WORLDWIDE
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:25 PM GMT

PDB ID : 3TVU
Title : Crystal Structure of the humanized carboxyltransferase domain of yeast Acetyl-coA caroxylase in complex with compound 3
Authors : Rajamohan, F.; Marr, E.; Reyes, A.; Landro, J.A.; Anderson, M.D; Corbett, J.W.; Dirico, K.J.; Harwood, J.H.; Tu, M.; Vajdos, F.F.
Deposited on : 2011-09-20
Resolution : 2.40 Å(reported)

The following versions of software and data (see references ①) were used in the production of this report:

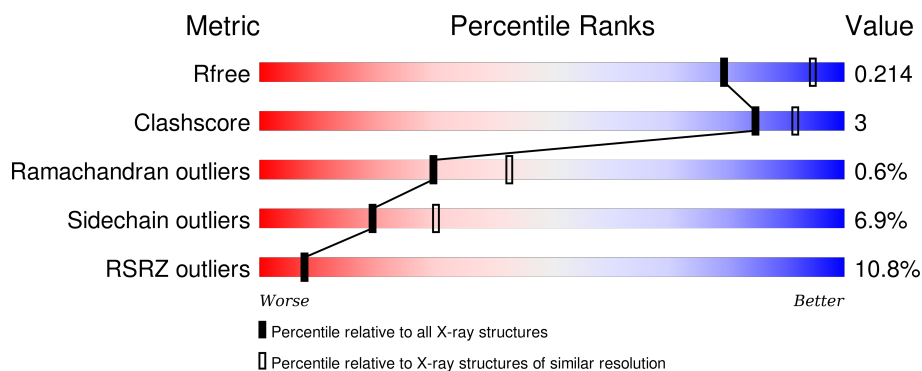|		
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA,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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	Percentile Ranks	Value
Rfree		0.214
Clashscore		3
Ramachandran outliers		0.6%
Sidechain outliers		6.9%
RSRZ outliers		10.8%

Worse — *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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 <=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	769	6% / 80% / 10% · 9%
1	B	769	12% / 77% / 11% · 10%
1	C	769	11% / 76% / 11% · 11%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 17661 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 carboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	696	Total	C	N	O	S	0	1	0
			5561	3539	960	1045	17			
1	B	690	Total	C	N	O	S	0	0	0
			5513	3510	949	1037	17			
1	C	681	Total	C	N	O	S	0	0	0
			5437	3454	939	1027	17			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1473	MET	-	EXPRESSION TAG	UNP Q00955
A	1474	ALA	-	EXPRESSION TAG	UNP Q00955
A	1475	SER	-	EXPRESSION TAG	UNP Q00955
A	1760	SER	PRO	ENGINEERED MUTATION	UNP Q00955
A	1762	LEU	ILE	ENGINEERED MUTATION	UNP Q00955
A	1765	VAL	MET	ENGINEERED MUTATION	UNP Q00955
A	1919	GLN	GLU	ENGINEERED MUTATION	UNP Q00955
A	1920	ALA	PRO	ENGINEERED MUTATION	UNP Q00955
A	1925	PHE	HIS	ENGINEERED MUTATION	UNP Q00955
A	2028	GLU	GLN	ENGINEERED MUTATION	UNP Q00955
A	2030	THR	MET	ENGINEERED MUTATION	UNP Q00955
A	2032	GLU	GLY	ENGINEERED MUTATION	UNP Q00955
A	2234	LEU	-	EXPRESSION TAG	UNP Q00955
A	2235	GLU	-	EXPRESSION TAG	UNP Q00955
A	2236	HIS	-	EXPRESSION TAG	UNP Q00955
A	2237	HIS	-	EXPRESSION TAG	UNP Q00955
A	2238	HIS	-	EXPRESSION TAG	UNP Q00955
A	2239	HIS	-	EXPRESSION TAG	UNP Q00955
A	2240	HIS	-	EXPRESSION TAG	UNP Q00955
A	2241	HIS	-	EXPRESSION TAG	UNP Q00955
B	1473	MET	-	EXPRESSION TAG	UNP Q00955
B	1474	ALA	-	EXPRESSION TAG	UNP Q00955
B	1475	SER	-	EXPRESSION TAG	UNP Q00955

