



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:52 PM UTC

PDB ID : 1RR2 / pdb_00001rr2
Title : Propionibacterium shermanii transcarboxylase 5S subunit bound to 2-ketobutyric acid
Authors : Hall, P.R.; Zheng, R.; Antony, L.; Pusztai-Carey, M.; Carey, P.R.; Yee, V.C.
Deposited on : 2003-12-08
Resolution : 2.00 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

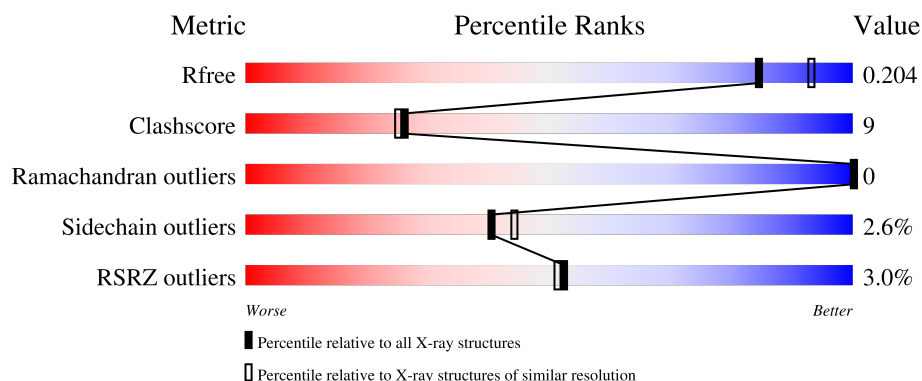
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	540	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	KCX	A	184[A]	-	X	-	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	2KT	A	530	-	X	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3943 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 transcarboxylase 5S subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	472	3675	2309	635	702	29	0	2	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	cloning artifact	GB 38304072
A	-9	ALA	-	cloning artifact	GB 38304072
A	-8	ILE	-	cloning artifact	GB 38304072
A	-7	SER	-	cloning artifact	GB 38304072
A	-6	ARG	-	cloning artifact	GB 38304072
A	-5	GLU	-	cloning artifact	GB 38304072
A	-4	LEU	-	cloning artifact	GB 38304072
A	-3	VAL	-	cloning artifact	GB 38304072
A	-2	ASP	-	cloning artifact	GB 38304072
A	-1	PRO	-	cloning artifact	GB 38304072
A	0	ASN	-	cloning artifact	GB 38304072
A	1	SER	-	cloning artifact	GB 38304072
A	184	KCX	LYS	microheterogeneity	GB 38304072
A	506	THR	-	cloning artifact	GB 38304072
A	507	ARG	-	cloning artifact	GB 38304072
A	508	ALA	-	cloning artifact	GB 38304072
A	509	SER	-	cloning artifact	GB 38304072
A	510	GLN	-	cloning artifact	GB 38304072
A	511	PRO	-	cloning artifact	GB 38304072
A	512	GLU	-	cloning artifact	GB 38304072
A	513	LEU	-	cloning artifact	GB 38304072
A	514	ALA	-	cloning artifact	GB 38304072
A	515	PRO	-	cloning artifact	GB 38304072
A	516	GLU	-	cloning artifact	GB 38304072
A	517	ASP	-	cloning artifact	GB 38304072
A	518	PRO	-	cloning artifact	GB 38304072
A	519	GLU	-	cloning artifact	GB 38304072

Continued on next page...

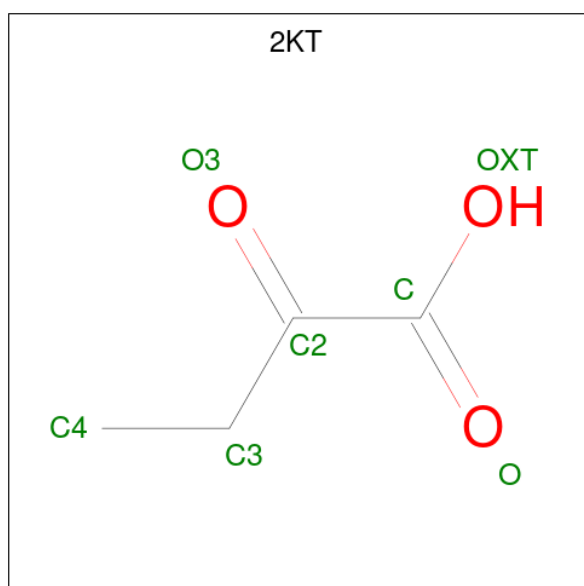
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	520	ASP	-	cloning artifact	GB 38304072
A	521	LEU	-	cloning artifact	GB 38304072
A	522	GLU	-	cloning artifact	GB 38304072
A	523	HIS	-	cloning artifact	GB 38304072
A	524	HIS	-	cloning artifact	GB 38304072
A	525	HIS	-	cloning artifact	GB 38304072
A	526	HIS	-	cloning artifact	GB 38304072
A	527	HIS	-	cloning artifact	GB 38304072
A	528	HIS	-	cloning artifact	GB 38304072

