



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 02:25 am GMT

PDB ID : 3P0W
Title : Crystal structure of D-Glucarate dehydratase from *Ralstonia solanacearum* complexed with Mg and D-glucarate
Authors : Fedorov, A.A.; Fedorov, E.V.; Gerlt, J.A.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2010-09-29
Resolution : 1.71 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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

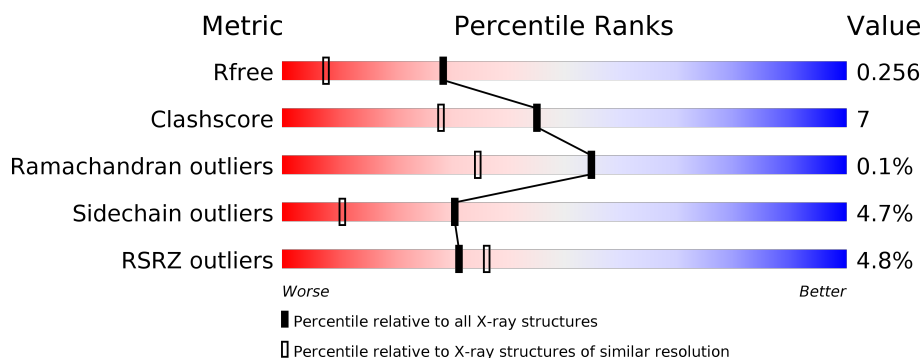
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.71 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}	100719	4385 (1.74-1.70)
Clashscore	112137	4841 (1.74-1.70)
Ramachandran outliers	110173	4771 (1.74-1.70)
Sidechain outliers	110143	4771 (1.74-1.70)
RSRZ outliers	101464	4426 (1.74-1.70)

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	470	<div> <div>2%</div> <div> <div></div> <div>78%</div> <div>11%</div> <div>•</div> <div>10%</div> </div> </div>
1	B	470	<div> <div>6%</div> <div> <div></div> <div>77%</div> <div>13%</div> <div>•</div> <div>9%</div> </div> </div>
1	C	470	<div> <div>4%</div> <div> <div></div> <div>71%</div> <div>17%</div> <div>•</div> <div>10%</div> </div> </div>
1	D	470	<div> <div>5%</div> <div> <div></div> <div>72%</div> <div>17%</div> <div>•</div> <div>10%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13261 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 Mandelate racemase/muconate lactonizing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	424	Total	C	N	O	S	0	0	0
			3237	2040	587	590	20			
1	B	428	Total	C	N	O	S	0	0	0
			3270	2061	592	597	20			
1	C	421	Total	C	N	O	S	0	0	0
			3220	2031	583	586	20			
1	D	425	Total	C	N	O	S	0	0	0
			3244	2044	588	592	20			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP B2UIZ1
A	2	SER	-	EXPRESSION TAG	UNP B2UIZ1
A	3	LEU	-	EXPRESSION TAG	UNP B2UIZ1
A	463	GLU	-	EXPRESSION TAG	UNP B2UIZ1
A	464	GLY	-	EXPRESSION TAG	UNP B2UIZ1
A	465	HIS	-	EXPRESSION TAG	UNP B2UIZ1
A	466	HIS	-	EXPRESSION TAG	UNP B2UIZ1
A	467	HIS	-	EXPRESSION TAG	UNP B2UIZ1
A	468	HIS	-	EXPRESSION TAG	UNP B2UIZ1
A	469	HIS	-	EXPRESSION TAG	UNP B2UIZ1
A	470	HIS	-	EXPRESSION TAG	UNP B2UIZ1
B	1	MET	-	EXPRESSION TAG	UNP B2UIZ1
B	2	SER	-	EXPRESSION TAG	UNP B2UIZ1
B	3	LEU	-	EXPRESSION TAG	UNP B2UIZ1
B	463	GLU	-	EXPRESSION TAG	UNP B2UIZ1
B	464	GLY	-	EXPRESSION TAG	UNP B2UIZ1
B	465	HIS	-	EXPRESSION TAG	UNP B2UIZ1
B	466	HIS	-	EXPRESSION TAG	UNP B2UIZ1
B	467	HIS	-	EXPRESSION TAG	UNP B2UIZ1
B	468	HIS	-	EXPRESSION TAG	UNP B2UIZ1
B	469	HIS	-	EXPRESSION TAG	UNP B2UIZ1