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1760	SER	PRO	ENGINEERED MUTATION	UNP Q00955
B	1762	LEU	ILE	ENGINEERED MUTATION	UNP Q00955
B	1765	VAL	MET	ENGINEERED MUTATION	UNP Q00955
B	1919	GLN	GLU	ENGINEERED MUTATION	UNP Q00955
B	1920	ALA	PRO	ENGINEERED MUTATION	UNP Q00955
B	1925	PHE	HIS	ENGINEERED MUTATION	UNP Q00955
B	2028	GLU	GLN	ENGINEERED MUTATION	UNP Q00955
B	2030	THR	MET	ENGINEERED MUTATION	UNP Q00955
B	2032	GLU	GLY	ENGINEERED MUTATION	UNP Q00955
B	2234	LEU	-	EXPRESSION TAG	UNP Q00955
B	2235	GLU	-	EXPRESSION TAG	UNP Q00955
B	2236	HIS	-	EXPRESSION TAG	UNP Q00955
B	2237	HIS	-	EXPRESSION TAG	UNP Q00955
B	2238	HIS	-	EXPRESSION TAG	UNP Q00955
B	2239	HIS	-	EXPRESSION TAG	UNP Q00955
B	2240	HIS	-	EXPRESSION TAG	UNP Q00955
B	2241	HIS	-	EXPRESSION TAG	UNP Q00955
C	1473	MET	-	EXPRESSION TAG	UNP Q00955
C	1474	ALA	-	EXPRESSION TAG	UNP Q00955
C	1475	SER	-	EXPRESSION TAG	UNP Q00955
C	1760	SER	PRO	ENGINEERED MUTATION	UNP Q00955
C	1762	LEU	ILE	ENGINEERED MUTATION	UNP Q00955
C	1765	VAL	MET	ENGINEERED MUTATION	UNP Q00955
C	1919	GLN	GLU	ENGINEERED MUTATION	UNP Q00955
C	1920	ALA	PRO	ENGINEERED MUTATION	UNP Q00955
C	1925	PHE	HIS	ENGINEERED MUTATION	UNP Q00955
C	2028	GLU	GLN	ENGINEERED MUTATION	UNP Q00955
C	2030	THR	MET	ENGINEERED MUTATION	UNP Q00955
C	2032	GLU	GLY	ENGINEERED MUTATION	UNP Q00955
C	2234	LEU	-	EXPRESSION TAG	UNP Q00955
C	2235	GLU	-	EXPRESSION TAG	UNP Q00955
C	2236	HIS	-	EXPRESSION TAG	UNP Q00955
C	2237	HIS	-	EXPRESSION TAG	UNP Q00955
C	2238	HIS	-	EXPRESSION TAG	UNP Q00955
C	2239	HIS	-	EXPRESSION TAG	UNP Q00955
C	2240	HIS	-	EXPRESSION TAG	UNP Q00955
C	2241	HIS	-	EXPRESSION TAG	UNP Q00955

- Molecule 2 is 4-({4-[(2-METHYLQUINOLIN-6-YL)METHYL]PIPERIDIN-1-YL}CARBONYL)-2-PHENYLQUINOLINE (three-letter code: B37) (formula: $C_{32}H_{29}N_3O$).
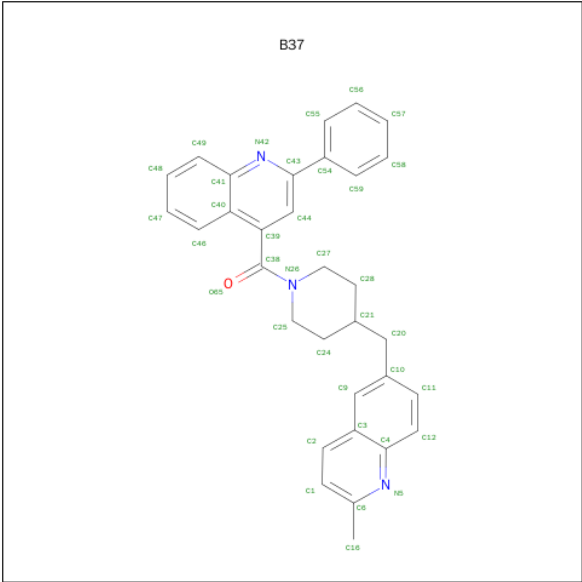
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 36	C 32	N 3	O 1	0	0
2	B	1	Total 36	C 32	N 3	O 1	0	0
2	C	1	Total 36	C 32	N 3	O 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	382	Total 382	O 382	0	0
3	B	339	Total 339	O 339	0	0
3	C	321	Total 321	O 321	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: Acetyl-CoA carboxylase

