



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 2, 2026 – 10:57 PM JST

PDB ID : 9V37 / pdb_00009v37
Title : crystal structure of ACAT2
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Deposited on : 2025-05-21
Resolution : 2.17 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

<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

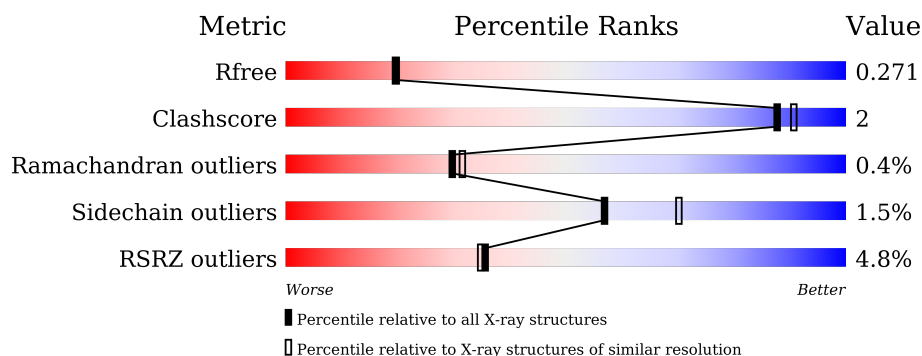
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.17 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	8975 (2.20-2.16)
Clashscore	190562	9786 (2.20-2.16)
Ramachandran outliers	187476	9664 (2.20-2.16)
Sidechain outliers	187428	9664 (2.20-2.16)
RSRZ outliers	180081	8979 (2.20-2.16)

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	405	<div> <div>5%</div> <div>90%</div> <div>6%</div> </div>
1	B	405	<div> <div>6%</div> <div>90%</div> <div>7%</div> </div>
1	C	405	<div> <div>3%</div> <div>92%</div> <div>5%</div> </div>
1	D	405	<div> <div>4%</div> <div>91%</div> <div>6%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11620 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 Acetyl-CoA acetyltransferase, cytosolic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	394	Total	C	N	O	S	0	0	0
			2870	1801	505	544	20			
1	C	394	Total	C	N	O	S	0	0	0
			2870	1801	505	544	20			
1	A	394	Total	C	N	O	S	0	0	0
			2870	1801	505	544	20			
1	B	394	Total	C	N	O	S	0	0	0
			2870	1801	505	544	20			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	2	ASP	ASN	conflict	UNP Q9BWD1
D	398	LEU	-	expression tag	UNP Q9BWD1
D	399	GLU	-	expression tag	UNP Q9BWD1
D	400	HIS	-	expression tag	UNP Q9BWD1
D	401	HIS	-	expression tag	UNP Q9BWD1
D	402	HIS	-	expression tag	UNP Q9BWD1
D	403	HIS	-	expression tag	UNP Q9BWD1
D	404	HIS	-	expression tag	UNP Q9BWD1
D	405	HIS	-	expression tag	UNP Q9BWD1
C	2	ASP	ASN	conflict	UNP Q9BWD1
C	398	LEU	-	expression tag	UNP Q9BWD1
C	399	GLU	-	expression tag	UNP Q9BWD1
C	400	HIS	-	expression tag	UNP Q9BWD1
C	401	HIS	-	expression tag	UNP Q9BWD1
C	402	HIS	-	expression tag	UNP Q9BWD1
C	403	HIS	-	expression tag	UNP Q9BWD1
C	404	HIS	-	expression tag	UNP Q9BWD1
C	405	HIS	-	expression tag	UNP Q9BWD1
A	2	ASP	ASN	conflict	UNP Q9BWD1
A	398	LEU	-	expression tag	UNP Q9BWD1
A	399	GLU	-	expression tag	UNP Q9BWD1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	400	HIS	-	expression tag	UNP Q9BWD1
A	401	HIS	-	expression tag	UNP Q9BWD1
A	402	HIS	-	expression tag	UNP Q9BWD1
A	403	HIS	-	expression tag	UNP Q9BWD1
A	404	HIS	-	expression tag	UNP Q9BWD1
A	405	HIS	-	expression tag	UNP Q9BWD1
B	2	ASP	ASN	conflict	UNP Q9BWD1
B	398	LEU	-	expression tag	UNP Q9BWD1
B	399	GLU	-	expression tag	UNP Q9BWD1
B	400	HIS	-	expression tag	UNP Q9BWD1
B	401	HIS	-	expression tag	UNP Q9BWD1
B	402	HIS	-	expression tag	UNP Q9BWD1
B	403	HIS	-	expression tag	UNP Q9BWD1
B	404	HIS	-	expression tag	UNP Q9BWD1
B	405	HIS	-	expression tag	UNP Q9BWD1

