



Full wwPDB X-ray Structure Validation Report

Mar 31, 2014 – 02:27 PM BST

PDB ID : 4J0E
Title : Crystal structure of 3-hydroxyacyl-CoA dehydrogenase from *Caenorhabditis elegans* in P1 space group
Authors : Xu, Y.; Sun, F.; Zhai, Y.
Deposited on : 2013-01-30
Resolution : 1.60 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

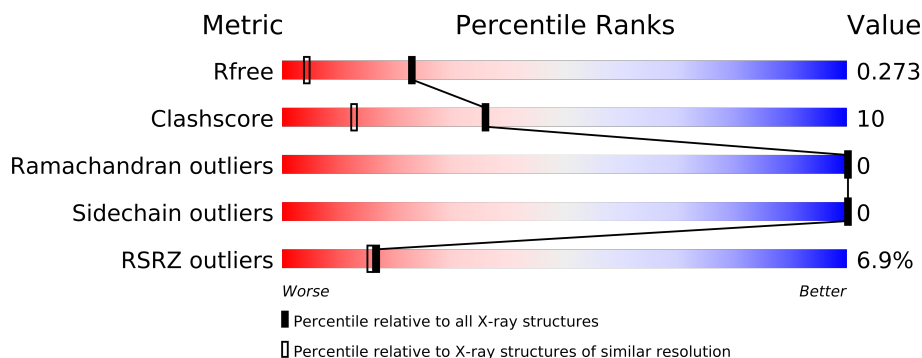
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable23004
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable23004

1 Overall quality at a glance

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}	66092	1872 (1.60-1.60)
Clashscore	79885	2199 (1.60-1.60)
Ramachandran outliers	78287	2126 (1.60-1.60)
Sidechain outliers	78261	2125 (1.60-1.60)
RSRZ outliers	66119	1872 (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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	320	
1	B	320	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4692 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Probable 3-hydroxyacyl-CoA dehydrogenase F54C8.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	296	Total	C	N	O	S	41	0	0
			2257	1429	377	435	16			
1	B	283	Total	C	N	O	S	34	3	0
			2171	1380	359	416	16			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	EXPRESSION TAG	UNP P34439
A	-1	GLY	-	EXPRESSION TAG	UNP P34439
A	0	SER	-	EXPRESSION TAG	UNP P34439
A	299	GLU	-	EXPRESSION TAG	UNP P34439
A	300	PHE	-	EXPRESSION TAG	UNP P34439
A	301	GLY	-	EXPRESSION TAG	UNP P34439
A	302	THR	-	EXPRESSION TAG	UNP P34439
A	303	SER	-	EXPRESSION TAG	UNP P34439
A	304	SER	-	EXPRESSION TAG	UNP P34439
A	305	THR	-	EXPRESSION TAG	UNP P34439
A	306	GLY	-	EXPRESSION TAG	UNP P34439
A	307	SER	-	EXPRESSION TAG	UNP P34439
A	308	SER	-	EXPRESSION TAG	UNP P34439
A	309	GLY	-	EXPRESSION TAG	UNP P34439
A	310	SER	-	EXPRESSION TAG	UNP P34439
A	311	SER	-	EXPRESSION TAG	UNP P34439
A	312	LEU	-	EXPRESSION TAG	UNP P34439
A	313	GLU	-	EXPRESSION TAG	UNP P34439
A	314	VAL	-	EXPRESSION TAG	UNP P34439
A	315	LEU	-	EXPRESSION TAG	UNP P34439
A	316	PHE	-	EXPRESSION TAG	UNP P34439
A	317	GLN	-	EXPRESSION TAG	UNP P34439
B	-2	MET	-	EXPRESSION TAG	UNP P34439
B	-1	GLY	-	EXPRESSION TAG	UNP P34439
B	0	SER	-	EXPRESSION TAG	UNP P34439