- Molecule 1: Acetyl-CoA carboxylase

• Molecule 1: Acetyl-CoA carboxylase

Chain C:
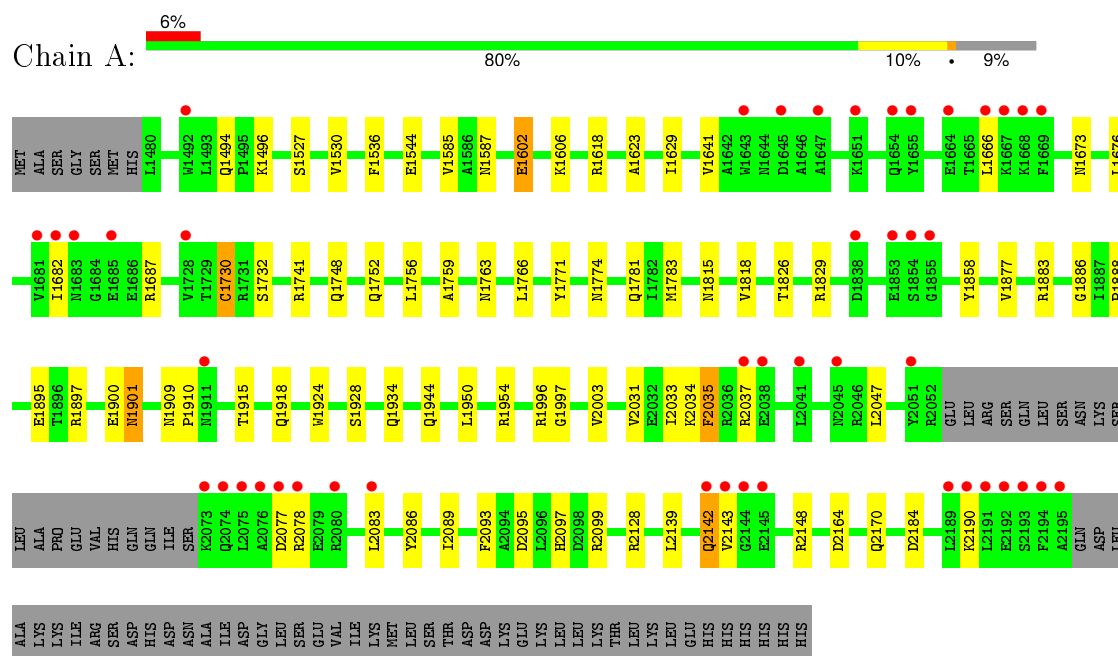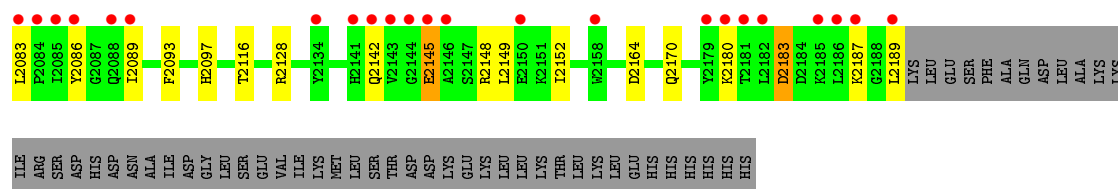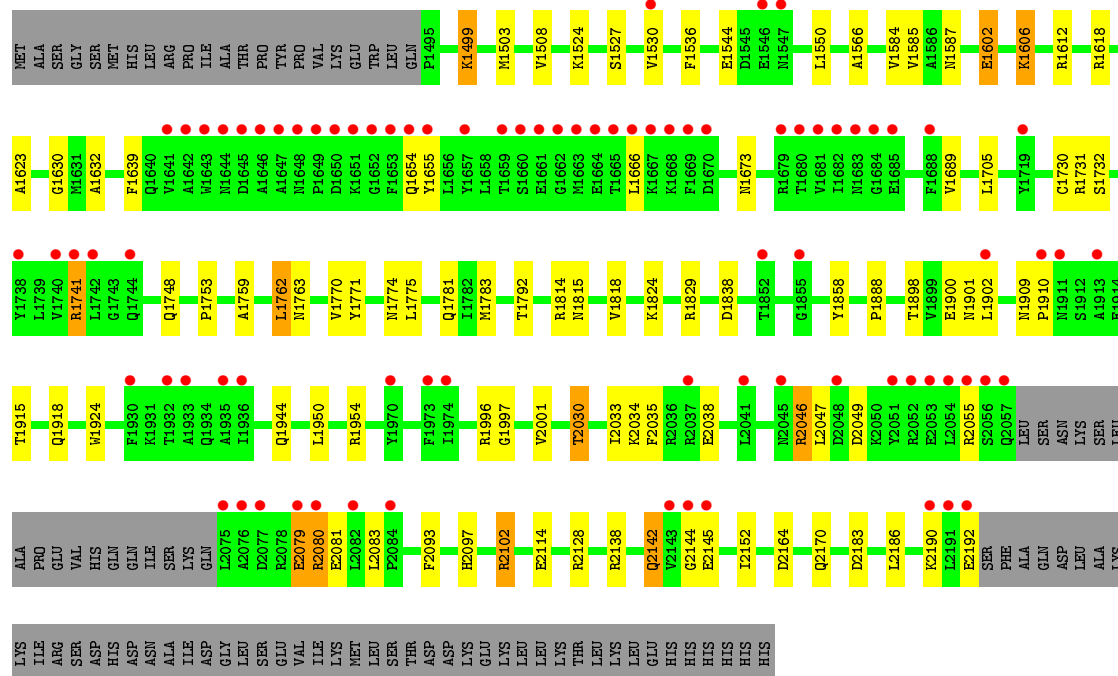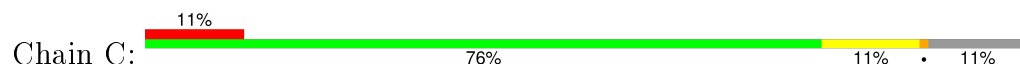
4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	246.99Å 123.18Å 146.16Å 90.00° 94.20° 90.00°	Depositor
Resolution (Å)	43.55 – 2.40 43.55 – 2.40	Depositor EDS
% Data completeness (in resolution range)	96.4 (43.55-2.40) 96.4 (43.55-2.40)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.08 (at 2.39Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.202 , 0.223 0.191 , 0.214	Depositor DCC
R_{free} test set	16364 reflections (11.06%)	DCC
Wilson B-factor (Å^2)	52.6	Xtriage
Anisotropy	0.406	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 71.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< |L| > = 0.51, < L^2 > = 0.35$	Xtriage
Outliers	0 of 164285 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	17661	wwPDB-VP
Average B, all atoms (Å^2)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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 ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: B37

