



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jul 24, 2017 – 05:07 AM EDT

PDB ID : 5ARE
EMDB ID: : EMD-3165
Title : Bovine mitochondrial ATP synthase state 1b
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 : 7.40 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
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

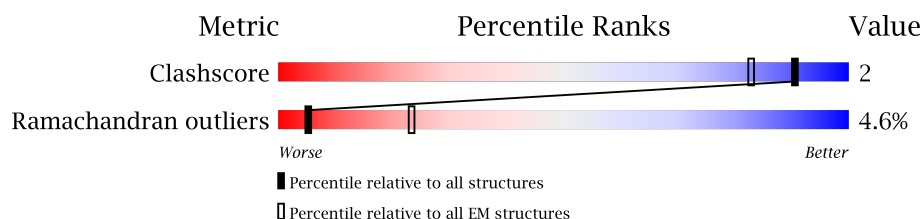
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	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 ≥ 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	87% 12% .
1	B	510	83% 10% . 6%
1	C	510	86% 9% . 5%
2	D	482	86% 11% .
2	E	482	84% 11% . .
2	F	482	87% 10% .
3	G	273	85% 11% . . .
4	H	146	68% 21% 10%
5	I	50	86% 6% . 6%
6	J	72	97% .
6	K	72	99% .

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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	 56% 25% 6% . 12%
8	T	174	 87% 11% .
9	U	124	 78% 17% . .
10	V	77	 62% 21% . 13%
11	W	217	 96% . .

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 18545 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	67	Total	C	N	O	0	1
			265	132	67	66		

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

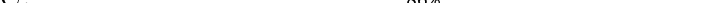
Mol	Chain	Residues	Atoms				AltConf	Trace
11	W	217	Total	C	N	O	0	0
			869	434	217	218		

- Molecule 1: ATP SYNTHASE SUBUNIT ALPHA, MITOCHONDRIAL

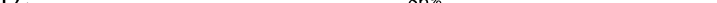
T193	T194	I202	K209	D224	T235	F257	G261	K262	H263	P289	M313	G319	A323	A336	P362	A364	I365	Y397	A401	F406	S408	D409	Q432	M436	G448	G451	Q475	H476	Q477	K488	F504	F508	E509	E510						
GL1	K2	I11	E13	E14	L17	G18	A19	D20	T21	S22	G35	A39	R40	V41	H42	G43	L44	A49	G61	N78	D79	V88	K89	D86	G100	A114	I115	E144	P145	M146	G149	G160	R164	R171	Q172	T173	G174	K187	D191	G193

Chain B: 83% 10% • 6%

SER	ASP	L410		R161	G162		GLN
				R171			LYS
		G421		R172			THR
				G172			THR
				T173			ALA
		Q430		G174			GLU
				K175			VAL
		Y433					
		S434		D194			SER
		P435		E195			ILE
		M436		K196			LEU
				K197			GLU
		K488		K198			GLU
							ARG
		L505		I202			ILE
							LEU
		F508		K209			GLY
							ALA
		E509		D224			ASP
		A510					THR
				V232			SER
							V23
				A236			
				S237			G35
				D238			
							I38
				R258			
							R45
				G261			V46
				K262			V47
							Q48
				I267			A49
							E50
				P289			
				G290			S57
				N313			L66
							E67
				G317			
				G318			N73
				G319			
							G100
				I327			
				E328			V107
				I361			I121
				G375			R127
				Q379			L131
				V400			S141
				A401			V142
				ALA			R143
				PHE			E144
				ALA			ALA
				GLN			G149
				PHE			
				GLY			G160

Chain C:  86% 9% 5%

D194	E195	K196	K209	R210	V213	A214	D224	V232	D238	R258	D259	K260	G261	K262	H263	L285	R286	P287	P288	P289	L301	G319	S320	L321	A331	I365	A402	F403	A404	K429	P435	M436	G451	I500	A510									
GLV	LVS	THR	GLY	THR	ALA	GLU	VAL	SEN	SEN	ILE	LEU	GLU	GLU	ARG	ILE	LEU	GLY	ASP	THR	SEN	VAL	D94	G29	G35	H42	V47	Q48	A49	L59	S63	E67	T91	A125	R143	F144	P145	M146	G149	Q163	D170	R171	Q172	T173	G174

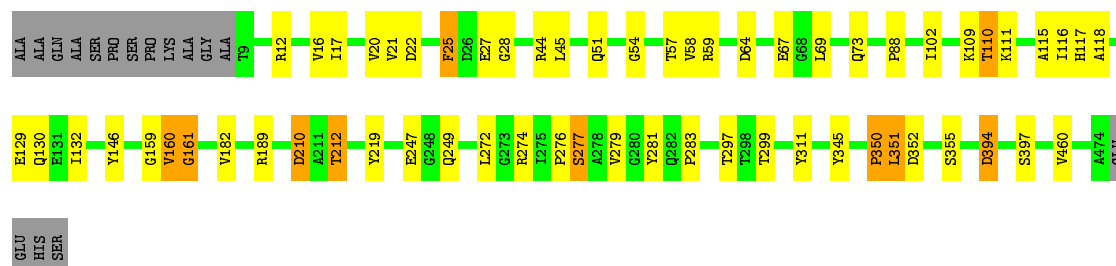
Chain D:  86% 11% .