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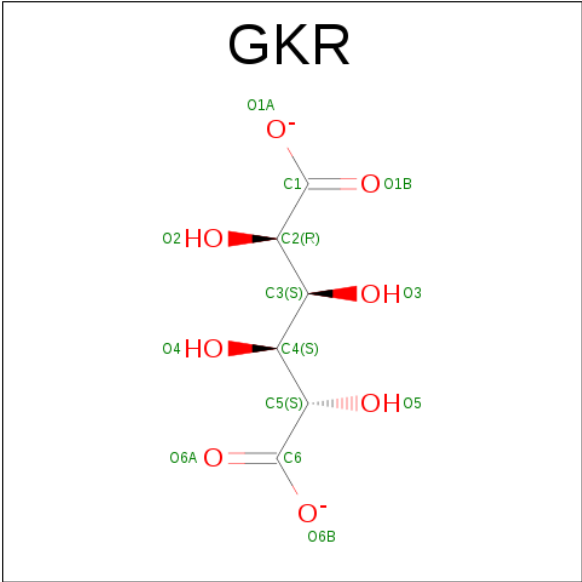
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Chain	Residue	Modelled	Actual	Comment	Reference
B	470	HIS	-	EXPRESSION TAG	UNP B2UIZ1
C	1	MET	-	EXPRESSION TAG	UNP B2UIZ1
C	2	SER	-	EXPRESSION TAG	UNP B2UIZ1
C	3	LEU	-	EXPRESSION TAG	UNP B2UIZ1
C	463	GLU	-	EXPRESSION TAG	UNP B2UIZ1
C	464	GLY	-	EXPRESSION TAG	UNP B2UIZ1
C	465	HIS	-	EXPRESSION TAG	UNP B2UIZ1
C	466	HIS	-	EXPRESSION TAG	UNP B2UIZ1
C	467	HIS	-	EXPRESSION TAG	UNP B2UIZ1
C	468	HIS	-	EXPRESSION TAG	UNP B2UIZ1
C	469	HIS	-	EXPRESSION TAG	UNP B2UIZ1
C	470	HIS	-	EXPRESSION TAG	UNP B2UIZ1
D	1	MET	-	EXPRESSION TAG	UNP B2UIZ1
D	2	SER	-	EXPRESSION TAG	UNP B2UIZ1
D	3	LEU	-	EXPRESSION TAG	UNP B2UIZ1
D	463	GLU	-	EXPRESSION TAG	UNP B2UIZ1
D	464	GLY	-	EXPRESSION TAG	UNP B2UIZ1
D	465	HIS	-	EXPRESSION TAG	UNP B2UIZ1
D	466	HIS	-	EXPRESSION TAG	UNP B2UIZ1
D	467	HIS	-	EXPRESSION TAG	UNP B2UIZ1
D	468	HIS	-	EXPRESSION TAG	UNP B2UIZ1
D	469	HIS	-	EXPRESSION TAG	UNP B2UIZ1
D	470	HIS	-	EXPRESSION TAG	UNP B2UIZ1

- 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
2	D	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0

- Molecule 3 is D-GLUCARATE (three-letter code: GKR) (formula: C₆H₈O₈).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			14	6	8		
3	B	1	Total	C	O	0	0
			14	6	8		
3	C	1	Total	C	O	0	0
			14	6	8		
3	D	1	Total	C	O	0	0
			14	6	8		

