMPLEX SUBUNIT C1, MITOCHONDRIAL

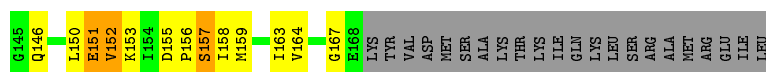
Chain Q:  97%



- Molecule 7: ATP SYNTHASE SUBUNIT O, MITOCHONDRIAL

Chain S:  60% 25% 12%





- Molecule 8: ATP SYNTHASE F(0) COMPLEX SUBUNIT B1, MITOCHONDRIAL

Chain T: 82% 14% .



- Molecule 9: ATP SYNTHASE SUBUNIT D, MITOCHONDRIAL

Chain U: 79% 15% . .



- Molecule 10: ATP SYNTHASE-COUPPLING FACTOR 6, MITOCHONDRIAL

Chain V: 74% 10% . 14%



- Molecule 11: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL

Chain W: 88% 11%



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	20104	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	EACH PARTICLE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	60.3	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4100	Depositor
Magnification	30487	Depositor
Image detector	GATAN K2 (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  > 2	RMSZ	# Z  > 2
1	A	1.81	3/2034 (0.1%)	1.42	17/2541 (0.7%)
1	B	1.85	3/1916 (0.2%)	1.42	18/2392 (0.8%)
1	C	1.83	3/1946 (0.2%)	1.42	17/2431 (0.7%)
10	V	0.79	0/263	1.06	0/327
11	W	2.53	5/868 (0.6%)	1.21	6/1082 (0.6%)
2	D	1.82	2/1866 (0.1%)	1.47	23/2331 (1.0%)
2	E	1.79	5/1862 (0.3%)	1.43	16/2326 (0.7%)
2	F	1.87	2/1862 (0.1%)	1.53	22/2326 (0.9%)
3	G	1.78	1/1050 (0.1%)	1.37	8/1308 (0.6%)
4	H	1.81	0/522	1.61	10/651 (1.5%)
5	I	1.63	0/186	1.40	2/231 (0.9%)
6	J	0.30	0/287	0.41	0/357
6	K	0.30	0/287	0.42	0/357
6	L	0.30	0/287	0.45	0/357
6	M	0.29	0/287	0.44	0/357
6	N	0.28	0/287	0.40	0/357
6	O	0.30	0/287	0.41	0/357
6	P	0.29	0/287	0.43	0/357
6	Q	0.30	0/287	0.44	0/357
7	S	1.63	3/668 (0.4%)	1.92	18/834 (2.2%)
8	T	1.24	6/696 (0.9%)	1.53	13/867 (1.5%)
9	U	0.87	0/484	1.37	4/604 (0.7%)
All	All	1.69	33/18519 (0.2%)	1.37	174/23107 (0.8%)

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	3
1	B	0	1
1	C	0	3

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	#Chirality outliers	#Planarity outliers
10	V	0	6
11	W	0	16
2	D	0	5
2	F	0	1
3	G	0	2
7	S	0	11
8	T	0	22
9	U	0	19
All	All	0	89

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	W	88	LEU	CA-C	62.36	3.15	1.52
11	W	88	LEU	N-CA	20.90	1.88	1.46
11	W	89	PRO	N-CA	-18.54	1.15	1.47
11	W	88	LEU	C-O	-14.20	0.96	1.23
8	T	160	THR	N-CA	9.37	1.65	1.46

The worst 5 of 174 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	S	73	THR	C-N-CA	16.48	162.91	121.70
7	S	110	SER	C-N-CA	-12.41	90.68	121.70
7	S	106	SER	CA-C-N	-12.23	90.30	117.20
11	W	89	PRO	N-CA-C	-10.49	84.82	112.10
9	U	78	VAL	CA-C-O	-9.60	99.94	120.10

There are no chirality outliers.

5 of 89 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	437	ALA	Mainchain,Peptide
1	A	485	THR	Mainchain
1	B	46	ASN	Mainchain
1	C	173	THR	Mainchain
1	C	336	ALA	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	2035	0	589	5	0
1	B	1918	0	553	7	0
1	C	1947	0	563	7	0
2	D	1867	0	533	4	0
2	E	1863	0	532	4	0
2	F	1863	0	532	8	0
3	G	1053	0	283	0	0
4	H	523	0	140	1	0
5	I	187	0	53	1	0
6	J	288	0	92	0	0
6	K	288	0	92	0	0
6	L	288	0	92	0	0
6	M	288	0	92	0	0
6	N	288	0	92	0	0
6	O	288	0	92	0	0
6	P	288	0	92	0	0
6	Q	288	0	92	0	0
7	S	669	0	178	8	0
8	T	697	0	182	1	0
9	U	485	0	118	0	0
10	V	264	0	71	0	0
11	W	869	0	226	4	0
All	All	18544	0	5289	43	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.

The worst 5 of 43 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)
11:W:88:LEU:CA	11:W:88:LEU:N	1.88	1.36
7:S:164:VAL:CA	7:S:167:GLY:O	2.28	0.80
2:F:84:ILE:H	2:F:114:ALA:H	1.42	0.68
1:B:49:ALA:H	2:F:69:LEU:H	1.43	0.67
1:A:49:ALA:H	2:E:69:LEU:N	2.00	0.59

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	507/510 (99%)	445 (88%)	35 (7%)	27 (5%)	2	26
1	B	476/510 (93%)	423 (89%)	30 (6%)	23 (5%)	2	28
1	C	485/510 (95%)	434 (90%)	28 (6%)	23 (5%)	3	28
2	D	465/482 (96%)	415 (89%)	30 (6%)	20 (4%)	3	29
2	E	464/482 (96%)	418 (90%)	34 (7%)	12 (3%)	6	40
2	F	464/482 (96%)	412 (89%)	32 (7%)	20 (4%)	3	29
3	G	258/273 (94%)	195 (76%)	43 (17%)	20 (8%)	1	17
4	H	129/146 (88%)	114 (88%)	10 (8%)	5 (4%)	3	31
5	I	45/50 (90%)	35 (78%)	7 (16%)	3 (7%)	1	21
6	J	70/72 (97%)	62 (89%)	6 (9%)	2 (3%)	5	38
6	K	70/72 (97%)	64 (91%)	5 (7%)	1 (1%)	13	54
6	L	70/72 (97%)	57 (81%)	13 (19%)	0	100	100
6	M	70/72 (97%)	64 (91%)	4 (6%)	2 (3%)	5	38
6	N	70/72 (97%)	61 (87%)	9 (13%)	0	100	100
6	O	70/72 (97%)	64 (91%)	5 (7%)	1 (1%)	13	54
6	P	70/72 (97%)	64 (91%)	5 (7%)	1 (1%)	13	54
6	Q	70/72 (97%)	61 (87%)	7 (10%)	2 (3%)	5	38
7	S	166/190 (87%)	110 (66%)	30 (18%)	26 (16%)	0	4
8	T	172/174 (99%)	154 (90%)	14 (8%)	4 (2%)	7	43
9	U	120/124 (97%)	95 (79%)	16 (13%)	9 (8%)	1	18
10	V	64/77 (83%)	51 (80%)	9 (14%)	4 (6%)	1	22
11	W	215/217 (99%)	192 (89%)	19 (9%)	4 (2%)	9	47
All	All	4590/4803 (96%)	3990 (87%)	391 (8%)	209 (5%)	5	28

5 of 209 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	THR
1	A	13	GLU
1	A	14	GLU
1	A	20	ASP
1	A	24	ASP

### 5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 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.