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Chain	Residue	Modelled	Actual	Comment	Reference
B	299	GLU	-	EXPRESSION TAG	UNP P34439
B	300	PHE	-	EXPRESSION TAG	UNP P34439
B	301	GLY	-	EXPRESSION TAG	UNP P34439
B	302	THR	-	EXPRESSION TAG	UNP P34439
B	303	SER	-	EXPRESSION TAG	UNP P34439
B	304	SER	-	EXPRESSION TAG	UNP P34439
B	305	THR	-	EXPRESSION TAG	UNP P34439
B	306	GLY	-	EXPRESSION TAG	UNP P34439
B	307	SER	-	EXPRESSION TAG	UNP P34439
B	308	SER	-	EXPRESSION TAG	UNP P34439
B	309	GLY	-	EXPRESSION TAG	UNP P34439
B	310	SER	-	EXPRESSION TAG	UNP P34439
B	311	SER	-	EXPRESSION TAG	UNP P34439
B	312	LEU	-	EXPRESSION TAG	UNP P34439
B	313	GLU	-	EXPRESSION TAG	UNP P34439
B	314	VAL	-	EXPRESSION TAG	UNP P34439
B	315	LEU	-	EXPRESSION TAG	UNP P34439
B	316	PHE	-	EXPRESSION TAG	UNP P34439
B	317	GLN	-	EXPRESSION TAG	UNP P34439

- Molecule 2 is water.

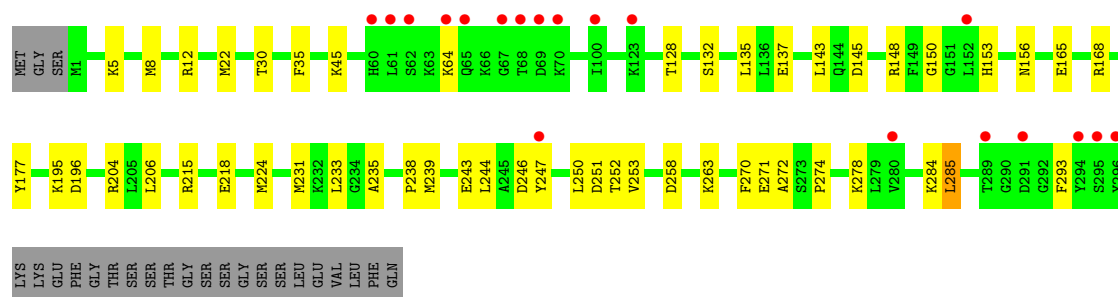
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	153	Total O 153 153	0	0
2	B	111	Total O 111 111	0	0

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.

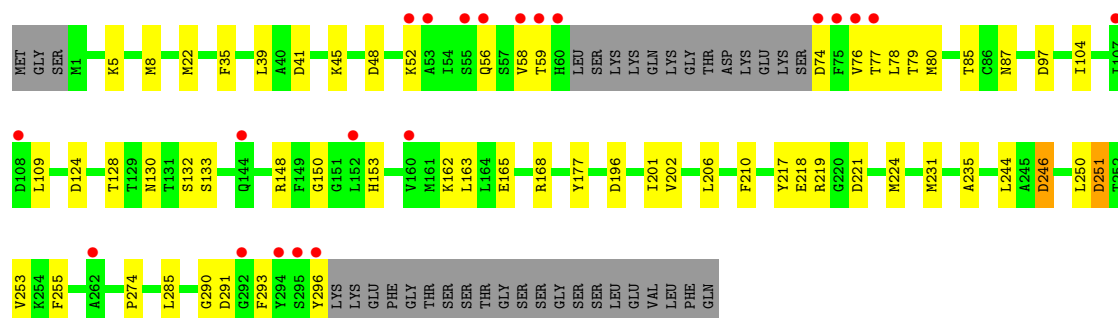
- Molecule 1: Probable 3-hydroxyacyl-CoA dehydrogenase F54C8.1

Chain A: 



- Molecule 1: Probable 3-hydroxyacyl-CoA dehydrogenase F54C8.1

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	55.71Å 55.22Å 56.07Å 80.45° 75.58° 72.42°	Depositor
Resolution (Å)	54.04 – 1.60 28.90 – 1.60	Depositor EDS
% Data completeness (in resolution range)	95.2 (54.04-1.60) 95.2 (28.90-1.60)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.88 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.223 , 0.270 0.226 , 0.273	Depositor DCC
R_{free} test set	3858 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	27.7	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.46 , 52.9	EDS
Estimated twinning fraction	0.009 for -h,-l,-k	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 77063 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4692	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.45% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	1.19	1/2292 (0.0%)	1.21	14/3087 (0.5%)
1	B	1.16	1/2215 (0.0%)	1.18	8/2987 (0.3%)
All	All	1.17	2/4507 (0.0%)	1.20	22/6074 (0.4%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	45	LYS	CA-CB	-5.14	1.42	1.53
1	A	284	LYS	CB-CG	5.02	1.66	1.52