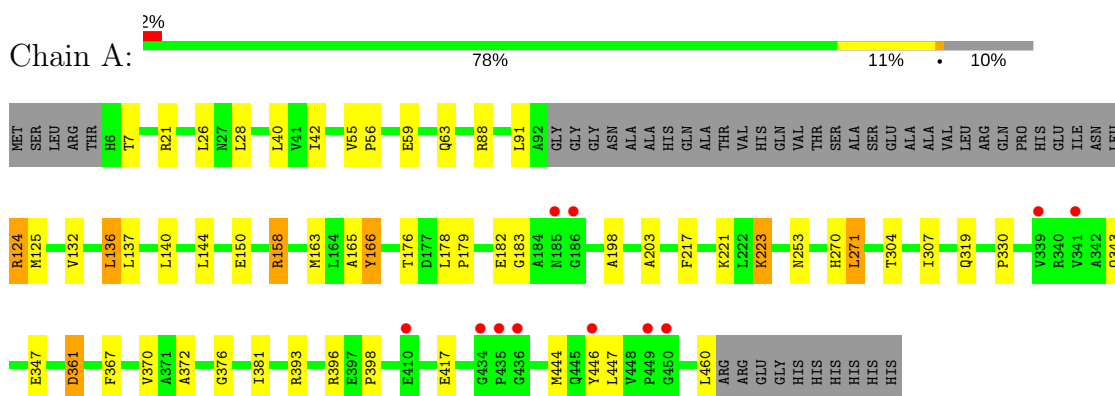
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	51	Total	O	0	0
			51	51		
4	B	99	Total	O	0	0
			99	99		
4	C	42	Total	O	0	0
			42	42		
4	D	38	Total	O	0	0
			38	38		

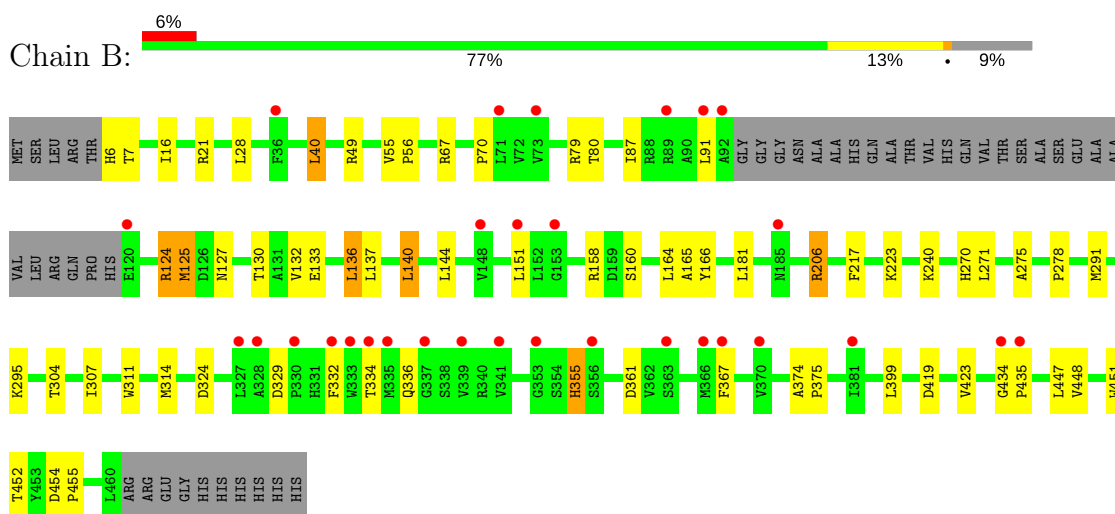
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

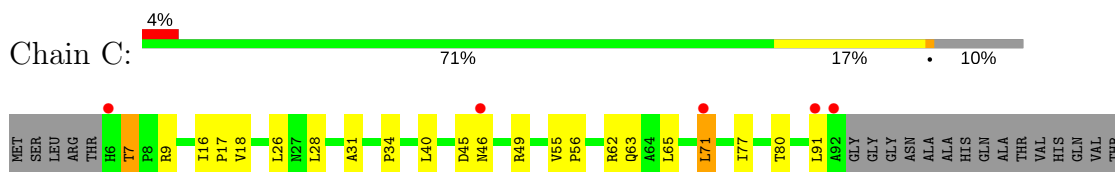
• Molecule 1: Mandelate racemase/muconate lactonizing protein

