



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 10:15 PM UTC

PDB ID : 2W6J / pdb_00002w6j
Title : Low resolution structures of bovine mitochondrial F1-ATPase during controlled dehydration: Hydration State 5.
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 : 3.84 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

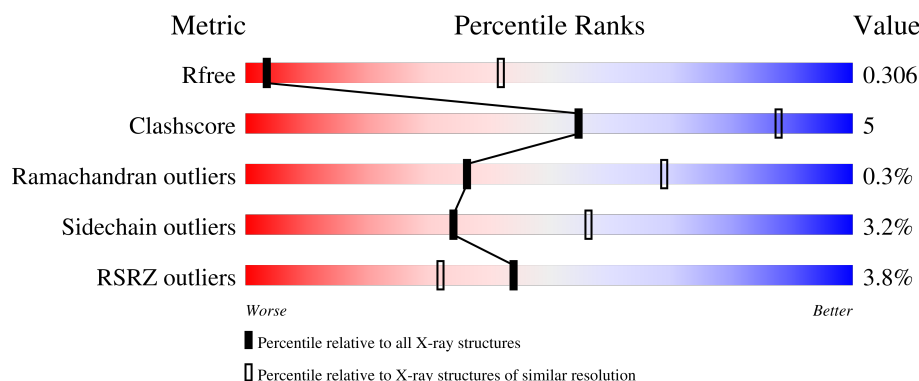
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.84 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))
R_{free}	180053	1169 (4.00-3.68)
Clashscore	190562	1211 (4.00-3.68)
Ramachandran outliers	187476	1156 (4.00-3.68)
Sidechain outliers	187428	1149 (4.00-3.68)
RSRZ outliers	180081	1168 (4.00-3.68)

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 of the lower 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 $\leq 5\%$. 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	4% 75% 11% 12%
1	B	553	3% 81% 5% 13%
1	C	553	5% 79% 9% 11%
2	D	528	3% 78% 9% 12%
2	E	528	4% 77% 9% 13%

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Mol	Chain	Length	Quality of chain
2	F	528	
3	G	298	
4	H	168	
5	I	51	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 23874 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	480	Total	C	N	O	S	0	0	0
			3663	2308	648	695	12			
1	C	490	Total	C	N	O	S	0	0	0
			3735	2353	659	711	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	458	Total	C	N	O	S	0	0	0
			3472	2201	592	669	10			
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	182	Total	C	N	O	S	0	0	1
			1397	881	250	260	6			

- Molecule 4 is a protein called F1-ATPASE DELTA SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	83	Total	C	N	O	S	0	0	0
			620	391	102	126	1			

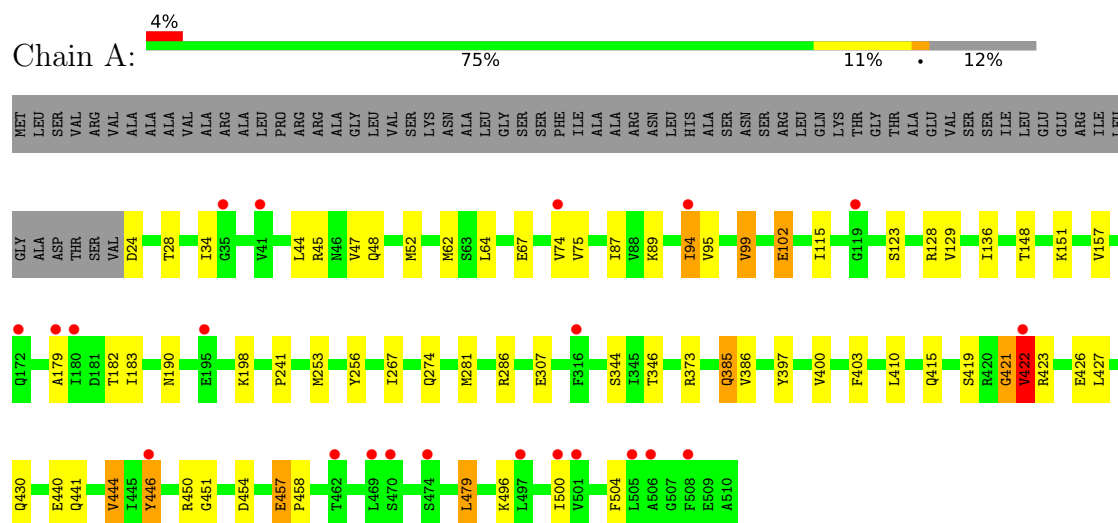
- Molecule 5 is a protein called ATP SYNTHASE SUBUNIT EPSILON, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	I	25	Total	C	N	O	S	0	0	0
			203	130	38	34	1			

