



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:11 AM GMT

PDB ID : 2W6G  
Title : LOW RESOLUTION STRUCTURES OF BOVINE MITOCHONDRIAL F1-ATPASE DURING CONTROLLED DEHYDRATION: HYDRATION STATE 3.  
Authors : Sanchez-Weatherby, J.; Felisaz, F.; Gobbo, A.; Huet, J.; Ravelli, R.B.G.; Bowler, M.W.; Cipriani, F.  
Deposited on : 2008-12-18  
Resolution : 6.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB 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/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

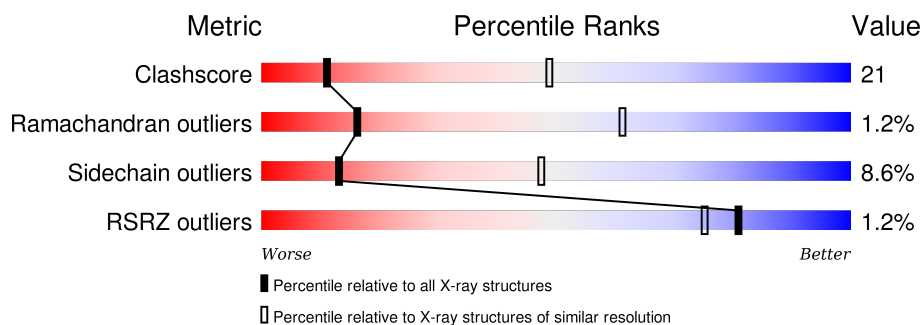
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 6.00 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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	1050 (8.30-3.70)
Ramachandran outliers	100387	1023 (8.30-3.66)
Sidechain outliers	100360	1012 (8.30-3.64)
RSRZ outliers	91569	1001 (8.30-3.66)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	553	<div> <div>2%</div> <div> <div>47%</div> <div>33%</div> <div>7%</div> <div>12%</div> </div> </div>
1	B	553	<div> <div>47%</div> <div>33%</div> <div>6%</div> <div>13%</div> </div>
1	C	553	<div> <div>51%</div> <div>33%</div> <div>11%</div> </div>
2	D	528	<div> <div>%</div> <div>55%</div> <div>28%</div> <div>12%</div> </div>
2	E	528	<div> <div>%</div> <div>45%</div> <div>36%</div> <div>6%</div> <div>12%</div> </div>
2	F	528	<div> <div>%</div> <div>57%</div> <div>28%</div> <div>12%</div> </div>
3	G	298	<div> <div>3%</div> <div>34%</div> <div>12%</div> <div>53%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 22795 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 HEART ISOFORM, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	487	Total	C	N	O	S	0	0	0
			3715	2341	656	706	12			
1	B	479	Total	C	N	O	S	0	0	0
			3656	2303	647	694	12			
1	C	492	Total	C	N	O	S	0	0	0
			3748	2360	661	715	12			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	467	Total	C	N	O	S	0	0	0
			3539	2243	601	684	11			
2	E	466	Total	C	N	O	S	0	0	0
			3530	2238	600	681	11			
2	F	466	Total	C	N	O	S	0	0	0
			3530	2238	600	681	11			