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	0/5689	0.72	1/7704 (0.0%)
1	B	0.50	0/5633	0.73	2/7631 (0.0%)
1	C	0.50	0/5551	0.74	2/7512 (0.0%)
All	All	0.50	0/16873	0.73	5/22847 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	2079	GLU	C-N-CA	7.22	139.75	121.70
1	B	2080	ARG	C-N-CA	7.14	139.56	121.70
1	C	2080	ARG	C-N-CA	6.11	136.99	121.70
1	B	1786	ASN	CB-CA-C	-5.87	98.65	110.40
1	A	1730	CYS	N-CA-C	-5.07	97.32	111.00

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	5561	0	5492	30	0
1	B	5513	0	5450	39	0
1	C	5437	0	5373	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	36	0	29	0	0
2	B	36	0	29	0	0
2	C	36	0	29	0	0
3	A	382	0	0	3	0
3	B	339	0	0	0	0
3	C	321	0	0	3	0
All	All	17661	0	16402	95	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 3.

The worst 5 of 95 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:B:1815:ASN:H	1:B:1944:GLN:HE22	1.18	0.88
1:C:1815:ASN:H	1:C:1944:GLN:HE22	1.21	0.86
1:C:1763:ASN:HD21	1:C:1771:TYR:H	1.22	0.84
1:A:1763:ASN:HD21	1:A:1771:TYR:H	1.24	0.84
1:A:1815:ASN:H	1:A:1944:GLN:HE22	1.19	0.84

There are no symmetry-related clashes.

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	693/769 (90%)	670 (97%)	21 (3%)	2 (0%)	46	63
1	B	686/769 (89%)	658 (96%)	23 (3%)	5 (1%)	26	38
1	C	677/769 (88%)	651 (96%)	20 (3%)	6 (1%)	21	30
All	All	2056/2307 (89%)	1979 (96%)	64 (3%)	13 (1%)	30	43

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	2081	GLU
1	C	2144	GLY
1	A	1997	GLY
1	A	2143	VAL
1	B	1997	GLY

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	591/658 (90%)	559 (95%)	32 (5%)	27	43
1	B	586/658 (89%)	542 (92%)	44 (8%)	17	26
1	C	578/658 (88%)	533 (92%)	45 (8%)	16	24
All	All	1755/1974 (89%)	1634 (93%)	121 (7%)	19	30

5 of 121 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1824	LYS
1	B	2128	ARG
1	C	2079	GLU
1	B	1843	VAL
1	B	2033	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1748	GLN
1	B	1815	ASN
1	C	2045	ASN
1	B	1752	GLN
1	B	1774	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)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#|Z| > 2$	Counts	RMSZ	$\#|Z| > 2$
2	B37	A	2242	-	41,41,41	1.24	5 (12%)	58,58,58	1.40	7 (12%)
2	B37	B	2242	-	41,41,41	1.15	3 (7%)	58,58,58	1.27	5 (8%)
2	B37	C	2242	-	41,41,41	1.15	5 (12%)	58,58,58	1.25	5 (8%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	B37	A	2242	-	-	0/16/26/26	0/6/6/6
2	B37	B	2242	-	-	0/16/26/26	0/6/6/6
2	B37	C	2242	-	-	0/16/26/26	0/6/6/6

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2242	B37	C54-C43	-3.38	1.43	1.48
2	C	2242	B37	C54-C43	-3.03	1.44	1.48
2	B	2242	B37	C54-C43	-2.93	1.44	1.48
2	C	2242	B37	C39-C40	-2.32	1.38	1.43
2	A	2242	B37	C39-C40	-2.30	1.38	1.43

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2242	B37	C39-C44-C43	-5.25	117.37	120.68
2	B	2242	B37	C39-C44-C43	-5.15	117.43	120.68
2	C	2242	B37	C39-C44-C43	-4.04	118.13	120.68
2	A	2242	B37	C28-C27-N26	-3.20	106.43	111.07
2	B	2242	B37	O65-C38-C39	-2.20	116.19	120.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	696/769 (90%)	0.22	46 (6%)	22	22	38, 56, 111, 147	0
1	B	690/769 (89%)	0.46	94 (13%)	4	4	40, 61, 119, 159	0
1	C	681/769 (88%)	0.42	83 (12%)	5	5	38, 59, 123, 153	0
All	All	2067/2307 (89%)	0.37	223 (10%)	8	8	38, 58, 118, 159	0

The worst 5 of 223 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2144	GLY	10.5
1	B	2075	LEU	9.3
1	C	2144	GLY	8.6
1	A	2195	ALA	7.9
1	A	2194	PHE	7.4

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)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors($Å^2$)	Q<0.9
2	B37	C	2242	36/36	0.92	0.15	0.20	51,60,76,77	0
2	B37	A	2242	36/36	0.93	0.14	0.03	49,55,77,79	0
2	B37	B	2242	36/36	0.91	0.15	-0.31	59,67,82,84	0

6.5 Other polymers ⓘ

There are no such residues in this entry.