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	246	ASP	CB-CG-OD1	7.24	124.82	118.30
1	A	196	ASP	CB-CG-OD1	6.14	123.83	118.30
1	A	278	LYS	CD-CE-NZ	-5.71	98.56	111.70
1	A	143	LEU	CB-CG-CD1	-5.69	101.33	111.00
1	B	231	MET	CG-SD-CE	-5.66	91.15	100.20
1	B	196	ASP	CB-CG-OD2	5.62	123.36	118.30
1	A	12	ARG	NE-CZ-NH2	-5.61	117.50	120.30
1	A	195	LYS	CD-CE-NZ	5.58	124.53	111.70
1	B	251	ASP	CB-CG-OD1	5.57	123.31	118.30
1	B	246	ASP	CB-CG-OD1	5.39	123.15	118.30
1	A	204	ARG	NE-CZ-NH2	-5.37	117.62	120.30
1	A	45	LYS	CG-CD-CE	-5.34	95.88	111.90
1	B	48	ASP	CB-CG-OD1	5.33	123.09	118.30
1	A	64	LYS	CA-CB-CG	5.24	124.92	113.40
1	A	258	ASP	CB-CG-OD1	5.19	122.97	118.30
1	B	221	ASP	CB-CG-OD2	5.19	122.97	118.30
1	A	270	PHE	CB-CG-CD1	-5.19	117.17	120.80
1	A	215	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	A	12	ARG	CD-NE-CZ	-5.17	116.37	123.60
1	B	219	ARG	NE-CZ-NH2	-5.16	117.72	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	97	ASP	CB-CG-OD2	5.15	122.93	118.30
1	A	285	LEU	CB-CG-CD2	5.06	119.61	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2257	0	2284	36	0
1	B	2171	0	2189	64	0
2	A	153	0	0	2	0
2	B	111	0	0	1	0
All	All	4692	0	4473	90	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 10.

All (90) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:210[B]:PHE:HE1	1:B:244:LEU:HD23	1.19	1.06
1:A:271:GLU:HB2	2:A:428:HOH:O	1.59	1.01
1:B:104:ILE:HG13	1:B:109:LEU:HD23	1.53	0.90
1:B:210[B]:PHE:CE1	1:B:244:LEU:HD23	2.05	0.90
1:B:224:MET:CE	1:B:293:PHE:HB3	2.04	0.87
1:B:104:ILE:HD11	1:B:109:LEU:HD22	1.55	0.86
1:B:153:HIS:HD2	1:B:165:GLU:OE1	1.58	0.85
1:B:290:GLY:O	1:B:291:ASP:OD1	1.97	0.82
1:B:104:ILE:CG1	1:B:109:LEU:CD2	2.59	0.81
1:B:104:ILE:HG13	1:B:109:LEU:CD2	2.11	0.80
1:B:224:MET:HE3	1:B:293:PHE:HB3	1.64	0.79
1:B:41:ASP:O	1:B:87:ASN:HA	1.83	0.79
1:A:231:MET:CE	1:B:201:ILE:HG22	2.16	0.75
1:A:231:MET:HE1	1:B:201:ILE:HG22	1.69	0.75