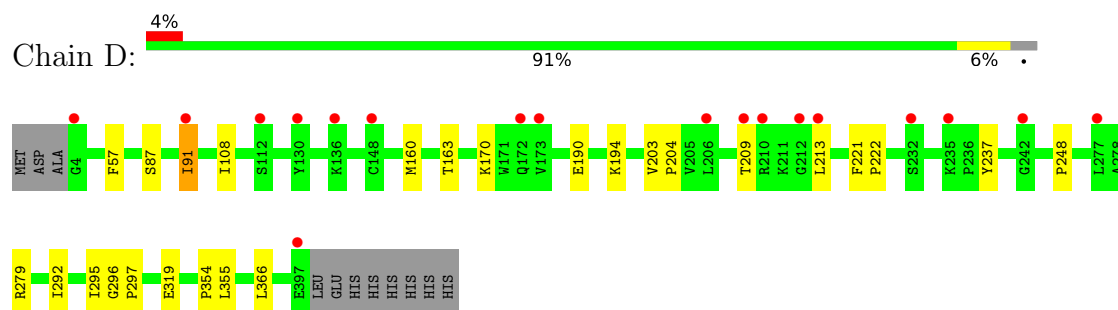
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	46	Total O 46 46	0	0
2	C	37	Total O 37 37	0	0
2	A	26	Total O 26 26	0	0
2	B	31	Total O 31 31	0	0

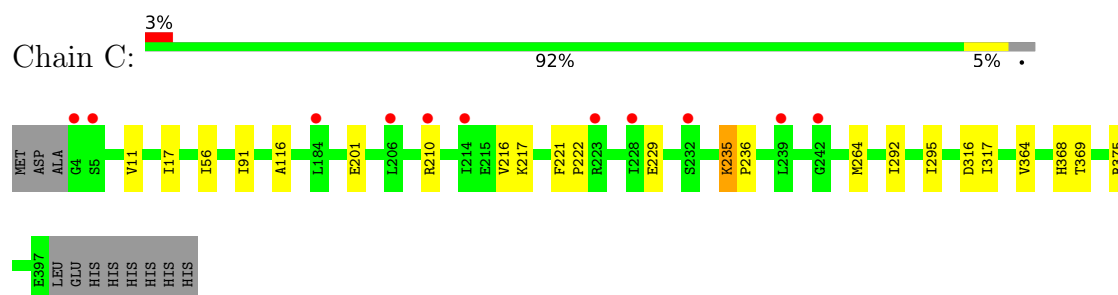
3 Residue-property plots [i](#)

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.

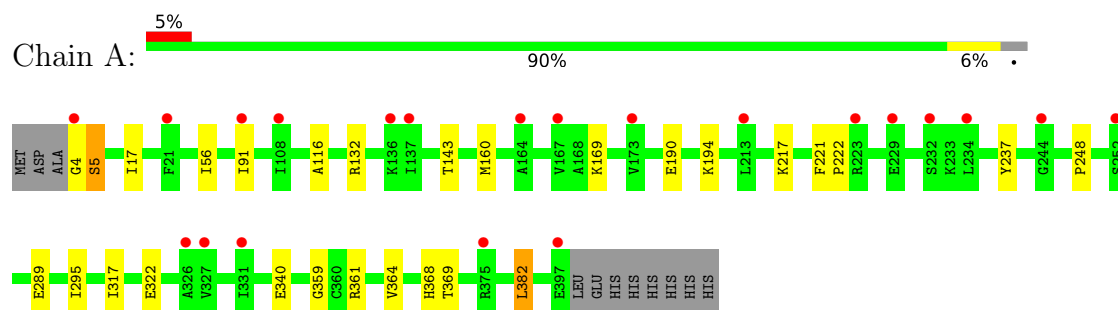
- Molecule 1: Acetyl-CoA acetyltransferase, cytosolic