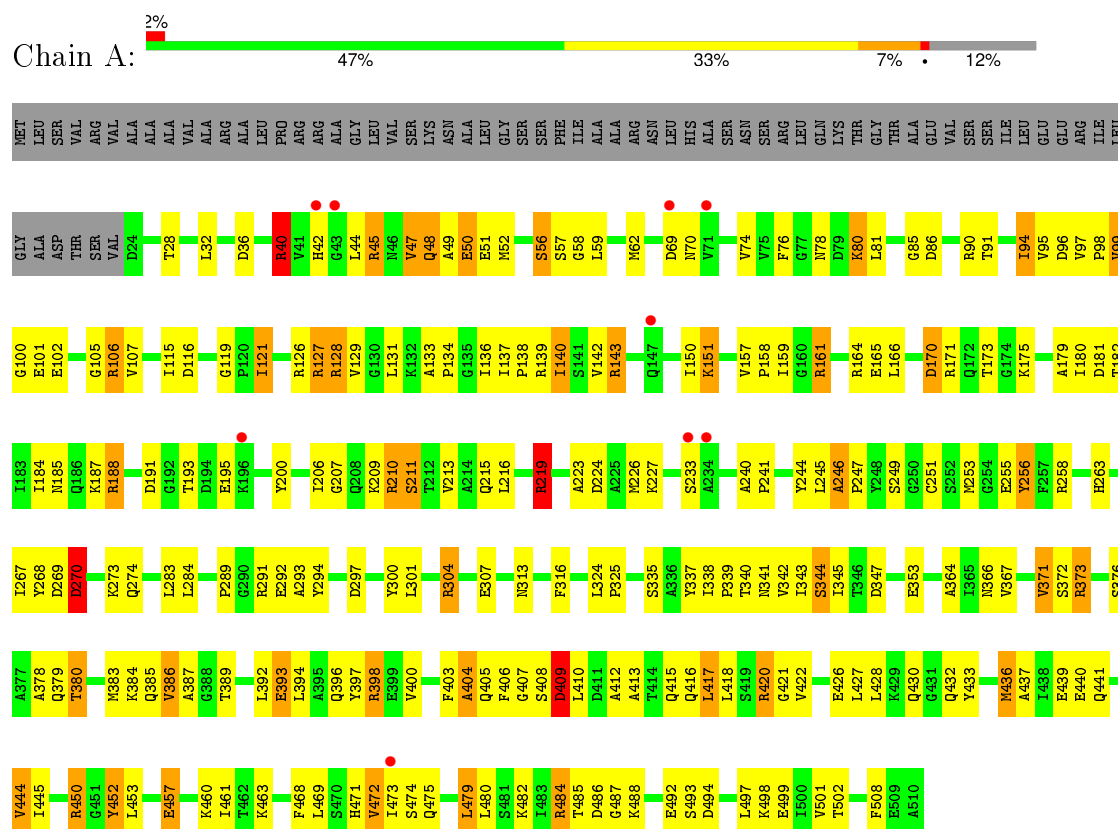
- Molecule 3 is a protein called ATP SYNTHASE SUBUNIT GAMMA, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	140	Total	C	N	O	S	0	0	0
			1077	671	195	205	6			

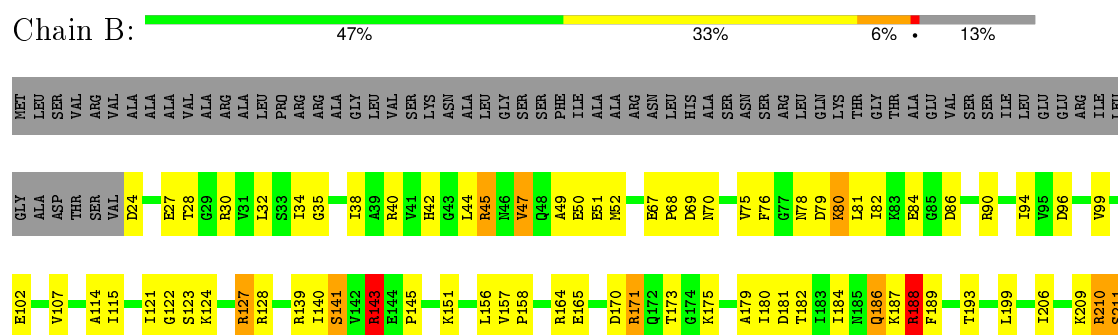
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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 HEART ISOFORM, MITOCHONDRIAL