[illegible]



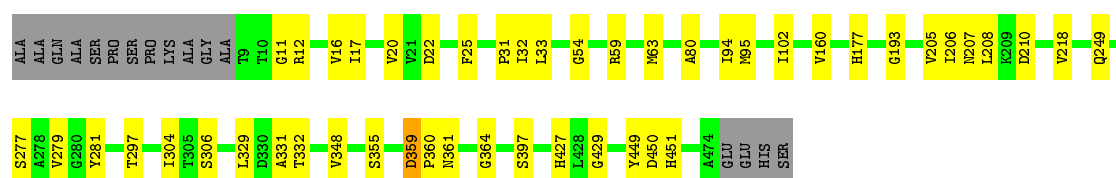
• Molecule 2: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL

Chain E: 84% 11%



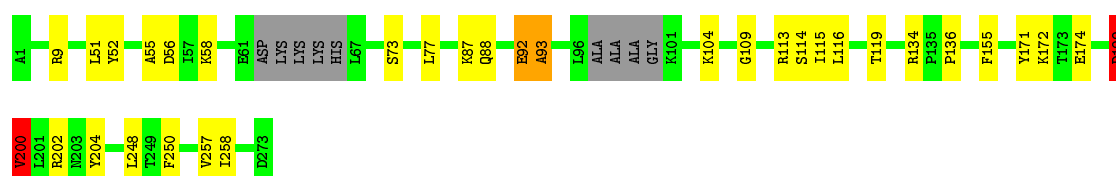
• Molecule 2: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL

Chain F: 87% 10%



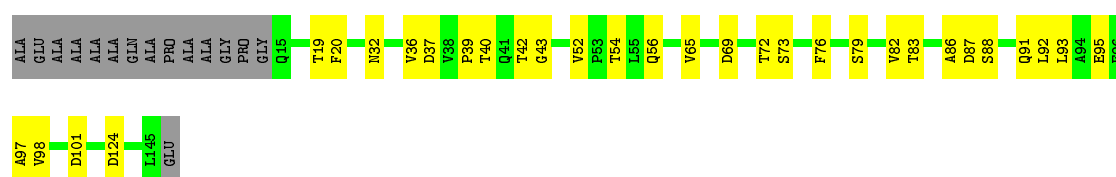
• Molecule 3: ATP SYNTHASE SUBUNIT GAMMA, MITOCHONDRIAL

Chain G: 85% 11%



• Molecule 4: ATP SYNTHASE SUBUNIT DELTA, MITOCHONDRIAL

Chain H: 68% 21% 10%



• Molecule 5: ATP SYNTHASE SUBUNIT EPSILON, MITOCHONDRIAL

Chain I: 86% 6% 6%



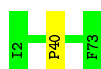
- Molecule 6: ATP SYNTHASE F(0) COMPLEX SUBUNIT C1, MITOCHONDRIAL

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.

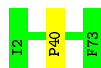
- Molecule 6: ATP SYNTHASE F(0) COMPLEX SUBUNIT C1, MITOCHONDRIAL

Chain O: 99%



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

Chain P: 99%



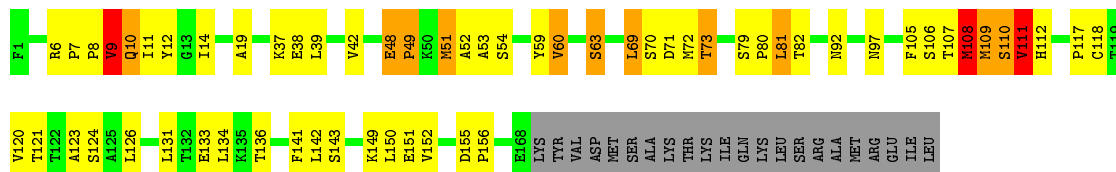
- Molecule 6: ATP SYNTHASE F(0) COMPLEX SUBUNIT C1, MITOCHONDRIAL

Chain Q:  97% .




- Molecule 7: ATP SYNTHASE SUBUNIT O, MITOCHONDRIAL

Chain S:  56% 25% 6% . 12%




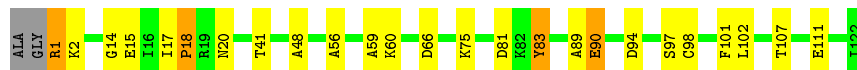
- Molecule 8: ATP SYNTHASE F(0) COMPLEX SUBUNIT B1, MITOCHONDRIAL

Chain T:  87% 11% .



- Molecule 9: ATP SYNTHASE SUBUNIT D, MITOCHONDRIAL

Chain U:  78% 17% . .



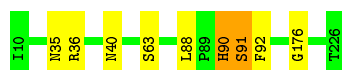
- Molecule 10: ATP SYNTHASE-COUPLING FACTOR 6, MITOCHONDRIAL

Chain V:  62% 21% . 13%



- Molecule 11: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL

Chain W:  96% . .