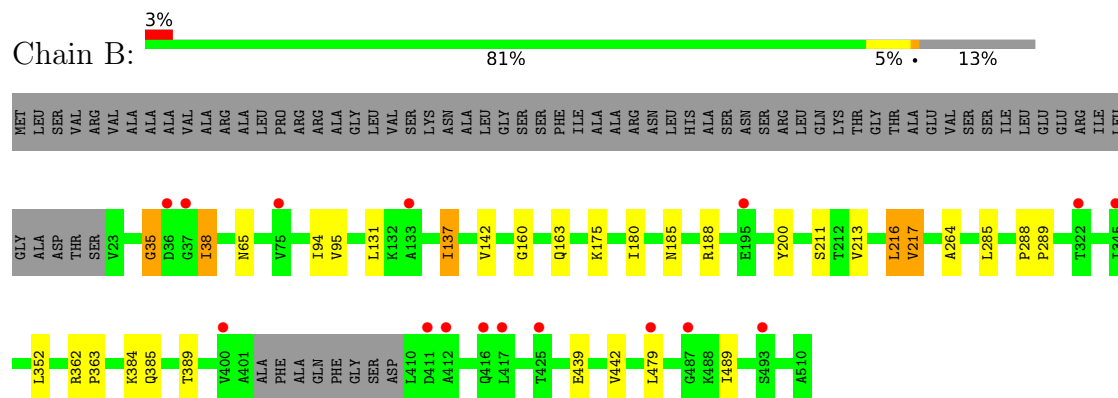
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 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.

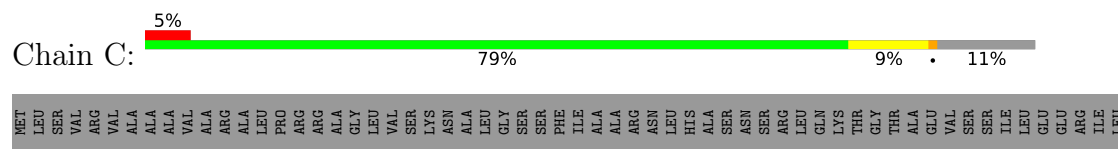
• Molecule 1: ATP SYNTHASE SUBUNIT ALPHA HEART ISOFORM, MITOCHONDRIAL

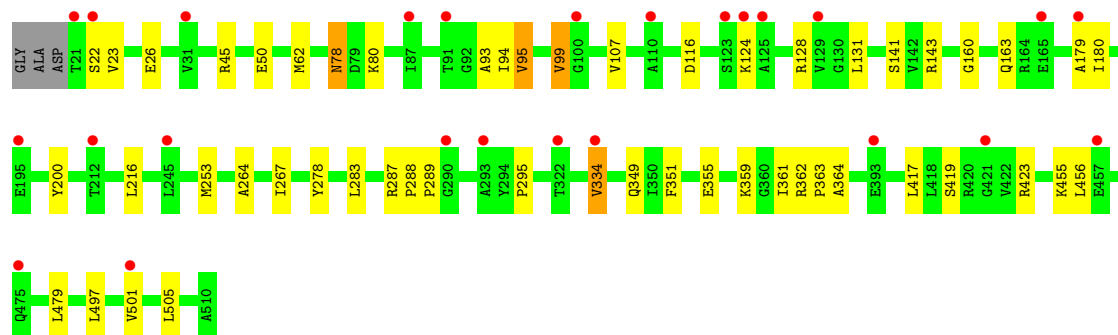


• Molecule 1: ATP SYNTHASE SUBUNIT ALPHA HEART ISOFORM, MITOCHONDRIAL

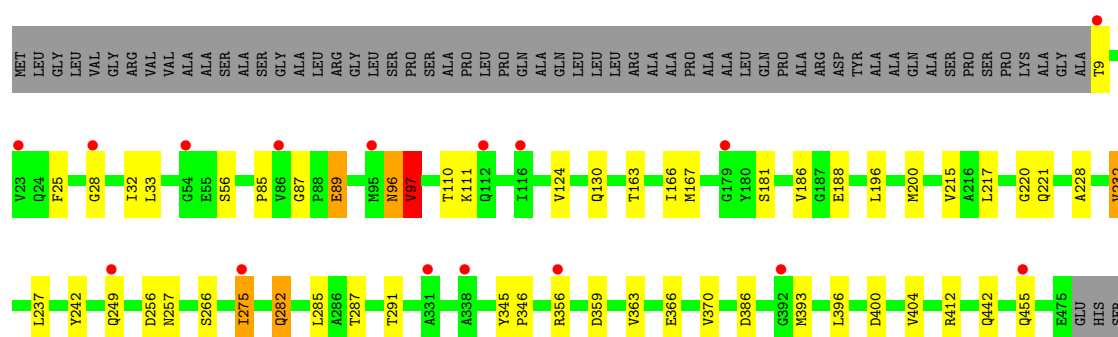
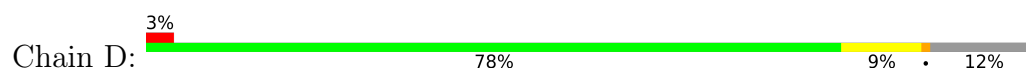


