



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:25 PM GMT

PDB ID : 3TW7
Title : Structure of Rhizobium etli pyruvate carboxylase T882A crystallized without acetyl coenzyme-A
Authors : St Maurice, M.; Kumar, S.; Lietzan, A.D.
Deposited on : 2011-09-21
Resolution : 3.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

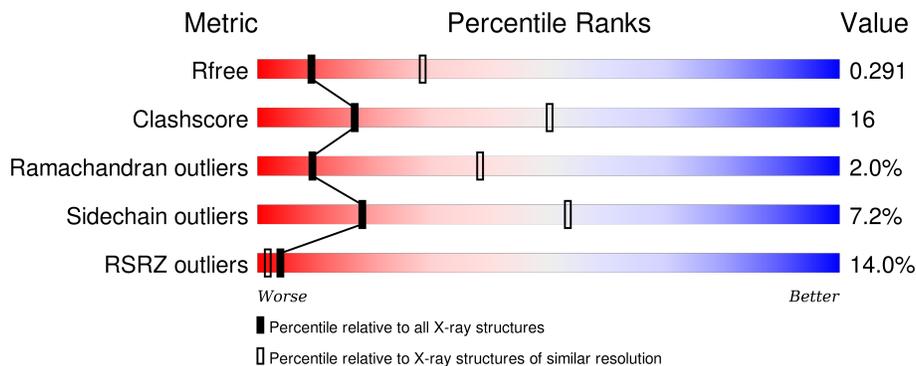
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1114 (3.14-3.06)
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)
RSRZ outliers	91569	1119 (3.14-3.06)

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	1165	 14% 55% 28% • 14%
1	B	1165	 10% 58% 25% • 14%

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
2	MG	A	1200	-	-	-	X
2	MG	B	1200	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 15185 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 Pyruvate carboxylase protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1004	Total	C	N	O	S	0	15	0
			7544	4804	1275	1434	31			
1	B	1002	Total	C	N	O	S	0	16	0
			7623	4853	1290	1449	31			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	EXPRESSION TAG	UNP Q2K340
A	-9	HIS	-	EXPRESSION TAG	UNP Q2K340
A	-8	HIS	-	EXPRESSION TAG	UNP Q2K340
A	-7	HIS	-	EXPRESSION TAG	UNP Q2K340
A	-6	HIS	-	EXPRESSION TAG	UNP Q2K340
A	-5	HIS	-	EXPRESSION TAG	UNP Q2K340
A	-4	HIS	-	EXPRESSION TAG	UNP Q2K340
A	-3	HIS	-	EXPRESSION TAG	UNP Q2K340
A	-2	HIS	-	EXPRESSION TAG	UNP Q2K340
A	-1	HIS	-	EXPRESSION TAG	UNP Q2K340
A	0	GLY	-	EXPRESSION TAG	UNP Q2K340
A	1	GLY	-	EXPRESSION TAG	UNP Q2K340
A	882	ALA	THR	ENGINEERED MUTATION	UNP Q2K340
B	-10	MET	-	EXPRESSION TAG	UNP Q2K340
B	-9	HIS	-	EXPRESSION TAG	UNP Q2K340
B	-8	HIS	-	EXPRESSION TAG	UNP Q2K340
B	-7	HIS	-	EXPRESSION TAG	UNP Q2K340
B	-6	HIS	-	EXPRESSION TAG	UNP Q2K340
B	-5	HIS	-	EXPRESSION TAG	UNP Q2K340
B	-4	HIS	-	EXPRESSION TAG	UNP Q2K340
B	-3	HIS	-	EXPRESSION TAG	UNP Q2K340
B	-2	HIS	-	EXPRESSION TAG	UNP Q2K340
B	-1	HIS	-	EXPRESSION TAG	UNP Q2K340
B	0	GLY	-	EXPRESSION TAG	UNP Q2K340
B	1	GLY	-	EXPRESSION TAG	UNP Q2K340

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Chain	Residue	Modelled	Actual	Comment	Reference
B	882	ALA	THR	ENGINEERED MUTATION	UNP Q2K340

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Mg 1 1	0	0
2	A	1	Total Mg 1 1	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Zn 1 1	0	0
3	A	1	Total Zn 1 1	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Cl 1 1	0	0
4	A	1	Total Cl 1 1	0	0

