



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:07 PM GMT

PDB ID : 1NM8
Title : Structure of Human Carnitine Acetyltransferase: Molecular Basis for Fatty Acyl Transfer
Authors : Wu, D.; Govindasamy, L.; Lian, W.; Gu, Y.; Kukar, T.; Agbandje-McKenna, M.; McKenna, R.
Deposited on : 2003-01-09
Resolution : 1.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at 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.

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

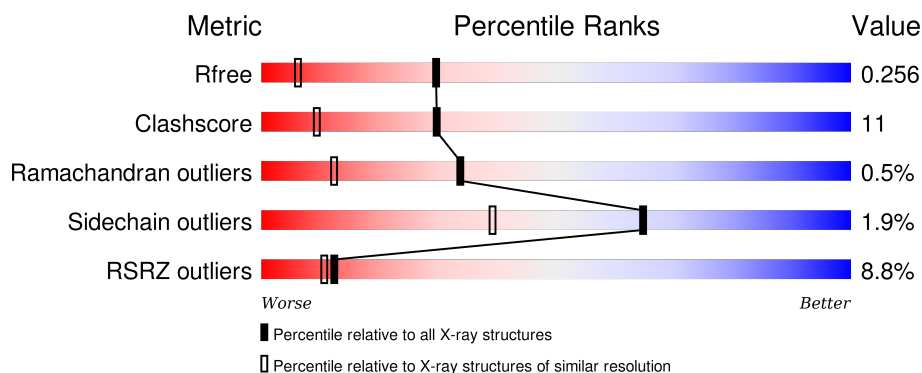
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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}	91344	2475 (1.60-1.60)
Clashscore	102246	2732 (1.60-1.60)
Ramachandran outliers	100387	2654 (1.60-1.60)
Sidechain outliers	100360	2653 (1.60-1.60)
RSRZ outliers	91569	2479 (1.60-1.60)

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 ≥ 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	616	<div> <div>8%</div> <div>77%</div> <div>17%</div> <div>• •</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5186 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 Carnitine O-acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	591	4714	3006	810	872	26	0	0	0

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	CLONING ARTIFACT	UNP P43155
A	2	ARG	-	CLONING ARTIFACT	UNP P43155
A	3	GLY	-	CLONING ARTIFACT	UNP P43155
A	4	SER	-	CLONING ARTIFACT	UNP P43155
A	5	HIS	-	CLONING ARTIFACT	UNP P43155
A	6	HIS	-	CLONING ARTIFACT	UNP P43155
A	7	HIS	-	CLONING ARTIFACT	UNP P43155
A	8	HIS	-	CLONING ARTIFACT	UNP P43155
A	9	HIS	-	CLONING ARTIFACT	UNP P43155
A	10	HIS	-	CLONING ARTIFACT	UNP P43155
A	11	THR	-	CLONING ARTIFACT	UNP P43155
A	12	ASP	-	CLONING ARTIFACT	UNP P43155
A	13	PRO	-	CLONING ARTIFACT	UNP P43155
A	67	GLU	GLY	VARIANT	UNP P43155
A	328	PRO	PHE	VARIANT	UNP P43155
A	496	ASP	GLY	VARIANT	UNP P43155
A	606	ILE	-	CLONING ARTIFACT	UNP P43155
A	607	SER	-	CLONING ARTIFACT	UNP P43155
A	608	GLU	-	CLONING ARTIFACT	UNP P43155
A	609	GLU	-	CLONING ARTIFACT	UNP P43155
A	610	ASP	-	CLONING ARTIFACT	UNP P43155
A	611	LEU	-	CLONING ARTIFACT	UNP P43155
A	612	SER	-	CLONING ARTIFACT	UNP P43155
A	613	LEU	-	CLONING ARTIFACT	UNP P43155
A	614	ILE	-	CLONING ARTIFACT	UNP P43155
A	615	SER	-	CLONING ARTIFACT	UNP P43155
A	616	GLY	-	CLONING ARTIFACT	UNP P43155