• Molecule 1: ATP SYNTHASE SUBUNIT ALPHA HEART ISOFORM, MITOCHONDRIAL

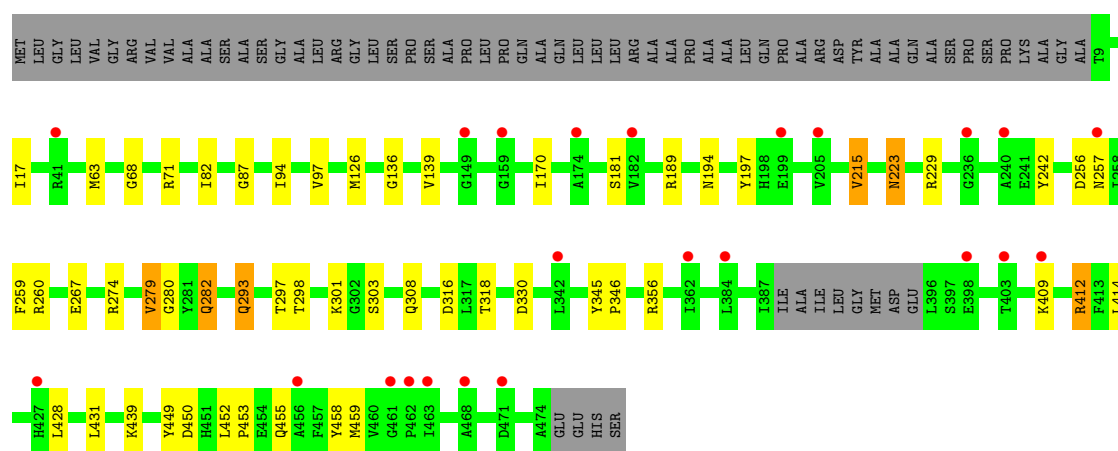
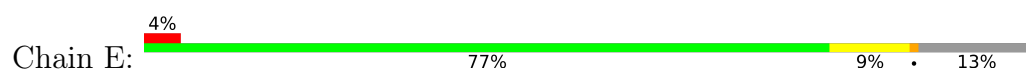




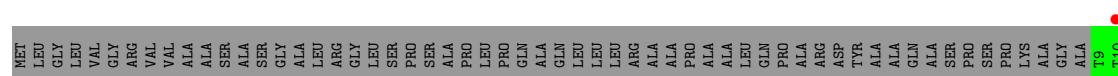
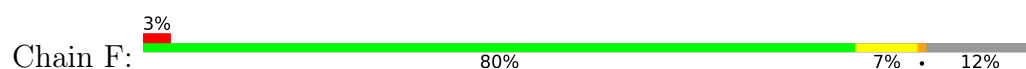
• Molecule 2: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL

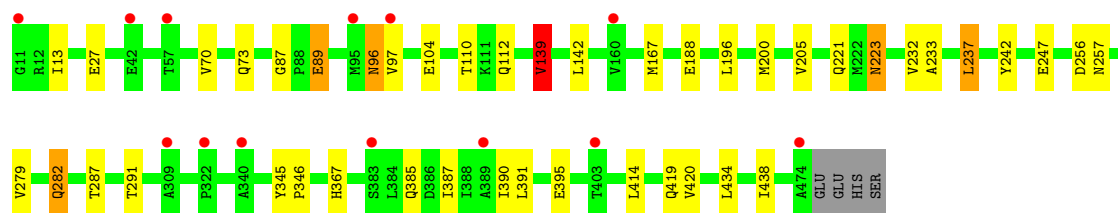


• Molecule 2: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL



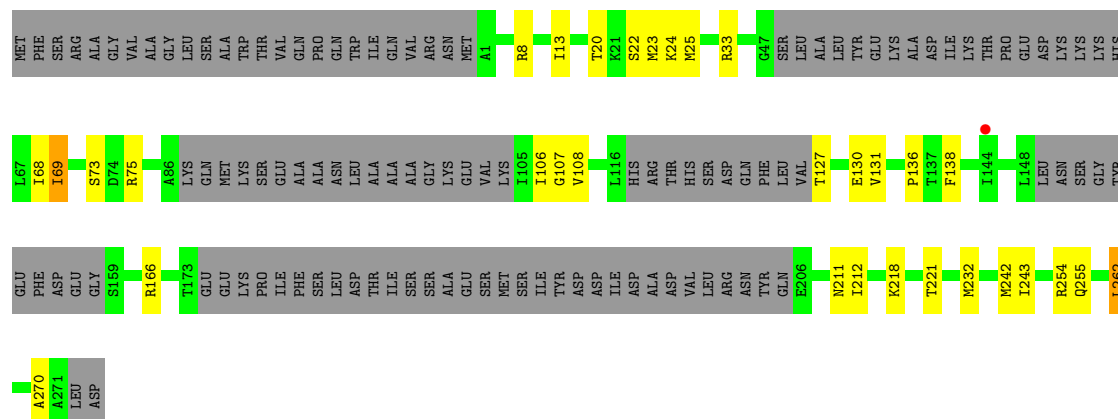
• Molecule 2: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL





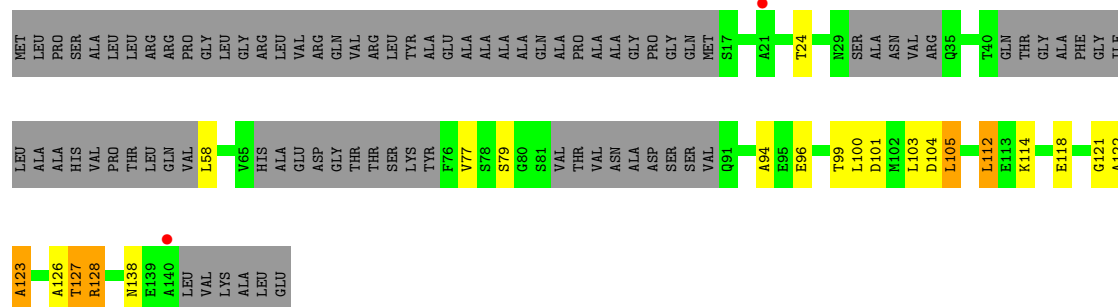
• Molecule 3: ATP SYNTHASE SUBUNIT GAMMA, MITOCHONDRIAL

Chain G: 50% 10% 39%



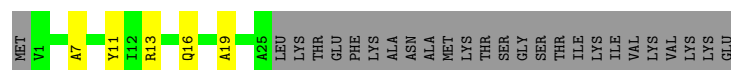
• Molecule 4: F1-ATPASE DELTA SUBUNIT

Chain H: 36% 10% 51%



• Molecule 5: ATP SYNTHASE SUBUNIT EPSILON, MITOCHONDRIAL

Chain I: 39% 10% 51%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	106.93Å 124.07Å 264.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	132.45 – 3.84 132.23 – 3.84	Depositor EDS
% Data completeness (in resolution range)	95.3 (132.45-3.84) 95.3 (132.23-3.84)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.52 (at 3.89Å)	Xtriage
Refinement program	REFMAC 5.5.0038	Depositor
R, R_{free}	0.305 , (Not available) 0.307 , 0.306	Depositor DCC
R_{free} test set	1665 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	73.4	Xtriage
Anisotropy	0.375	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 3.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.79	EDS
Total number of atoms	23874	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.09% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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	0.51	1/3766 (0.0%)	0.81	5/5080 (0.1%)
1	B	0.51	1/3711 (0.0%)	0.79	0/5005
1	C	0.48	0/3786	0.81	2/5108 (0.0%)
2	D	0.50	0/3596	0.77	3/4879 (0.1%)
2	E	0.48	0/3528	0.78	2/4786 (0.0%)
2	F	0.52	0/3587	0.79	1/4867 (0.0%)
3	G	0.52	1/1406 (0.1%)	0.84	0/1880
4	H	0.44	0/623	0.92	2/840 (0.2%)
5	I	0.50	0/207	0.83	0/279
All	All	0.50	3/24210 (0.0%)	0.80	15/32724 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	422	VAL	CA-CB	8.65	1.66	1.54
3	G	270	ALA	C-N	-6.98	1.23	1.33
1	B	137	ILE	CA-CB	5.01	1.57	1.53

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	256	ASP	CA-C-N	6.62	133.62	121.70
2	E	256	ASP	C-N-CA	6.62	133.62	121.70
4	H	127	THR	CA-C-N	6.17	132.80	121.70
4	H	127	THR	C-N-CA	6.17	132.80	121.70
1	A	421	GLY	CA-C-N	-5.93	111.30	121.97

There are no chirality outliers.