- Molecule 2 is COBALT (II) ION (CCD ID: CO) (formula: Co).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Co 1 1	0	0

- Molecule 3 is 2-KETOBUTYRIC ACID (CCD ID: 2KT) (formula: C₄H₆O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 7 4 3	0	0

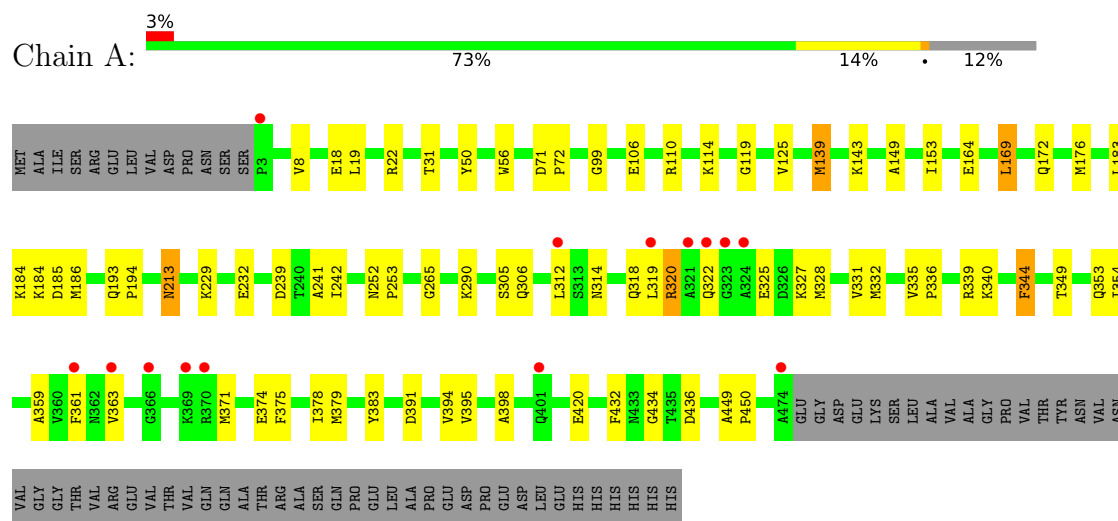
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	260	Total 260	O 260	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: transcarboxylase 5S subunit



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	96.17Å 146.13Å 78.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.29 – 2.00 27.29 – 2.00	Depositor EDS
% Data completeness (in resolution range)	85.4 (27.29-2.00) 85.4 (27.29-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.00 (at 1.89Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.173 , 0.205 0.173 , 0.204	Depositor DCC
R_{free} test set	1546 reflections (3.52%)	wwPDB-VP
Wilson B-factor (Å ²)	26.3	Xtriage
Anisotropy	0.122	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3943	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 4.97% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: KCX, CO, 2KT

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	0.82	9/3740 (0.2%)	1.00	9/5054 (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 (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	184[B]	LYS	CA-CB	-18.79	1.23	1.53
1	A	184[B]	LYS	CA-C	15.45	1.71	1.52
1	A	184[B]	LYS	C-O	-13.46	1.08	1.24
1	A	184[B]	LYS	N-CA	12.04	1.60	1.46
1	A	184[B]	LYS	CG-CD	9.96	1.82	1.52
1	A	184[B]	LYS	CB-CG	8.94	1.79	1.52
1	A	184[B]	LYS	CD-CE	-7.29	1.30	1.52
1	A	184[B]	LYS	C-N	7.21	1.42	1.33
1	A	185	ASP	C-N	6.91	1.43	1.34

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	184[B]	LYS	N-CA-C	-10.27	89.73	108.02
1	A	184[B]	LYS	CB-CG-CD	-7.42	94.23	111.30
1	A	184[B]	LYS	CA-CB-CG	-7.17	99.75	114.10
1	A	184[B]	LYS	CA-C-O	6.88	127.75	120.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	265	GLY	N-CA-C	-6.29	107.20	114.69
1	A	119	GLY	N-CA-C	5.86	123.21	114.95
1	A	344	PHE	CA-C-N	-5.31	114.91	120.38
1	A	344	PHE	C-N-CA	-5.31	114.91	120.38
1	A	99	GLY	N-CA-C	5.07	120.02	112.41

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	183	LEU	Peptide

5.2 Too-close contacts [i](#)

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	3675	0	3635	62	0
2	A	1	0	0	0	0
3	A	7	0	5	0	0
4	A	260	0	0	0	0
All	All	3943	0	3640	62	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 9.