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



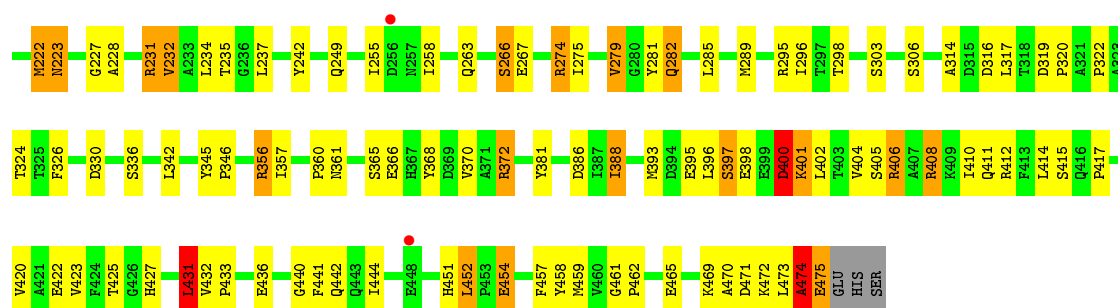


Frequency	Percentage
Daily	51%
Often	33%
Sometimes	11%
Never	3%

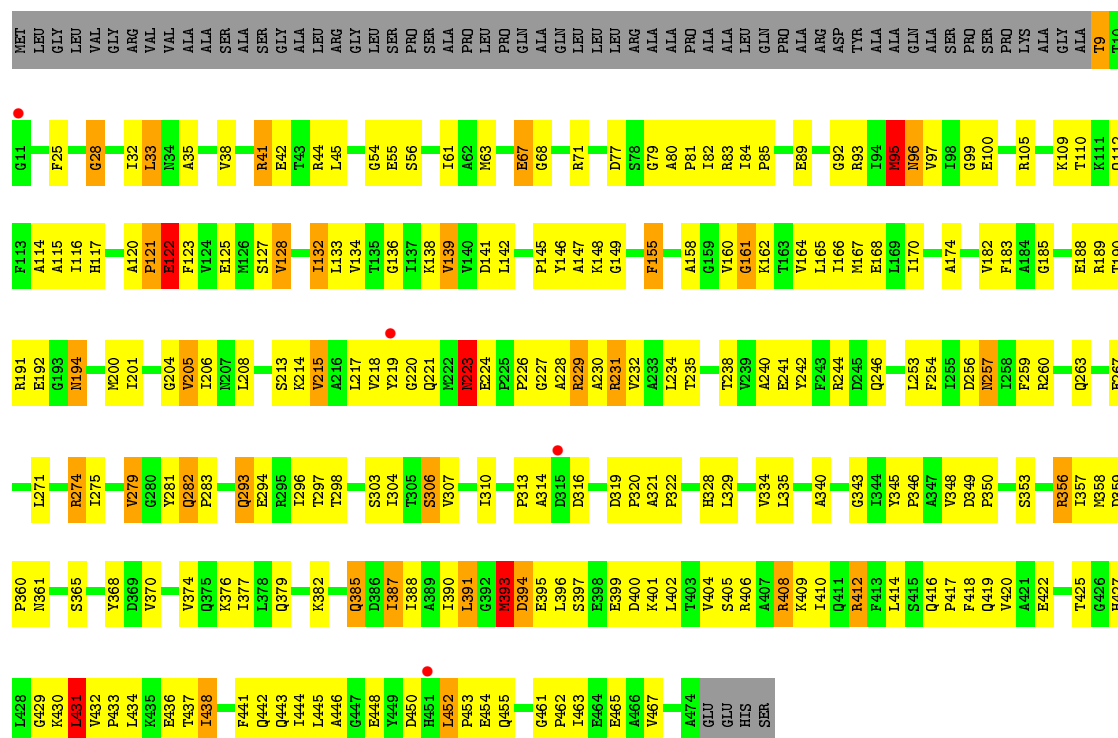


Response	Percentage
Doing a good job	55%
Not doing a good job	28%
Don't know	12%

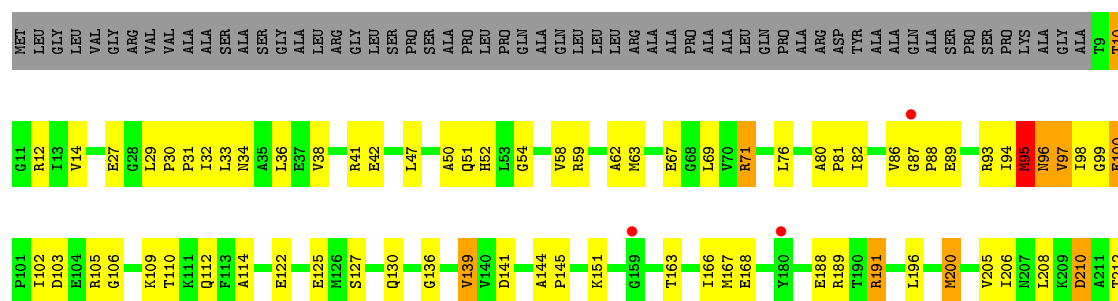


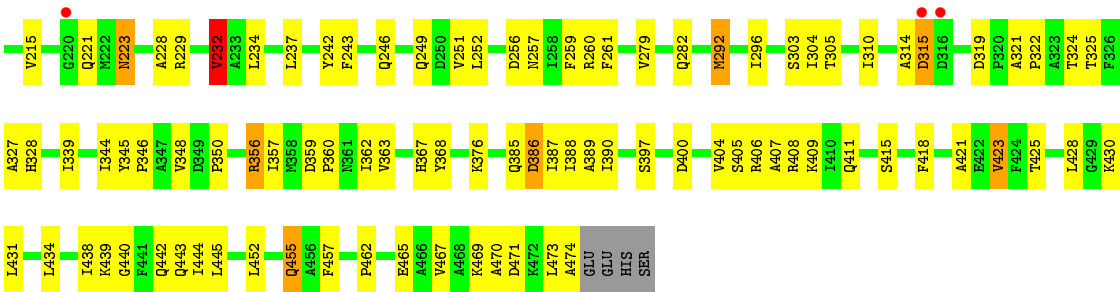


• Molecule 2: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL

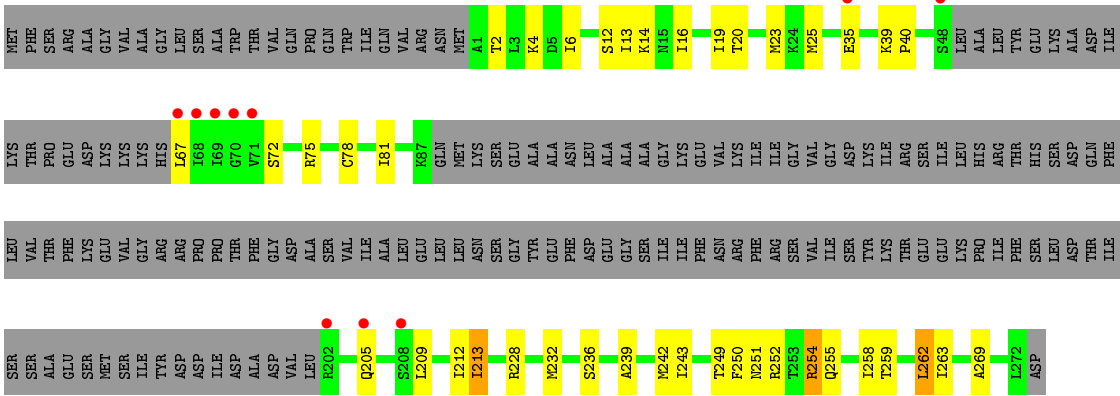
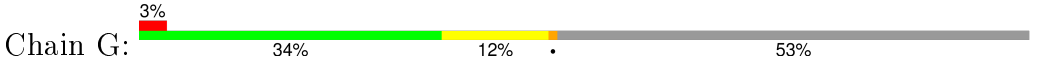


• Molecule 2: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL





• Molecule 3: ATP SYNTHASE SUBUNIT GAMMA, MITOCHONDRIAL



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.35Å 132.93Å 275.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	101.53 – 6.00 80.74 – 6.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (101.53-6.00) 65.8 (80.74-6.00)	Depositor EDS
$R_{merge}$	0.21	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 6.18Å)	Xtriage
Refinement program	REFMAC 5.5.0038	Depositor
R, $R_{free}$	0.330 , (Not available) 0.329 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	156.4	Xtriage
Anisotropy	0.372	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 37.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.36$ , $\langle L^2 \rangle = 0.20$	Xtriage
Outliers	0 of 6950 reflections	Xtriage
$F_o, F_c$ correlation	0.78	EDS
Total number of atoms	22795	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.56% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.



## 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	A	0.60	0/3766	1.31	29/5080 (0.6%)
1	B	0.61	0/3704	1.36	34/4995 (0.7%)
1	C	0.62	0/3799	1.38	24/5126 (0.5%)
2	D	0.62	0/3596	1.36	23/4879 (0.5%)
2	E	0.60	0/3587	1.32	18/4867 (0.4%)
2	F	0.62	0/3587	1.36	27/4867 (0.6%)
3	G	0.33	0/1083	0.69	2/1448 (0.1%)
All	All	0.60	0/23122	1.33	157/31262 (0.5%)

There are no bond length outliers.