There are no planarity outliers.

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	3715	0	3813	43	1
1	B	3663	0	3773	17	0
1	C	3735	0	3834	22	0
2	D	3539	0	3593	44	1
2	E	3472	0	3526	43	0
2	F	3530	0	3587	29	0
3	G	1397	0	1481	21	0
4	H	620	0	614	29	0
5	I	203	0	205	4	0
All	All	23874	0	24426	230	1

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 5.

The worst 5 of 230 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)
4:H:122:ALA:HA	4:H:123:ALA:CB	1.74	1.15
3:G:68:ILE:HB	3:G:69:ILE:HA	1.31	1.09
2:D:89:GLU:HG3	2:D:110:THR:HB	1.29	1.08
2:D:228:ALA:O	2:D:232:VAL:HG13	1.52	1.08
4:H:104:ASP:HA	4:H:105:LEU:HB2	1.31	1.06

All (1) 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:A:48:GLN:CD	2:D:111:LYS:NZ[4_545]	2.17	0.03

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 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%)	469 (97%)	15 (3%)	1 (0%)	43	74
1	B	476/553 (86%)	465 (98%)	10 (2%)	1 (0%)	43	74
1	C	488/553 (88%)	476 (98%)	12 (2%)	0	100	100
2	D	465/528 (88%)	445 (96%)	20 (4%)	0	100	100
2	E	454/528 (86%)	444 (98%)	9 (2%)	1 (0%)	43	74
2	F	464/528 (88%)	450 (97%)	13 (3%)	1 (0%)	43	74
3	G	170/298 (57%)	161 (95%)	8 (5%)	1 (1%)	21	55
4	H	73/168 (44%)	64 (88%)	6 (8%)	3 (4%)	2	21
5	I	23/51 (45%)	22 (96%)	1 (4%)	0	100	100
All	All	3098/3760 (82%)	2996 (97%)	94 (3%)	8 (0%)	36	69

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	H	123	ALA
4	H	128	ARG
4	H	105	LEU
2	E	279	VAL
1	B	35	GLY

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%)	378 (96%)	15 (4%)	29	53
1	B	389/444 (88%)	380 (98%)	9 (2%)	44	63
1	C	396/444 (89%)	384 (97%)	12 (3%)	36	57
2	D	377/417 (90%)	370 (98%)	7 (2%)	50	66
2	E	370/417 (89%)	361 (98%)	9 (2%)	43	63
2	F	376/417 (90%)	362 (96%)	14 (4%)	30	54
3	G	152/251 (61%)	142 (93%)	10 (7%)	15	42
4	H	66/128 (52%)	61 (92%)	5 (8%)	12	38
5	I	19/42 (45%)	19 (100%)	0	100	100
All	All	2538/3004 (84%)	2457 (97%)	81 (3%)	34	56

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	205	VAL
3	G	130	GLU
2	F	237	LEU
2	F	420	VAL
3	G	262	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	221	GLN
2	F	419	GLN
2	E	177	HIS
2	F	282	GLN
3	G	225	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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, 95th 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 ²)	Q < 0.9
1	A	487/553 (88%)	0.61	22 (4%)	38	28	10, 20, 20, 20	4 (0%)
1	B	480/553 (86%)	0.67	16 (3%)	49	34	15, 20, 20, 20	1 (0%)
1	C	490/553 (88%)	0.64	25 (5%)	33	26	20, 20, 20, 20	0
2	D	467/528 (88%)	0.59	16 (3%)	48	34	10, 20, 20, 20	2 (0%)
2	E	458/528 (86%)	0.68	23 (5%)	34	26	12, 20, 20, 20	2 (0%)
2	F	466/528 (88%)	0.64	14 (3%)	52	36	14, 20, 20, 20	3 (0%)
3	G	182/298 (61%)	0.50	1 (0%)	87	71	20, 20, 20, 20	0
4	H	83/168 (49%)	0.57	2 (2%)	59	42	20, 20, 20, 20	0
5	I	25/51 (49%)	0.38	0	100	100	20, 20, 20, 20	0
All	All	3138/3760 (83%)	0.63	119 (3%)	44	32	10, 20, 20, 20	12 (0%)

The worst 5 of 119 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	275	ILE	6.7
1	B	400	VAL	5.4
1	A	501	VAL	5.4
1	A	497	LEU	4.5
1	A	94	ILE	4.5

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 oligosaccharides 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.