



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 4, 2024 – 09:28 AM EST

PDB ID : 1EC8
Title : E. COLI GLUCARATE DEHYDRATASE BOUND TO PRODUCT 2,3-DIHYDROXY-5-OXO-HEXANEDIOATE
Authors : Gulick, A.M.; Hubbard, B.K.; Gerlt, J.A.; Rayment, I.
Deposited on : 2000-01-25
Resolution : 1.90 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

<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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

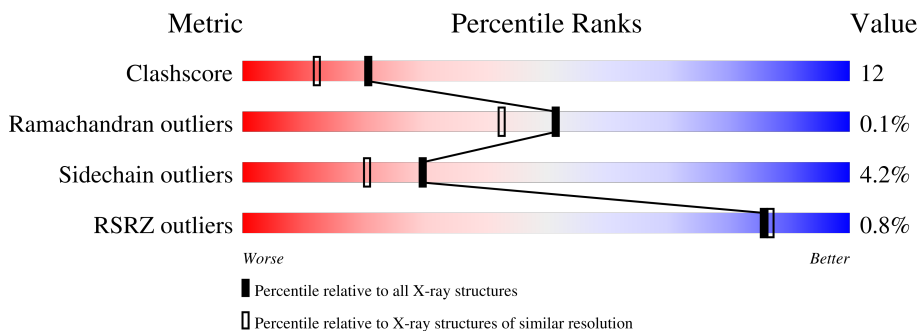
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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))
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	446	
1	B	446	
1	C	446	
1	D	446	

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
4	IPA	A	603	-	-	X	-
4	IPA	D	602	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14943 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.

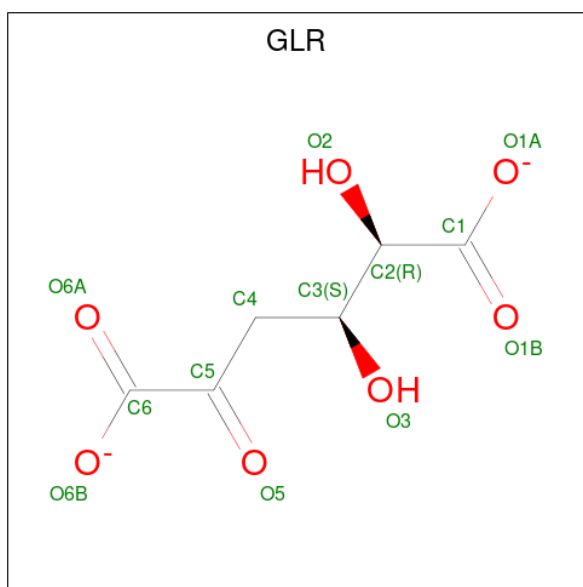
- Molecule 1 is a protein called GLUCARATE DEHYDRATASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	442	Total 3419	C 2161	N 599	O 638	S 21	0	0	0
1	B	442	Total 3408	C 2156	N 596	O 635	S 21	0	0	0
1	C	442	Total 3407	C 2154	N 595	O 637	S 21	0	0	0
1	D	442	Total 3403	C 2151	N 597	O 634	S 21	0	0	0

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

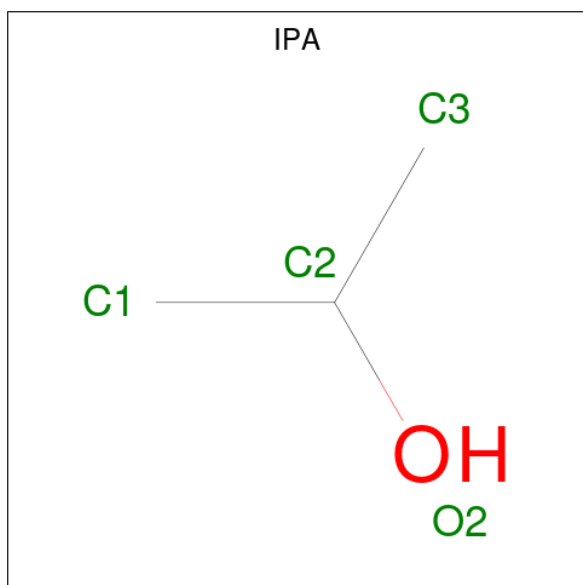
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Mg 1	0	0
2	B	1	Total 1	Mg 1	0	0
2	C	1	Total 1	Mg 1	0	0
2	D	1	Total 1	Mg 1	0	0

- Molecule 3 is 2,3-DIHYDROXY-5-OXO-HEXANEDIOATE (three-letter code: GLR) (formula: C₆H₆O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		
3	B	1	Total	C	O	0	0
			13	6	7		
3	C	1	Total	C	O	0	0
			13	6	7		
3	D	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C₃H₈O).