All (62) 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:432:PHE:CE1	1:A:434:GLY:HA2	2.14	0.81
1:A:371:MET:HE3	1:A:375:PHE:CD2	2.16	0.79
1:A:169:LEU:HA	1:A:172:GLN:HE21	1.55	0.72
1:A:378:ILE:HG12	1:A:383:TYR:CD1	2.28	0.68
1:A:335:VAL:HB	1:A:336:PRO:HD3	1.76	0.68
1:A:371:MET:HE1	1:A:398:ALA:HB2	1.78	0.66
1:A:314:ASN:O	1:A:318:GLN:HG3	1.96	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:GLN:HB3	1:A:194:PRO:HD3	1.79	0.64
1:A:125:VAL:CG2	1:A:139:MET:HE3	2.28	0.63
1:A:371:MET:HE3	1:A:375:PHE:HD2	1.62	0.59
1:A:339:ARG:HG2	1:A:344:PHE:HA	1.84	0.59
1:A:349:THR:HG23	1:A:353:GLN:HE22	1.68	0.59
1:A:106:GLU:O	1:A:110:ARG:HG2	2.02	0.59
1:A:378:ILE:HG12	1:A:383:TYR:HD1	1.68	0.59
1:A:139:MET:CE	1:A:149:ALA:HB1	2.34	0.58
1:A:340:LYS:HD3	1:A:344:PHE:CZ	2.39	0.57
1:A:139:MET:HE2	1:A:149:ALA:HB1	1.85	0.57
1:A:139:MET:HE2	1:A:139:MET:HA	1.87	0.57
1:A:229:LYS:HD3	1:A:232:GLU:OE1	2.07	0.54
1:A:320:ARG:C	1:A:320:ARG:HD3	2.32	0.53
1:A:354:ILE:CD1	1:A:378:ILE:HD11	2.38	0.53
1:A:125:VAL:HG21	1:A:139:MET:HE3	1.92	0.52
1:A:328:MET:HE2	1:A:332:MET:HG3	1.90	0.52
1:A:371:MET:HE1	1:A:398:ALA:CB	2.39	0.52
1:A:305:SER:O	1:A:306:GLN:HB2	2.10	0.52
1:A:139:MET:HG3	1:A:176:MET:HE3	1.92	0.51
1:A:328:MET:O	1:A:328:MET:HE3	2.11	0.51
1:A:320:ARG:HD3	1:A:320:ARG:O	2.10	0.51
1:A:22:ARG:HD2	1:A:22:ARG:C	2.37	0.50
1:A:139:MET:HG3	1:A:176:MET:CE	2.42	0.50
1:A:331:VAL:HA	1:A:363:VAL:HG21	1.93	0.50
1:A:354:ILE:HD12	1:A:378:ILE:HD11	1.93	0.49
1:A:320:ARG:CG	1:A:320:ARG:HH11	2.25	0.49
1:A:449:ALA:HB3	1:A:450:PRO:HD3	1.94	0.49
1:A:320:ARG:HH11	1:A:320:ARG:HB2	1.79	0.48
1:A:153:ILE:HG12	1:A:169:LEU:HD13	1.96	0.47
1:A:320:ARG:HH11	1:A:320:ARG:CB	2.28	0.47
1:A:169:LEU:HA	1:A:172:GLN:NE2	2.26	0.47
1:A:213:ASN:HD22	1:A:213:ASN:N	2.13	0.47
1:A:18:GLU:HB2	1:A:50:TYR:CE2	2.50	0.46
1:A:379:MET:HE2	1:A:394:VAL:HG12	1.98	0.46
1:A:164:GLU:H	1:A:164:GLU:CD	2.24	0.46
1:A:114:LYS:HE3	1:A:436:ASP:HB2	1.99	0.45
1:A:241:ALA:O	1:A:242:ILE:C	2.59	0.45
1:A:391:ASP:O	1:A:395:VAL:HG23	2.16	0.45
1:A:325:GLU:C	1:A:327:LYS:H	2.24	0.45
1:A:374:GLU:CD	1:A:374:GLU:H	2.26	0.44
1:A:363:VAL:O	1:A:363:VAL:HG12	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:LEU:HB3	1:A:325:GLU:HA	2.01	0.43
1:A:229:LYS:HD3	1:A:229:LYS:HA	1.84	0.42
1:A:8:VAL:HG12	1:A:232:GLU:HB3	2.02	0.42
1:A:19:LEU:HD11	1:A:239:ASP:HB3	2.02	0.42
1:A:374:GLU:CD	1:A:374:GLU:N	2.78	0.42
1:A:139:MET:O	1:A:143:LYS:HG2	2.20	0.42
1:A:331:VAL:HG22	1:A:363:VAL:HG21	2.02	0.41
1:A:359:ALA:O	1:A:363:VAL:HG23	2.20	0.41
1:A:340:LYS:CD	1:A:344:PHE:CZ	3.03	0.41
1:A:252:ASN:HA	1:A:253:PRO:HD3	1.88	0.41
1:A:361:PHE:N	1:A:361:PHE:CD2	2.89	0.41
1:A:71:ASP:HA	1:A:72:PRO:HD3	1.94	0.40
1:A:432:PHE:CE1	1:A:434:GLY:CA	2.97	0.40