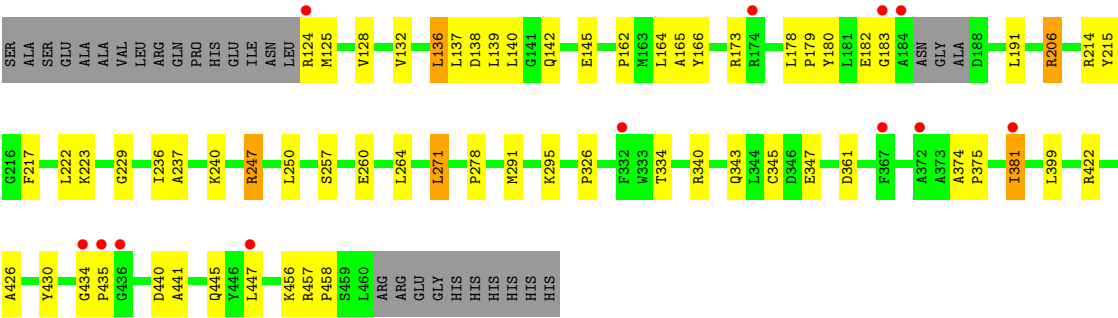


• Molecule 1: Mandelate racemase/muconate lactonizing protein

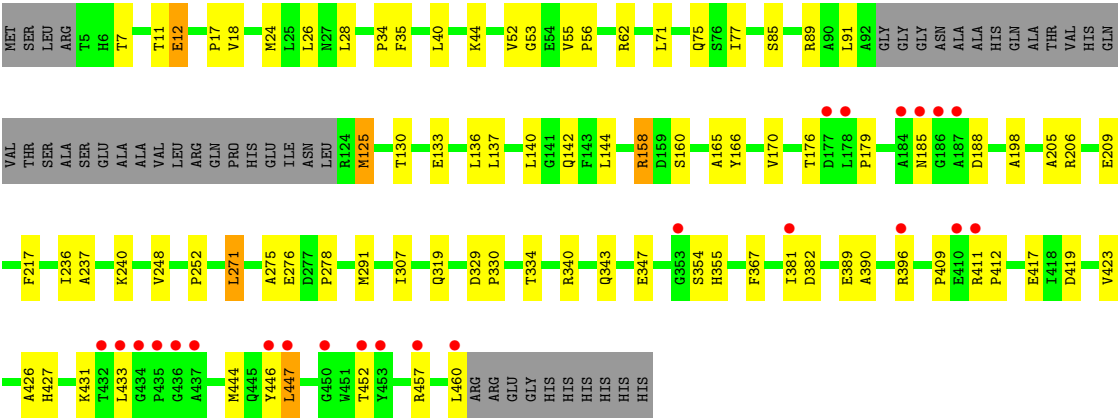


• Molecule 1: Mandelate racemase/muconate lactonizing protein





• Molecule 1: Mandelate racemase/muconate lactonizing protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.96Å 128.82Å 178.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.01 – 1.71 39.01 – 1.71	Depositor EDS
% Data completeness (in resolution range)	76.7 (39.01-1.71) 76.8 (39.01-1.71)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.83 (at 1.71Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.227 , 0.265 0.218 , 0.256	Depositor DCC
R_{free} test set	7644 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	34.7	Xtriage
Anisotropy	0.320	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 35.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13261	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.67% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.40	0/3312	0.58	0/4504
1	B	0.42	0/3345	0.60	0/4549
1	C	0.39	0/3294	0.55	0/4478
1	D	0.40	0/3319	0.55	0/4514
All	All	0.41	0/13270	0.57	0/18045

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	3237	0	3196	35	1
1	B	3270	0	3230	49	0
1	C	3220	0	3181	53	0
1	D	3244	0	3203	63	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	14	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	14	0	8	3	0
3	C	14	0	8	0	0
3	D	14	0	8	0	0
4	A	51	0	0	3	0
4	B	99	0	0	2	0
4	C	42	0	0	5	0
4	D	38	0	0	1	1
All	All	13261	0	12842	192	1

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 7.