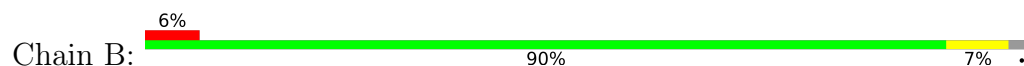
- Molecule 1: Acetyl-CoA acetyltransferase, cytosolic

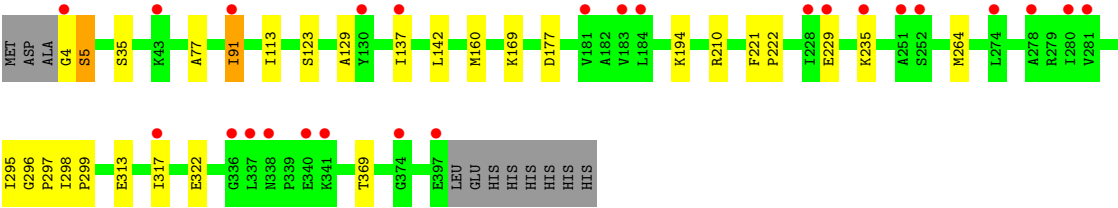


- Molecule 1: Acetyl-CoA acetyltransferase, cytosolic



- Molecule 1: Acetyl-CoA acetyltransferase, cytosolic





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	113.59Å 127.50Å 131.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.27 – 2.17 28.27 – 2.17	Depositor EDS
% Data completeness (in resolution range)	92.0 (28.27-2.17) 92.0 (28.27-2.17)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 2.18Å)	Xtriage
Refinement program	REFMAC 5.8.0430	Depositor
R, R_{free}	0.226 , 0.268 0.235 , 0.271	Depositor DCC
R_{free} test set	4872 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	43.7	Xtriage
Anisotropy	0.140	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 26.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11620	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 27.87 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.0381e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.52	0/2914	0.98	3/3950 (0.1%)
1	B	0.51	0/2914	0.98	2/3950 (0.1%)
1	C	0.52	0/2914	0.95	0/3950
1	D	0.51	0/2914	0.97	0/3950
All	All	0.51	0/11656	0.97	5/15800 (0.0%)

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	D	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	322	GLU	CB-CA-C	-7.02	101.98	111.88
1	B	194	LYS	CB-CA-C	-6.17	100.94	110.81
1	B	322	GLU	CB-CA-C	-5.59	103.80	112.07
1	A	289	GLU	CB-CA-C	5.18	118.22	109.67
1	A	143	THR	CA-CB-OG1	-5.11	101.93	109.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	279	ARG	Sidechain

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	2870	0	2940	13	0
1	B	2870	0	2940	12	0
1	C	2870	0	2940	11	0
1	D	2870	0	2940	11	0
2	A	26	0	0	0	0
2	B	31	0	0	0	0
2	C	37	0	0	0	0
2	D	46	0	0	1	0
All	All	11620	0	11760	46	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.