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	470/540 (87%)	454 (97%)	16 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	391/448 (87%)	381 (97%)	10 (3%)	40	44

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

Mol	Chain	Res	Type
1	A	31	THR
1	A	56	TRP
1	A	139	MET
1	A	169	LEU
1	A	213	ASN
1	A	290	LYS
1	A	312	LEU
1	A	320	ARG
1	A	322	GLN
1	A	420	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	GLN
1	A	211	GLN
1	A	213	ASN
1	A	269	ASN
1	A	318	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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
1	KCX	A	184[A]	2,1	10,11,12	4.60	9 (90%)	6,12,14	5.80	3 (50%)

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
1	KCX	A	184[A]	2,1	-	3/9/10/12	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	184[A]	KCX	CE-NZ	7.15	1.62	1.46
1	A	184[A]	KCX	CX-NZ	-5.94	1.24	1.35
1	A	184[A]	KCX	CB-CA	-5.88	1.44	1.53
1	A	184[A]	KCX	CD-CE	-5.02	1.31	1.51
1	A	184[A]	KCX	CG-CB	4.87	1.72	1.52
1	A	184[A]	KCX	OQ2-CX	-4.05	0.97	1.36
1	A	184[A]	KCX	CD-CG	-3.16	1.36	1.51
1	A	184[A]	KCX	CA-N	2.75	1.55	1.48
1	A	184[A]	KCX	O-C	-2.35	1.11	1.20

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	184[A]	KCX	OQ1-CX-NZ	-12.95	105.25	124.92
1	A	184[A]	KCX	CE-NZ-CX	5.05	130.55	121.98
1	A	184[A]	KCX	CD-CE-NZ	2.10	118.09	112.20

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	184[A]	KCX	O-C-CA-CB
1	A	184[A]	KCX	CG-CD-CE-NZ
1	A	184[A]	KCX	CA-CB-CG-CD

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
3	2KT	A	530	-	6,6,6	1.33	1 (16%)	7,7,7	1.61	3 (42%)

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
3	2KT	A	530	-	-	4/6/6/6	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	530	2KT	OXT-C	-2.86	1.22	1.30

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	530	2KT	OXT-C-C2	2.49	120.51	113.59
3	A	530	2KT	C3-C2-C	2.05	119.69	116.08
3	A	530	2KT	O-C-C2	-2.04	119.27	121.81

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	530	2KT	OXT-C-C2-C3
3	A	530	2KT	O-C-C2-C3
3	A	530	2KT	OXT-C-C2-O3
3	A	530	2KT	O-C-C2-O3

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	183:LEU	C	184[B]:LYS	N	1.15

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	471/540 (87%)	-0.30	14 (2%)	52	51	16, 29, 76, 100	1 (0%)

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	474	ALA	3.8
1	A	401	GLN	2.7
1	A	363	VAL	2.7
1	A	369	LYS	2.5
1	A	3	PRO	2.5
1	A	312	LEU	2.5
1	A	321	ALA	2.5
1	A	361	PHE	2.4
1	A	319	LEU	2.3
1	A	370	ARG	2.2
1	A	322	GLN	2.2
1	A	323	GLY	2.2
1	A	366	GLY	2.1
1	A	324	ALA	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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. 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	B-factors(Å ²)	Q < 0.9
1	KCX	A	184[A]	12/13	0.92	0.10	6,18,22,24	12

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
3	2KT	A	530	7/7	0.73	0.23	22,26,27,28	7
2	CO	A	529	1/1	1.00	0.04	24,24,24,24	0

6.5 Other polymers [i](#)

There are no such residues in this entry.