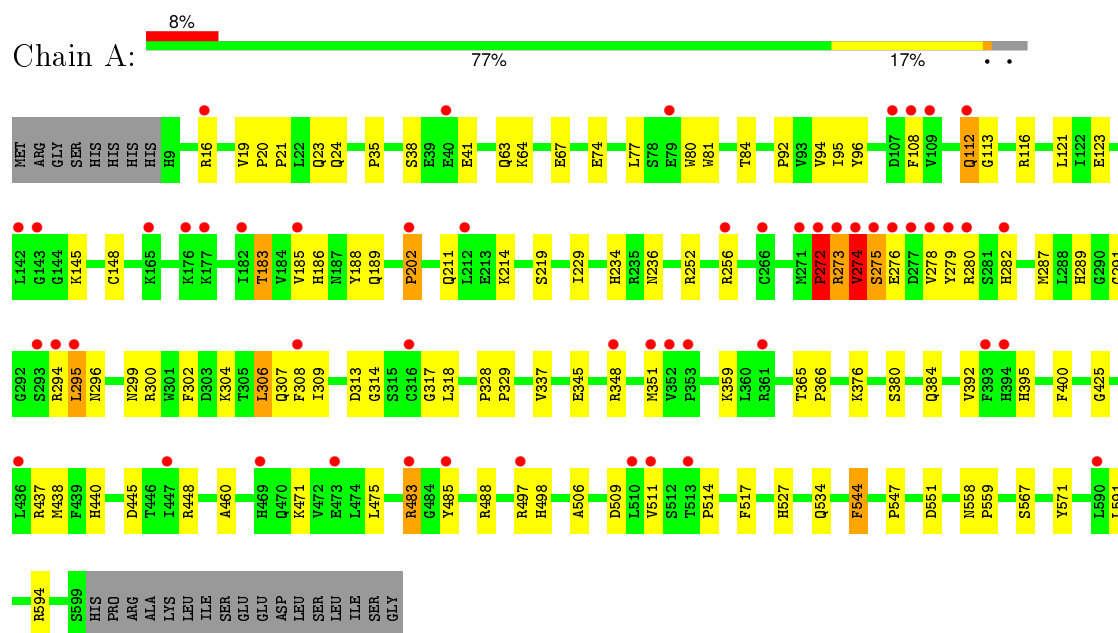
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	472	Total	O	0	0
			472	472		

3 Residue-property plots [i](#)

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: Carnitine O-acetyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	137.50 Å 84.50 Å 57.50 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.60 27.22 – 1.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-1.60) 87.0 (27.22-1.60)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.70 (at 1.60 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.208 , 0.232 0.235 , 0.256	Depositor DCC
R_{free} test set	2816 reflections (3.62%)	DCC
Wilson B-factor (Å ²)	16.0	Xtriage
Anisotropy	0.474	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 41.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 80597 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5186	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.54% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

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	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.51	5/4829 (0.1%)	0.70	11/6550 (0.2%)

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	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	302	PHE	N-CA	-12.39	1.21	1.46
1	A	448	ARG	N-CA	-12.36	1.21	1.46
1	A	35	PRO	CA-CB	9.01	1.71	1.53
1	A	296	ASN	N-CA	7.56	1.61	1.46
1	A	425	GLY	N-CA	-6.34	1.36	1.46

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	296	ASN	N-CA-CB	15.95	139.31	110.60
1	A	202	PRO	CA-N-CD	-8.75	99.25	111.50
1	A	35	PRO	N-CA-CB	-7.46	94.35	103.30
1	A	425	GLY	N-CA-C	-7.38	94.66	113.10
1	A	183	THR	N-CA-CB	6.29	122.25	110.30
1	A	448	ARG	N-CA-CB	6.12	121.61	110.60
1	A	296	ASN	N-CA-C	-6.05	94.67	111.00
1	A	19	VAL	N-CA-C	-5.65	95.73	111.00
1	A	274	VAL	C-N-CA	5.61	135.73	121.70
1	A	272	PRO	CA-N-CD	-5.32	104.05	111.50
1	A	35	PRO	CA-N-CD	5.11	118.86	111.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	295	LEU	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	4714	0	4689	105	2
2	A	472	0	0	8	2
All	All	5186	0	4689	105	2

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 11.