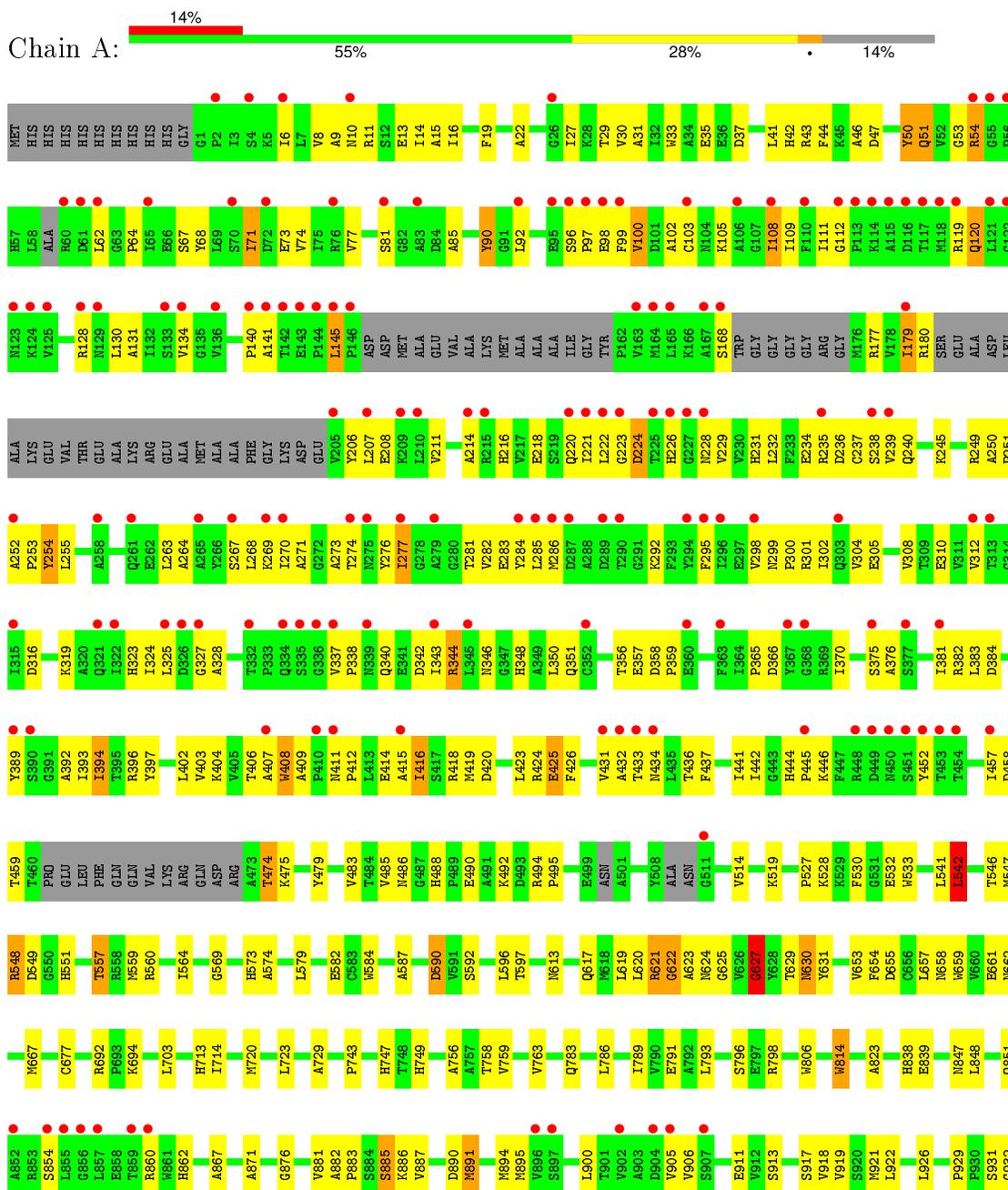
- Molecule 5 is water.

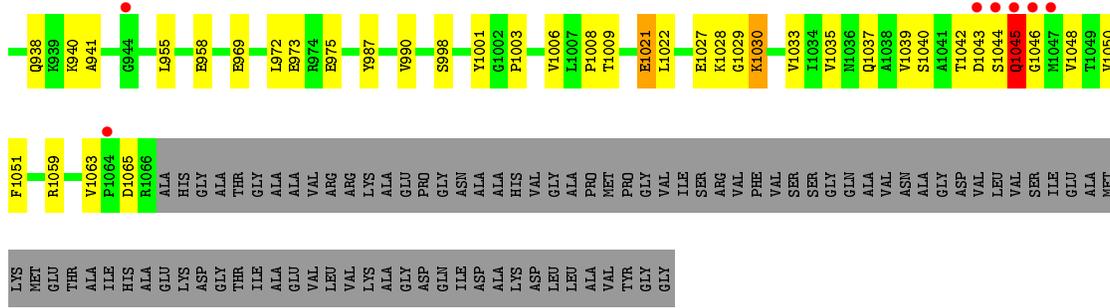
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	7	Total O 7 7	0	0
5	B	5	Total O 5 5	0	0