The worst 5 of 192 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:206:ARG:HH11	1:C:206:ARG:HG3	1.07	1.10
1:B:206:ARG:HH11	1:B:206:ARG:HG3	1.02	1.08
1:C:9:ARG:H	1:C:46:ASN:HB2	1.31	0.94
1:D:158:ARG:HH11	1:D:158:ARG:HG2	1.33	0.91
1:B:206:ARG:HG3	1:B:206:ARG:NH1	1.83	0.88

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:GLN:NE2	4:D:503:HOH:O[2_564]	2.18	0.02

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	420/470 (89%)	410 (98%)	10 (2%)	0	100	100
1	B	424/470 (90%)	413 (97%)	11 (3%)	0	100	100
1	C	415/470 (88%)	404 (97%)	10 (2%)	1 (0%)	51	31
1	D	421/470 (90%)	407 (97%)	14 (3%)	0	100	100
All	All	1680/1880 (89%)	1634 (97%)	45 (3%)	1 (0%)	55	35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	334	THR

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	325/361 (90%)	313 (96%)	12 (4%)	39	17
1	B	329/361 (91%)	314 (95%)	15 (5%)	31	11
1	C	324/361 (90%)	306 (94%)	18 (6%)	25	7
1	D	326/361 (90%)	310 (95%)	16 (5%)	29	9
All	All	1304/1444 (90%)	1243 (95%)	61 (5%)	30	11

5 of 61 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	7	THR
1	C	136	LEU
1	D	240	LYS
1	C	26	LEU
1	C	71	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	GKR	A	472	2	7,13,13	2.27	2 (28%)	10,18,18	1.62	1 (10%)
3	GKR	B	472	2	7,13,13	2.19	1 (14%)	10,18,18	2.06	3 (30%)
3	GKR	C	472	2	7,13,13	2.24	2 (28%)	10,18,18	1.62	1 (10%)
3	GKR	D	472	2	7,13,13	2.27	2 (28%)	10,18,18	1.90	3 (30%)

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	GKR	A	472	2	-	0/12/20/20	0/0/0/0
3	GKR	B	472	2	-	0/12/20/20	0/0/0/0
3	GKR	C	472	2	-	0/12/20/20	0/0/0/0
3	GKR	D	472	2	-	0/12/20/20	0/0/0/0

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	472	GKR	C4-C3	2.09	1.57	1.53
3	A	472	GKR	C4-C3	2.19	1.57	1.53
3	D	472	GKR	C4-C3	2.28	1.57	1.53
3	D	472	GKR	O2-C2	4.77	1.52	1.42
3	A	472	GKR	O2-C2	4.87	1.52	1.42

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	472	GKR	O4-C4-C3	2.07	114.41	109.46
3	D	472	GKR	O2-C2-C3	2.46	112.98	107.52
3	B	472	GKR	O2-C2-C3	2.49	113.03	107.52
3	B	472	GKR	O4-C4-C3	3.15	117.00	109.46
3	B	472	GKR	O5-C5-C4	4.16	116.75	107.52

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	472	GKR	3	0

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	424/470 (90%)	0.07	11 (2%) 56 62	31, 39, 51, 68	0
1	B	428/470 (91%)	0.24	30 (7%) 17 20	28, 37, 50, 69	0
1	C	421/470 (89%)	0.24	17 (4%) 39 44	30, 41, 55, 73	0
1	D	425/470 (90%)	0.31	24 (5%) 25 28	31, 41, 58, 70	0
All	All	1698/1880 (90%)	0.22	82 (4%) 31 36	28, 39, 55, 73	0

The worst 5 of 82 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	92	ALA	6.5
1	B	434	GLY	6.3
1	D	435	PRO	6.2
1	D	434	GLY	5.1
1	C	435	PRO	5.1

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(\AA^2)	Q<0.9
3	GKR	D	472	14/14	0.80	0.14	1.51	43,50,53,60	0
2	MG	B	471	1/1	0.94	0.15	1.12	38,38,38,38	0
2	MG	A	471	1/1	0.93	0.12	0.97	40,40,40,40	0
3	GKR	A	472	14/14	0.85	0.12	0.86	41,46,50,50	0
3	GKR	C	472	14/14	0.81	0.14	0.81	43,47,52,52	0
3	GKR	B	472	14/14	0.88	0.11	-0.06	35,41,42,44	0
2	MG	D	471	1/1	0.90	0.09	-0.46	45,45,45,45	0
2	MG	C	471	1/1	0.94	0.06	-1.61	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.