All (46) 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:C:292:ILE:O	1:C:295:ILE:HG13	1.99	0.62
1:C:235:LYS:HD2	1:C:236:PRO:HD2	1.83	0.61
1:D:292:ILE:O	1:D:295:ILE:HG13	2.02	0.60
1:B:129:ALA:HB2	1:B:142:LEU:HD23	1.83	0.59
1:B:317:ILE:HD13	1:B:369:THR:HG22	1.87	0.56
1:A:317:ILE:HD13	1:A:369:THR:HG22	1.88	0.55
1:B:4:GLY:O	1:B:5:SER:CB	2.55	0.55
1:C:221:PHE:N	1:C:222:PRO:CD	2.70	0.54
1:C:17:ILE:HG12	1:C:216:VAL:HG12	1.89	0.54
1:A:221:PHE:N	1:A:222:PRO:CD	2.73	0.50
1:A:132:ARG:HD2	1:B:123:SER:O	2.12	0.50
1:B:313:GLU:N	1:B:313:GLU:OE2	2.45	0.50
1:B:221:PHE:N	1:B:222:PRO:CD	2.75	0.50
1:D:221:PHE:N	1:D:222:PRO:CD	2.76	0.49
1:A:17:ILE:HG21	1:A:217:LYS:C	2.39	0.48
1:C:11:VAL:HG21	1:C:264:MET:HE3	1.95	0.48
1:B:298:ILE:HB	1:B:299:PRO:HD3	1.95	0.48
1:A:364:VAL:O	1:A:368:HIS:HD2	1.98	0.46
1:B:160:MET:HA	1:B:160:MET:HE2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:237:TYR:HB2	1:D:248:PRO:HD3	1.96	0.46
1:D:190:GLU:O	1:D:194:LYS:HG2	2.16	0.46
1:A:190:GLU:O	1:A:194:LYS:HG2	2.16	0.46
1:C:316:ASP:C	1:C:317:ILE:HG13	2.42	0.44
1:A:359:GLY:HA2	1:A:382:LEU:HD21	1.99	0.44
1:C:317:ILE:HD13	1:C:369:THR:HG22	1.98	0.44
1:B:296:GLY:N	1:B:297:PRO:CD	2.80	0.43
1:A:4:GLY:O	1:A:5:SER:HB3	2.18	0.43
1:D:296:GLY:N	1:D:297:PRO:CD	2.81	0.43
1:C:17:ILE:HG21	1:C:217:LYS:C	2.44	0.43
1:D:354:PRO:O	1:D:355:LEU:C	2.62	0.42
1:A:295:ILE:HD12	1:A:295:ILE:C	2.44	0.42
1:B:113:ILE:HG12	1:B:264:MET:HE2	2.01	0.42
1:C:364:VAL:O	1:C:368:HIS:HD2	2.02	0.42
1:B:35:SER:HA	1:B:77:ALA:HB2	2.02	0.42
1:D:203:VAL:HA	1:D:204:PRO:HD3	1.95	0.42
1:B:295:ILE:HB	1:B:298:ILE:HD12	2.01	0.42
1:C:56:ILE:O	1:C:116:ALA:HA	2.20	0.41
1:D:319:GLU:HG3	1:D:366:LEU:HB2	2.02	0.41
1:D:170:LYS:HE3	2:D:538:HOH:O	2.20	0.41
1:D:57:PHE:O	1:D:87:SER:HA	2.20	0.41
1:C:201:GLU:HB3	1:C:368:HIS:CD2	2.56	0.41
1:A:56:ILE:O	1:A:116:ALA:HA	2.21	0.41
1:A:361:ARG:O	1:A:361:ARG:HD2	2.21	0.41
1:D:160:MET:O	1:D:163:THR:OG1	2.36	0.40
1:A:160:MET:HA	1:A:160:MET:HE2	2.02	0.40
1:A:237:TYR:HB2	1:A:248:PRO:HD3	2.02	0.40

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 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	392/405 (97%)	377 (96%)	13 (3%)	2 (0%)	24	25
1	B	392/405 (97%)	375 (96%)	15 (4%)	2 (0%)	24	25
1	C	392/405 (97%)	379 (97%)	12 (3%)	1 (0%)	36	39
1	D	392/405 (97%)	378 (96%)	13 (3%)	1 (0%)	36	39
All	All	1568/1620 (97%)	1509 (96%)	53 (3%)	6 (0%)	30	31

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	5	SER
1	C	91	ILE
1	A	5	SER
1	A	91	ILE
1	B	91	ILE
1	D	91	ILE