All (105) 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:81:TRP:CD2	1:A:497:ARG:NH2	2.14	1.16
1:A:280:ARG:NH1	1:A:392:VAL:HG21	1.65	1.10
1:A:81:TRP:CE2	1:A:497:ARG:NH2	2.19	1.10
1:A:280:ARG:HH12	1:A:392:VAL:HG21	1.21	1.04
1:A:274:VAL:HB	2:A:1045:HOH:O	0.86	1.03
1:A:278:VAL:HG12	1:A:282:HIS:CD2	1.93	1.03
1:A:278:VAL:HG12	1:A:282:HIS:HD2	1.22	0.95
1:A:287:MET:HE3	1:A:309:ILE:HD12	1.48	0.95
1:A:274:VAL:HG23	1:A:275:SER:H	1.31	0.94
1:A:77:LEU:HD21	1:A:497:ARG:NH1	1.83	0.92
1:A:280:ARG:NH1	1:A:392:VAL:CG2	2.32	0.90
1:A:497:ARG:NH2	2:A:665:HOH:O	2.07	0.87
1:A:289:HIS:HD2	1:A:291:GLY:H	1.23	0.85
1:A:278:VAL:CG1	1:A:282:HIS:CD2	2.63	0.82
1:A:544:PHE:HB3	1:A:567:SER:OG	1.81	0.80
1:A:274:VAL:HG23	1:A:275:SER:N	1.97	0.80
1:A:291:GLY:C	1:A:295:LEU:HD12	2.02	0.80
1:A:234:HIS:HE1	1:A:236:ASN:HD22	1.30	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:VAL:O	1:A:278:VAL:HG12	1.84	0.77
1:A:514:PRO:HG2	1:A:517:PHE:CD2	2.20	0.77
1:A:287:MET:HE1	1:A:309:ILE:HB	1.67	0.77
1:A:483:ARG:HG3	1:A:483:ARG:O	1.85	0.74
1:A:145:LYS:HB2	1:A:438:MET:HE2	1.70	0.72
1:A:81:TRP:CE3	1:A:497:ARG:CZ	2.74	0.71
1:A:280:ARG:HH12	1:A:392:VAL:CG2	2.00	0.70
1:A:234:HIS:CE1	1:A:236:ASN:HD22	2.09	0.70
1:A:328:PRO:HB2	1:A:329:PRO:HD3	1.73	0.70
1:A:16:ARG:HD3	2:A:674:HOH:O	1.90	0.70
1:A:252:ARG:O	1:A:256:ARG:HG3	1.91	0.70
1:A:289:HIS:CD2	1:A:291:GLY:H	2.09	0.69
1:A:274:VAL:CG2	1:A:275:SER:H	2.04	0.67
1:A:280:ARG:HH11	1:A:392:VAL:CG2	2.08	0.67
1:A:20:PRO:HG2	1:A:498:HIS:ND1	2.11	0.66
1:A:514:PRO:HG2	1:A:517:PHE:HD2	1.59	0.66
1:A:287:MET:CE	1:A:309:ILE:HD12	2.23	0.64
1:A:278:VAL:CG1	1:A:282:HIS:HD2	2.01	0.63
1:A:81:TRP:CD2	1:A:497:ARG:CZ	2.81	0.62
1:A:534:GLN:HE21	1:A:559:PRO:HG2	1.64	0.61
1:A:272:PRO:O	1:A:273:ARG:C	2.38	0.60
1:A:299:ASN:C	1:A:300:ARG:HG2	2.22	0.59
1:A:278:VAL:CG1	1:A:278:VAL:O	2.53	0.56
1:A:64:LYS:HD3	1:A:64:LYS:O	2.05	0.56
1:A:280:ARG:HH11	1:A:392:VAL:HG23	1.70	0.56
1:A:274:VAL:CB	2:A:1045:HOH:O	1.74	0.56
1:A:64:LYS:HD3	1:A:64:LYS:C	2.26	0.55
1:A:94:VAL:HG12	1:A:95:ILE:HG13	1.88	0.55
1:A:81:TRP:CE3	1:A:497:ARG:NH1	2.76	0.54
1:A:188:TYR:H	1:A:299:ASN:HD22	1.55	0.54
1:A:189:GLN:HE21	1:A:359:LYS:NZ	2.06	0.54
1:A:186:HIS:HE1	2:A:629:HOH:O	1.91	0.53
1:A:527:HIS:HE1	1:A:551:ASP:OD1	1.90	0.53
1:A:112:GLN:O	1:A:116:ARG:HG2	2.08	0.53