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:153:HIS:CD2	1:B:165:GLU:OE1	2.41	0.73
1:A:153:HIS:HD2	1:A:165:GLU:OE1	1.73	0.71
1:B:59:THR:HA	1:B:76:VAL:HG21	1.74	0.70
1:B:224:MET:HE1	1:B:293:PHE:HB3	1.73	0.69
1:A:231:MET:HE2	1:B:202:VAL:HG22	1.74	0.69
1:A:137:GLU:HG3	2:A:534:HOH:O	1.94	0.68
1:B:59:THR:HA	1:B:76:VAL:CG2	2.24	0.68
1:B:210[B]:PHE:CE1	1:B:244:LEU:CD2	2.77	0.67
1:B:251:ASP:HB3	1:B:285:LEU:HD22	1.76	0.66
1:B:5:LYS:HA	1:B:8:MET:HE2	1.78	0.66
1:B:104:ILE:CD1	1:B:109:LEU:HD22	2.25	0.65
1:B:8:MET:HE1	1:B:35:PHE:HZ	1.62	0.65
1:A:251:ASP:OD1	1:A:252:THR:N	2.31	0.63
1:B:52:LYS:O	1:B:56:GLN:HG2	1.99	0.63
1:A:239:MET:HE2	1:A:243:GLU:HB3	1.81	0.63
1:B:210[A]:PHE:HZ	1:B:293:PHE:CZ	2.17	0.62
1:A:145:ASP:OD2	1:A:148:ARG:NH1	2.32	0.61
1:B:58:VAL:HG21	1:B:80:MET:HE3	1.82	0.61
1:B:124:ASP:HA	1:B:148:ARG:HH11	1.66	0.61
1:A:153:HIS:CD2	1:A:165:GLU:OE1	2.54	0.61
1:B:210[B]:PHE:CZ	1:B:244:LEU:HG	2.36	0.60
1:B:22:MET:HE2	1:B:130[B]:ASN:HD21	1.67	0.59
1:B:210[A]:PHE:HZ	1:B:293:PHE:HZ	1.50	0.59
1:A:231:MET:HE1	1:B:202:VAL:HA	1.85	0.58
1:A:233:LEU:HD22	1:B:163:LEU:HB2	1.85	0.57
1:B:22:MET:CE	1:B:130[B]:ASN:HD21	2.18	0.56
1:A:233:LEU:O	1:A:233:LEU:HD23	2.06	0.55
1:B:210[A]:PHE:CZ	1:B:293:PHE:CZ	2.95	0.54
1:B:74:ASP:O	1:B:78:LEU:N	2.27	0.54
1:A:132:SER:OG	1:A:153:HIS:HE1	1.92	0.53
1:B:218:GLU:OE2	1:B:274:PRO:HD2	2.08	0.53
1:B:132:SER:OG	1:B:153:HIS:HE1	1.92	0.52
1:B:104:ILE:CG1	1:B:109:LEU:HD22	2.37	0.52
1:B:217:TYR:CE1	1:B:224:MET:HG3	2.44	0.51
1:A:231:MET:HE3	1:B:201:ILE:HG22	1.93	0.50
1:A:233:LEU:HD21	1:B:162:LYS:HB3	1.91	0.50
1:A:271:GLU:HG2	1:A:272:ALA:N	2.26	0.50
1:A:218:GLU:OE2	1:A:274:PRO:HD2	2.13	0.49
1:A:224:MET:HE1	1:A:293:PHE:HB3	1.95	0.49
1:B:224:MET:HE3	1:B:293:PHE:CB	2.41	0.49
1:A:231:MET:CE	1:B:202:VAL:HA	2.44	0.47
1:B:58:VAL:HG21	1:B:80:MET:CE	2.42	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:235:ALA:HB2	1:B:206:LEU:HD11	1.97	0.47
1:B:217:TYR:CD1	1:B:224:MET:HG3	2.50	0.47
1:B:210[A]:PHE:CZ	1:B:293:PHE:CE2	3.02	0.47
1:B:224:MET:HB3	1:B:224:MET:HE2	1.71	0.47
1:A:5:LYS:HA	1:A:8:MET:HE2	1.96	0.46
1:B:104:ILE:CD1	1:B:109:LEU:CD2	2.90	0.46
1:B:124:ASP:OD1	1:B:148:ARG:NH1	2.48	0.46
1:B:58:VAL:CG2	1:B:80:MET:HE3	2.46	0.46
1:A:239:MET:HE1	1:A:247:TYR:HB2	1.98	0.46
1:B:246:ASP:OD2	1:B:296:TYR:OH	2.29	0.45
1:A:168:ARG:HB3	1:A:177:TYR:CD1	2.51	0.45
1:B:128:THR:HA	1:B:150:GLY:O	2.17	0.45
1:B:210[B]:PHE:HZ	1:B:244:LEU:HG	1.81	0.44
1:A:206:LEU:HD11	1:B:235:ALA:HB2	1.99	0.44
1:A:128:THR:HA	1:A:150:GLY:O	2.18	0.44
1:B:79:THR:HG22	1:B:80:MET:HE2	2.00	0.43
1:B:39:LEU:O	1:B:85:THR:HA	2.17	0.43
1:B:133:SER:HG	1:B:255:PHE:HE2	1.64	0.43
1:B:250:LEU:HA	1:B:253:VAL:HG22	2.00	0.43
1:A:239:MET:HE2	1:A:243:GLU:CB	2.48	0.43
1:A:233:LEU:HD23	1:A:233:LEU:C	2.39	0.43
1:B:8:MET:CE	1:B:35:PHE:HZ	2.29	0.43
1:A:239:MET:HE1	1:A:244:LEU:HA	2.02	0.42
1:A:22:MET:SD	1:A:156:ASN:HB2	2.59	0.42
1:B:77:THR:OG1	1:B:78:LEU:N	2.52	0.42
1:A:239:MET:HE1	1:A:243:GLU:O	2.21	0.41
1:A:250:LEU:HA	1:A:253:VAL:HG22	2.03	0.41
1:B:76:VAL:O	1:B:80:MET:HG2	2.21	0.41
1:B:124:ASP:HA	1:B:148:ARG:NH1	2.33	0.41
1:B:168:ARG:HB3	1:B:177:TYR:CD1	2.55	0.41
1:A:135:LEU:CD1	1:A:263:LYS:HE2	2.50	0.41
1:A:238:PRO:HD2	2:B:495:HOH:O	2.21	0.41
1:A:251:ASP:HB3	1:A:285:LEU:HD22	2.03	0.40
1:A:30:THR:HG22	1:A:35:PHE:HB2	2.03	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	294/320 (92%)	287 (98%)	7 (2%)	0	100	100
1	B	282/320 (88%)	278 (99%)	4 (1%)	0	100	100
All	All	576/640 (90%)	565 (98%)	11 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	244/264 (92%)	244 (100%)	0	100	100
1	B	235/264 (89%)	235 (100%)	0	100	100
All	All	479/528 (91%)	479 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	153	HIS
1	B	21	GLN
1	B	153	HIS