The worst 5 of 157 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	D	408	ARG	CD-NE-CZ	23.30	156.22	123.60
2	E	408	ARG	CD-NE-CZ	13.97	143.16	123.60
1	C	291	ARG	NE-CZ-NH2	-13.30	113.65	120.30
1	B	40	ARG	NE-CZ-NH1	13.08	126.84	120.30
1	B	279	ARG	NE-CZ-NH1	12.73	126.67	120.30

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	3715	0	3813	184	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3656	0	3764	156	58
1	C	3748	0	3843	163	56
2	D	3539	0	3593	158	0
2	E	3530	0	3587	217	0
2	F	3530	0	3587	124	2
3	G	1077	0	1139	66	0
All	All	22795	0	23326	961	58

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 21.

The worst 5 of 961 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:F:390:ILE:HD11	3:G:242:MET:CE	1.54	1.36
2:F:390:ILE:CD1	3:G:242:MET:CE	2.07	1.29
2:E:390:ILE:HG13	3:G:25:MET:SD	1.75	1.25
1:C:127:ARG:HH12	1:C:255:GLU:HB2	1.00	1.13
2:F:390:ILE:CD1	3:G:242:MET:HE3	1.77	1.09

The worst 5 of 58 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:314:ASP:O	1:C:22:SER:C[4_455]	0.42	1.78
1:B:314:ASP:CA	1:C:22:SER:N[4_455]	0.82	1.38
1:B:318:GLY:C	1:C:20:ASP:OD2[4_455]	0.87	1.33
1:B:314:ASP:O	1:C:23:VAL:N[4_455]	0.93	1.27
1:B:314:ASP:OD1	1:C:20:ASP:O[4_455]	0.94	1.26

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	485/553 (88%)	443 (91%)	35 (7%)	7 (1%)	14	58
1	B	475/553 (86%)	427 (90%)	41 (9%)	7 (2%)	13	57
1	C	490/553 (89%)	444 (91%)	38 (8%)	8 (2%)	12	56
2	D	465/528 (88%)	419 (90%)	43 (9%)	3 (1%)	30	74
2	E	464/528 (88%)	407 (88%)	48 (10%)	9 (2%)	10	52
2	F	464/528 (88%)	432 (93%)	30 (6%)	2 (0%)	39	80
3	G	134/298 (45%)	130 (97%)	3 (2%)	1 (1%)	26	71
All	All	2977/3541 (84%)	2702 (91%)	238 (8%)	37 (1%)	16	61

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	407	GLY
2	E	393	MET
1	A	57	SER
1	A	405	GLN
1	A	409	ASP

### 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 X-ray entries followed by that with respect to entries of similar resolution.

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	393/444 (88%)	351 (89%)	42 (11%)	8	36
1	B	388/444 (87%)	341 (88%)	47 (12%)	6	31
1	C	397/444 (89%)	369 (93%)	28 (7%)	18	55
2	D	377/417 (90%)	346 (92%)	31 (8%)	14	49
2	E	376/417 (90%)	344 (92%)	32 (8%)	13	48
2	F	376/417 (90%)	354 (94%)	22 (6%)	24	61
3	G	116/251 (46%)	110 (95%)	6 (5%)	29	65
All	All	2423/2834 (86%)	2215 (91%)	208 (9%)	13	47

5 of 208 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	87	ILE
1	C	505	LEU
2	F	223	ASN
1	C	164	ARG
1	C	349	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	328	HIS
2	E	51	GLN
3	G	82	HIS
2	D	442	GLN
2	E	194	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	487/553 (88%)	0.05	9 (1%) 71 66	20, 20, 20, 20	0
1	B	479/553 (86%)	0.03	2 (0%) 93 90	20, 20, 20, 20	0
1	C	492/553 (88%)	-0.09	1 (0%) 95 94	20, 20, 20, 20	0
2	D	467/528 (88%)	-0.02	4 (0%) 85 81	20, 20, 20, 20	0
2	E	466/528 (88%)	-0.09	4 (0%) 85 81	20, 20, 20, 20	0
2	F	466/528 (88%)	-0.02	6 (1%) 79 73	20, 20, 20, 20	0
3	G	140/298 (46%)	0.55	10 (7%) 19 21	36, 59, 81, 89	0
All	All	2997/3541 (84%)	0.01	36 (1%) 81 75	20, 20, 20, 89	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	G	67	LEU	4.3
1	A	234	ALA	3.7
3	G	202	ARG	3.6
1	B	489	ILE	3.4
3	G	69	ILE	3.3

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.