3 Residue-property plots

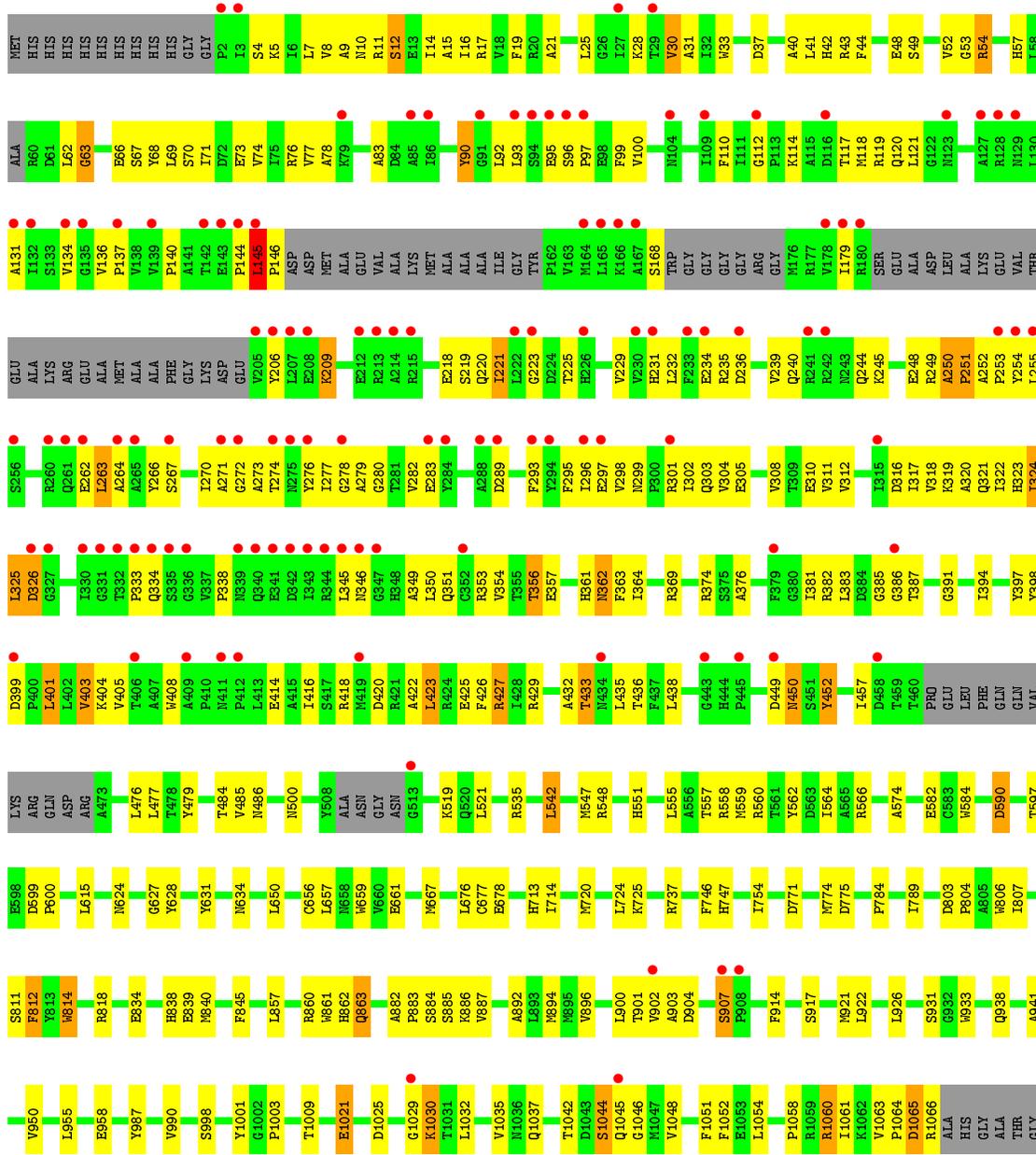
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Pyruvate carboxylase protein





• Molecule 1: Pyruvate carboxylase protein



ALA
ALA
VAL
ARG
ARG
LYS
ALA
GLU
PRO
GLY
GLN
ASN
ALA
ALA
HIS
VAL
GLY
ALA
ALA
PRO
MET
PRO
GLY
VAL
ILE
SER
ARG
VAL
PHE
VAL
SER
SER
SER
GLY
GLN
ALA
ALA
VAL
ASN
ALA
GLY
ASP
VAL
LEU
VAL
SER
ILE
GLU
ALA
MET
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MET
MET
GLU
THR
ALA
ILE
HIS
ALA
GLU
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ASP
GLY
THR
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ALA
GLU
VAL
LEU
VAL
LYS
ALA
GLY
ASP
GLN
ILE
ASP
ALA
LYS
ASP
LEU
LEU
ALA
VAL
TYR
GLY
GLY