1:A:291:GLY:CA	1:A:295:LEU:HD12	2.38	0.53
1:A:23:GLN:HG3	2:A:700:HOH:O	2.09	0.53
1:A:74:GLU:OE1	1:A:440:HIS:HE1	1.93	0.52
1:A:485:TYR:HD1	1:A:488:ARG:HH22	1.57	0.52
1:A:291:GLY:O	1:A:295:LEU:HD12	2.09	0.51
1:A:81:TRP:CE3	1:A:497:ARG:NH2	2.71	0.51
1:A:80:TRP:O	1:A:84:THR:HG23	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:TYR:H	1:A:299:ASN:ND2	2.09	0.50
1:A:287:MET:HE2	1:A:318:LEU:N	2.27	0.50
1:A:345:GLU:OE2	1:A:348:ARG:HG2	2.11	0.50
1:A:185:VAL:HG22	1:A:299:ASN:ND2	2.26	0.50
1:A:291:GLY:HA3	1:A:295:LEU:HD12	1.93	0.49
1:A:287:MET:HE3	1:A:309:ILE:CD1	2.33	0.49
1:A:123:GLU:HG2	2:A:1018:HOH:O	2.13	0.49
1:A:547:PRO:HD2	1:A:571:TYR:CZ	2.48	0.49
1:A:365:THR:HB	1:A:366:PRO:HD2	1.95	0.48
1:A:211:GLN:HE22	1:A:214:LYS:NZ	2.11	0.48
1:A:299:ASN:O	1:A:300:ARG:HG2	2.13	0.48
1:A:21:PRO:HG2	1:A:24:GLN:CB	2.44	0.48
1:A:108:PHE:CZ	1:A:314:GLY:HA2	2.49	0.48
1:A:112:GLN:HE21	1:A:113:GLY:N	2.10	0.48
1:A:287:MET:CE	1:A:309:ILE:HB	2.42	0.48
1:A:186:HIS:HD2	1:A:219:SER:OG	1.96	0.47
1:A:306:LEU:HD23	1:A:307:GLN:N	2.29	0.47
1:A:279:TYR:OH	1:A:313:ASP:OD2	2.31	0.47
1:A:318:LEU:C	1:A:318:LEU:HD12	2.35	0.47
1:A:92:PRO:HG2	1:A:96:TYR:CE2	2.50	0.47
1:A:148:CYS:O	1:A:437:ARG:HD2	2.15	0.46
1:A:279:TYR:HE2	2:A:873:HOH:O	1.98	0.46
1:A:63:GLN:O	1:A:67:GLU:HG3	2.15	0.46
1:A:395:HIS:CG	1:A:591:LEU:HD21	2.52	0.45
1:A:229:ILE:HD13	1:A:376:LYS:HG2	1.99	0.45
1:A:475:LEU:HD23	1:A:475:LEU:C	2.37	0.45
1:A:506:ALA:HB1	1:A:511:VAL:HG23	1.98	0.45
1:A:460:ALA:O	1:A:471:LYS:HE2	2.16	0.44
1:A:400:PHE:CZ	1:A:594:ARG:HG3	2.52	0.44
1:A:81:TRP:CZ2	1:A:497:ARG:NH2	2.81	0.44
1:A:38:SER:OG	1:A:41:GLU:HG3	2.17	0.44
1:A:121:LEU:HD12	1:A:337:VAL:HG12	2.00	0.43
1:A:485:TYR:CD1	1:A:488:ARG:NH2	2.85	0.43
1:A:112:GLN:C	1:A:112:GLN:NE2	2.72	0.43
1:A:21:PRO:HG2	1:A:24:GLN:HB3	2.01	0.43
1:A:304:LYS:HD2	1:A:304:LYS:HA	1.77	0.43
1:A:306:LEU:HD21	1:A:308:PHE:CE1	2.53	0.43
1:A:294:ARG:O	1:A:294:ARG:HG3	2.17	0.43
1:A:287:MET:CE	1:A:318:LEU:N	2.82	0.42
1:A:287:MET:HE1	1:A:317:GLY:C	2.40	0.42
1:A:77:LEU:HD21	1:A:497:ARG:HH11	1.77	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:LYS:HD2	1:A:438:MET:CE	2.49	0.42
1:A:380:SER:HB3	1:A:384:GLN:HE22	1.85	0.42
1:A:445:ASP:OD1	1:A:497:ARG:HG2	2.19	0.41
1:A:92:PRO:HG2	1:A:96:TYR:CD2	2.55	0.41
1:A:445:ASP:CG	1:A:497:ARG:HG2	2.42	0.40