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates 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	296/320 (92%)	0.35	19 (6%)	19 18	22, 31, 49, 69	16 (5%)
1	B	283/320 (88%)	0.46	21 (7%)	14 13	21, 33, 51, 66	11 (3%)
All	All	579/640 (90%)	0.40	40 (6%)	17 15	21, 32, 50, 69	27 (4%)

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	76	VAL	5.9
1	B	75	PHE	5.7
1	A	61	LEU	5.1
1	B	56	GLN	4.8
1	A	68	THR	4.7
1	A	296	TYR	4.6
1	A	123	LYS	4.6
1	B	52	LYS	4.6
1	B	296	TYR	4.6
1	B	77	THR	4.5
1	B	60	HIS	4.5
1	A	70	LYS	4.3
1	B	59	THR	4.2
1	B	55	SER	3.8
1	B	58	VAL	3.6
1	B	74	ASP	3.4
1	A	289	THR	3.0
1	A	64	LYS	2.9
1	B	262	ALA	2.8
1	A	65	GLN	2.8
1	B	292	GLY	2.7
1	B	295	SER	2.7
1	B	144	GLN	2.6
1	A	69	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	100	ILE	2.6
1	B	160	VAL	2.6
1	B	53	ALA	2.6
1	B	107	ILE	2.5
1	A	291	ASP	2.5
1	B	294	TYR	2.4
1	A	295	SER	2.4
1	B	152	LEU	2.3
1	A	67	GLY	2.3
1	A	152	LEU	2.3
1	A	62	SER	2.3
1	A	60	HIS	2.2
1	A	294	TYR	2.1
1	A	247	TYR	2.1
1	A	280	VAL	2.0
1	B	108	ASP	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 ⓘ

There are no such residues in this entry.