4 Data and refinement statistics

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, α , β , γ	264.16Å 264.16Å 91.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.10 45.30 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-3.10) 100.0 (45.30-3.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.13 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.250 , 0.292 0.248 , 0.291	Depositor DCC
R_{free} test set	2964 reflections (5.42%)	DCC
Wilson B-factor (Å ²)	54.7	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 66.1	EDS
Estimated twinning fraction	0.023 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 57689 reflections	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	15185	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.61% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, KCX, CL

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	0.69	8/7719 (0.1%)	0.79	7/10500 (0.1%)
1	B	0.70	2/7799 (0.0%)	0.84	6/10603 (0.1%)
All	All	0.70	10/15518 (0.1%)	0.82	13/21103 (0.1%)

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
1	B	0	1
All	All	0	2

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	98[A]	GLU	CD-OE1	7.78	1.34	1.25
1	A	98[B]	GLU	CD-OE1	7.78	1.34	1.25
1	A	269	LYS	CE-NZ	7.16	1.67	1.49
1	A	1045	GLN	CD-NE2	6.86	1.50	1.32
1	A	1045	GLN	CG-CD	6.82	1.66	1.51

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	145	LEU	CA-CB-CG	7.13	131.69	115.30
1	A	548	ARG	NE-CZ-NH2	6.72	123.66	120.30
1	A	542	LEU	CA-CB-CG	-6.47	100.42	115.30
1	A	798	ARG	NE-CZ-NH2	-6.16	117.22	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	542	LEU	CA-CB-CG	-6.16	101.13	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1046	GLY	Peptide
1	B	1065	ASP	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	7544	0	7260	247	0
1	B	7623	0	7392	249	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	7	0	0	0	0
5	B	5	0	0	0	0
All	All	15185	0	14652	492	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 16.

The worst 5 of 492 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:4:SER:O	1:B:28:LYS:HG3	1.53	1.08
1:A:359:PRO:HD3	1:A:433:THR:O	1.55	1.06
1:A:90:TYR:HB2	1:A:301:ARG:HH11	1.21	1.05
1:A:1029:GLY:HA3	1:A:1030:LYS:HB2	1.39	1.04
1:B:1029:GLY:CA	1:B:1030:LYS:HB2	1.88	1.04

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	1001/1165 (86%)	875 (87%)	107 (11%)	19 (2%)	10	40
1	B	1002/1165 (86%)	899 (90%)	82 (8%)	21 (2%)	9	37
All	All	2003/2330 (86%)	1774 (89%)	189 (9%)	40 (2%)	9	38

5 of 40 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	92	LEU
1	A	622	GLY
1	A	623	ALA
1	A	1030	LYS
1	B	92	LEU

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	749/933 (80%)	699 (93%)	50 (7%)	20	56
1	B	769/933 (82%)	709 (92%)	60 (8%)	16	49
All	All	1518/1866 (81%)	1408 (93%)	110 (7%)	18	53

5 of 110 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1045	GLN
1	B	219	SER
1	B	907[B]	SER
1	B	30	VAL
1	B	120	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	10	ASN
1	B	220	GLN
1	B	873	GLN
1	B	57	HIS
1	B	120	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

2 non-standard protein/DNA/RNA residues 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
1	KCX	A	718[A]	1,3	7,11,12	0.76	0	7,12,14	1.24	1 (14%)
1	KCX	B	718[A]	1,3	7,11,12	0.98	0	7,12,14	1.11	0

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	718[A]	1,3	-	0/6/10/12	0/0/0/0
1	KCX	B	718[A]	1,3	-	0/6/10/12	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	718[A]	KCX	CD-CG-CB	-2.37	105.24	113.66

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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	1003/1165 (86%)	0.55	161 (16%) 3 1	19, 72, 163, 191	8 (0%)
1	B	1001/1165 (85%)	0.33	120 (11%) 6 2	19, 56, 139, 190	7 (0%)
All	All	2004/2330 (86%)	0.44	281 (14%) 4 2	19, 65, 156, 191	15 (0%)

The worst 5 of 281 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	335	SER	11.4
1	A	142	THR	8.3
1	B	288	ALA	7.9
1	A	285	LEU	7.7
1	B	346	ASN	7.2

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. 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
1	KCX	A	718[A]	12/13	0.98	0.13	-	20,21,22,22	0
1	KCX	B	718[A]	12/13	0.98	0.12	-	19,21,22,22	0

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	MG	B	1200	1/1	0.88	0.24	5.07	40,40,40,40	0
2	MG	A	1200	1/1	0.80	0.19	2.15	25,25,25,25	0
3	ZN	B	1201	1/1	0.98	0.06	-4.17	59,59,59,59	0
3	ZN	A	1201	1/1	0.97	0.09	-	56,56,56,56	0
4	CL	B	1202	1/1	0.97	0.11	-	30,30,30,30	0
4	CL	A	1202	1/1	0.97	0.17	-	24,24,24,24	0

6.5 Other polymers [i](#)

There are no such residues in this entry.