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	22935	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	1.82	6/2034 (0.3%)	1.48	22/2541 (0.9%)
1	B	1.85	4/1916 (0.2%)	1.53	21/2392 (0.9%)
1	C	1.76	6/1946 (0.3%)	1.50	16/2431 (0.7%)
10	V	0.78	0/264	1.31	1/329 (0.3%)
11	W	0.44	0/868	0.72	1/1082 (0.1%)
2	D	1.77	5/1866 (0.3%)	1.51	27/2331 (1.2%)
2	E	1.78	3/1862 (0.2%)	1.56	30/2326 (1.3%)
2	F	1.78	5/1862 (0.3%)	1.49	23/2326 (1.0%)
3	G	1.68	2/1050 (0.2%)	1.52	13/1308 (1.0%)
4	H	1.93	0/522	1.83	16/651 (2.5%)
5	I	1.68	0/186	1.35	1/231 (0.4%)
6	J	0.30	0/287	0.42	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	0.30	0/287	0.42	0/357
6	Q	0.30	0/287	0.44	0/357
7	S	1.01	5/668 (0.7%)	1.79	16/834 (1.9%)
8	T	0.87	2/696 (0.3%)	1.05	3/867 (0.3%)
9	U	0.77	0/484	1.18	1/604 (0.2%)
All	All	1.55	38/18520 (0.2%)	1.39	191/23109 (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	4
1	B	0	3
1	C	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	V	0	16
11	W	0	5
2	D	0	1
2	E	0	5
2	F	0	4
3	G	0	5
4	H	0	2
7	S	0	38
8	T	0	16
9	U	0	30
All	All	0	132

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	T	93	ASP	N-CA	9.53	1.65	1.46
2	D	429	GLY	CA-C	-7.32	1.40	1.51
7	S	6	ARG	CA-C	6.89	1.70	1.52
1	C	35	GLY	CA-C	-6.80	1.41	1.51
7	S	6	ARG	C-N	6.77	1.47	1.34

The worst 5 of 191 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	S	48	GLU	O-C-N	13.96	147.63	121.10
7	S	48	GLU	CA-C-N	-11.40	85.17	117.10
7	S	6	ARG	CA-C-O	-9.20	100.79	120.10
7	S	108	MET	CA-C-O	-9.10	100.99	120.10
1	A	407	GLY	N-CA-C	-9.02	90.54	113.10

There are no chirality outliers.

5 of 132 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	406	PHE	Mainchain,Peptide
1	A	408	SER	Mainchain
1	A	509	GLU	Mainchain
1	B	379	GLN	Peptide
1	B	78	ASN	Mainchain

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	10	0
1	B	1918	0	553	7	0
1	C	1947	0	562	8	0
2	D	1867	0	533	3	0
2	E	1863	0	532	8	0
2	F	1863	0	532	1	0
3	G	1053	0	283	1	0
4	H	523	0	140	1	0
5	I	187	0	53	0	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	179	6	0
8	T	697	0	182	0	0
9	U	485	0	121	0	0
10	V	265	0	68	1	0
11	W	869	0	226	1	0
All	All	18545	0	5289	44	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 44 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)
1:A:17:LEU:CA	7:S:81:LEU:O	2.45	0.64
7:S:108:MET:O	7:S:112:HIS:CA	2.51	0.58
4:H:65:VAL:H	4:H:73:SER:H	1.55	0.55
7:S:106:SER:CA	7:S:109:MET:H	2.20	0.54
1:B:261:GLY:HA2	1:B:317:GLY:HA3	1.90	0.53

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%)	441 (87%)	42 (8%)	24 (5%)	3	28
1	B	476/510 (93%)	420 (88%)	31 (6%)	25 (5%)	2	26
1	C	485/510 (95%)	433 (89%)	34 (7%)	18 (4%)	4	33
2	D	465/482 (96%)	404 (87%)	44 (10%)	17 (4%)	4	33
2	E	464/482 (96%)	413 (89%)	31 (7%)	20 (4%)	3	29
2	F	464/482 (96%)	414 (89%)	33 (7%)	17 (4%)	4	33
3	G	258/273 (94%)	204 (79%)	35 (14%)	19 (7%)	1	18
4	H	129/146 (88%)	110 (85%)	8 (6%)	11 (8%)	1	15
5	I	45/50 (90%)	34 (76%)	7 (16%)	4 (9%)	1	15
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%)	112 (68%)	28 (17%)	26 (16%)	0	4
8	T	172/174 (99%)	156 (91%)	9 (5%)	7 (4%)	3	30
9	U	120/124 (97%)	103 (86%)	10 (8%)	7 (6%)	2	24
10	V	65/77 (84%)	49 (75%)	10 (15%)	6 (9%)	1	14
11	W	215/217 (99%)	192 (89%)	20 (9%)	3 (1%)	13	54
All	All	4591/4803 (96%)	3982 (87%)	396 (9%)	213 (5%)	5	28

5 of 213 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	13	GLU
1	A	14	GLU
1	A	224	ASP
1	A	262	LYS
1	A	365	ILE

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.