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	306/316 (97%)	303 (99%)	3 (1%)	68	79
1	B	306/316 (97%)	299 (98%)	7 (2%)	44	56
1	C	306/316 (97%)	302 (99%)	4 (1%)	61	74
1	D	306/316 (97%)	302 (99%)	4 (1%)	61	74
All	All	1224/1264 (97%)	1206 (98%)	18 (2%)	57	70

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	91	ILE
1	D	108	ILE
1	D	209	THR
1	D	213	LEU
1	C	210	ARG

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Mol	Chain	Res	Type
1	C	229	GLU
1	C	235	LYS
1	C	375	ARG
1	A	169	LYS
1	A	340	GLU
1	A	382	LEU
1	B	91	ILE
1	B	137	ILE
1	B	169	LYS
1	B	177	ASP
1	B	210	ARG
1	B	229	GLU
1	B	235	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	22	ASN
1	C	368	HIS
1	A	59	HIS
1	A	67	GLN
1	A	368	HIS
1	B	172	GLN
1	B	187	ASN
1	B	395	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	394/405 (97%)	0.69	21 (5%)	32 31	35, 46, 71, 111	0
1	B	394/405 (97%)	0.81	25 (6%)	26 25	36, 49, 73, 115	0
1	C	394/405 (97%)	0.62	11 (2%)	55 54	34, 45, 70, 124	0
1	D	394/405 (97%)	0.67	18 (4%)	37 36	34, 46, 70, 113	0
All	All	1576/1620 (97%)	0.70	75 (4%)	35 35	34, 46, 71, 124	0

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	4	GLY	5.2
1	D	213	LEU	3.8
1	B	4	GLY	3.7
1	D	172	GLN	3.6
1	D	4	GLY	3.6
1	B	91	ILE	3.6
1	D	173	VAL	3.1
1	B	130	TYR	3.0
1	B	137	ILE	3.0
1	C	206	LEU	2.9
1	D	397	GLU	2.9
1	D	91	ILE	2.9
1	A	326	ALA	2.9
1	A	136	LYS	2.8
1	D	235	LYS	2.8
1	D	136	LYS	2.8
1	B	184	LEU	2.6
1	C	5	SER	2.6
1	A	223	ARG	2.6
1	C	232	SER	2.6
1	A	21	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	234	LEU	2.5
1	A	137	ILE	2.5
1	A	232	SER	2.5
1	B	274	LEU	2.4
1	A	252	SER	2.4
1	C	184	LEU	2.4
1	D	212	GLY	2.4
1	A	91	ILE	2.4
1	B	43	LYS	2.4
1	B	341	LYS	2.4
1	B	251	ALA	2.3
1	C	214	ILE	2.3
1	B	336	GLY	2.3
1	B	229	GLU	2.3
1	D	148	CYS	2.3
1	B	338	ASN	2.3
1	D	242	GLY	2.3
1	D	232	SER	2.3
1	A	173	VAL	2.3
1	C	223	ARG	2.3
1	B	235	LYS	2.3
1	B	278	ALA	2.3
1	D	206	LEU	2.3
1	B	397	GLU	2.2
1	A	375	ARG	2.2
1	D	112	SER	2.2
1	B	228	ILE	2.2
1	A	327	VAL	2.2
1	B	181	VAL	2.2
1	B	281	VAL	2.2
1	A	213	LEU	2.2
1	B	337	LEU	2.2
1	D	210	ARG	2.2
1	C	210	ARG	2.2
1	B	252	SER	2.2
1	D	130	TYR	2.2
1	A	397	GLU	2.1
1	B	183	VAL	2.1
1	C	242	GLY	2.1
1	D	277	LEU	2.1
1	A	108	ILE	2.1
1	A	331	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	4	GLY	2.1
1	A	244	GLY	2.1
1	B	374	GLY	2.1
1	A	167	VAL	2.1
1	A	164	ALA	2.1
1	A	229	GLU	2.1
1	B	280	ILE	2.1
1	C	228	ILE	2.0
1	B	317	ILE	2.0
1	B	340	GLU	2.0
1	C	239	LEU	2.0
1	D	209	THR	2.0

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.