All (2) 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:273:ARG:NH2	2:A:933:HOH:O[2_565]	1.74	0.46
1:A:351:MET:SD	2:A:880:HOH:O[4_556]	1.78	0.42

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	589/616 (96%)	574 (98%)	12 (2%)	3 (0%)	34 12

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	274	VAL
1	A	276	GLU
1	A	273	ARG

5.3.2 Protein sidechains [i](#)

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	521/543 (96%)	511 (98%)	10 (2%)	65	39

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	112	GLN
1	A	183	THR
1	A	202	PRO
1	A	272	PRO
1	A	275	SER
1	A	306	LEU
1	A	483	ARG
1	A	509	ASP
1	A	544	PHE
1	A	558	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	91	GLN
1	A	166	GLN
1	A	186	HIS
1	A	189	GLN
1	A	211	GLN
1	A	236	ASN
1	A	282	HIS
1	A	289	HIS
1	A	299	ASN
1	A	377	GLN
1	A	384	GLN
1	A	440	HIS
1	A	470	GLN
1	A	527	HIS
1	A	529	HIS
1	A	534	GLN
1	A	558	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	591/616 (95%)	0.89	52 (8%) 12 11	9, 15, 27, 44	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	274	VAL	13.0
1	A	279	TYR	11.1
1	A	273	ARG	8.2
1	A	351	MET	6.9
1	A	176	LYS	6.7
1	A	278	VAL	6.3
1	A	276	GLU	6.2
1	A	277	ASP	6.0
1	A	294	ARG	4.9
1	A	109	VAL	4.5
1	A	275	SER	4.3
1	A	511	VAL	4.1
1	A	177	LYS	4.0
1	A	280	ARG	4.0
1	A	483	ARG	3.9
1	A	272	PRO	3.8
1	A	295	LEU	3.8
1	A	107	ASP	3.7
1	A	40	GLU	3.7
1	A	143	GLY	3.6
1	A	293	SER	3.6
1	A	485	TYR	3.2
1	A	16	ARG	3.2
1	A	271	MET	3.1
1	A	182	ILE	3.0
1	A	497	ARG	2.9
1	A	256	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	352	VAL	2.8
1	A	202	PRO	2.7
1	A	282	HIS	2.7
1	A	316	CYS	2.6
1	A	353	PRO	2.6
1	A	348	ARG	2.6
1	A	112	GLN	2.6
1	A	308	PHE	2.5
1	A	165	LYS	2.5
1	A	510	LEU	2.4
1	A	142	LEU	2.3
1	A	469	HIS	2.3
1	A	79	GLU	2.3
1	A	361	ARG	2.3
1	A	212	LEU	2.2
1	A	447	ILE	2.2
1	A	185	VAL	2.2
1	A	108	PHE	2.2
1	A	393	PHE	2.2
1	A	473	GLU	2.1
1	A	394	HIS	2.1
1	A	513	THR	2.1
1	A	436	LEU	2.1
1	A	590	LEU	2.1
1	A	266	CYS	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.