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

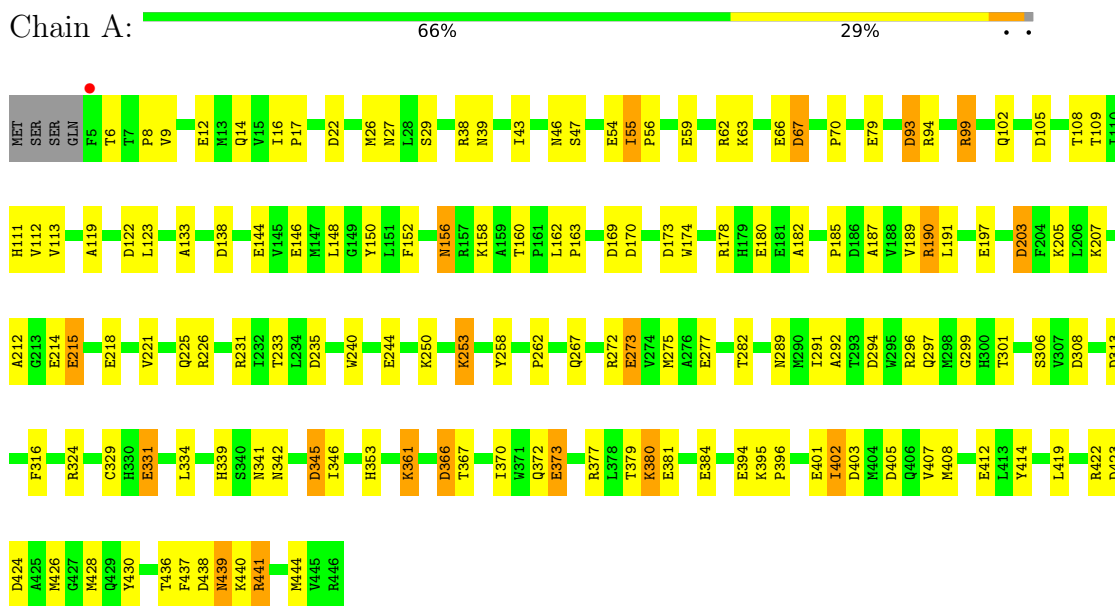
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	342	Total	O	0	0
			342	342		
5	B	259	Total	O	0	0
			259	259		
5	C	344	Total	O	0	0
			344	344		
5	D	289	Total	O	0	0
			289	289		

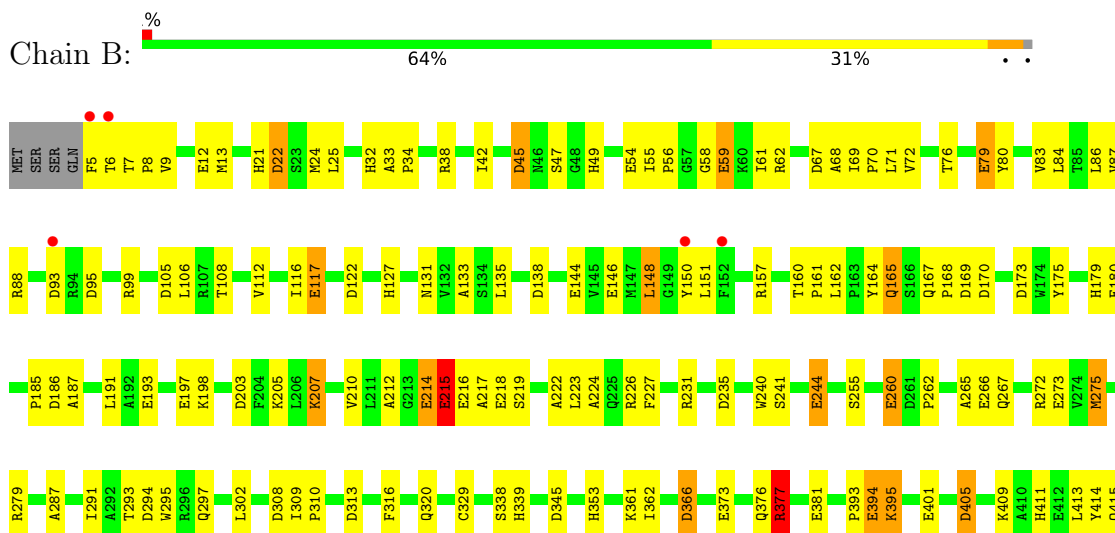
3 Residue-property plots

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: GLUCARATE DEHYDRATASE

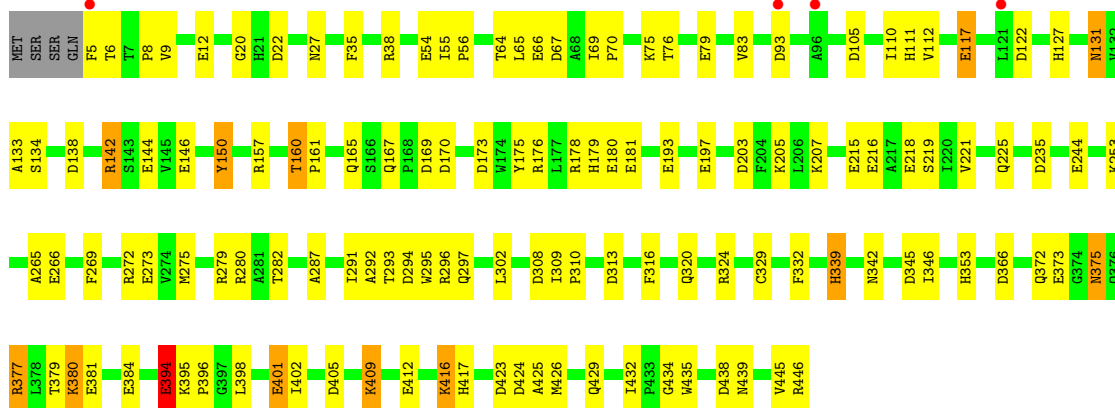


• Molecule 1: GLUCARATE DEHYDRATASE

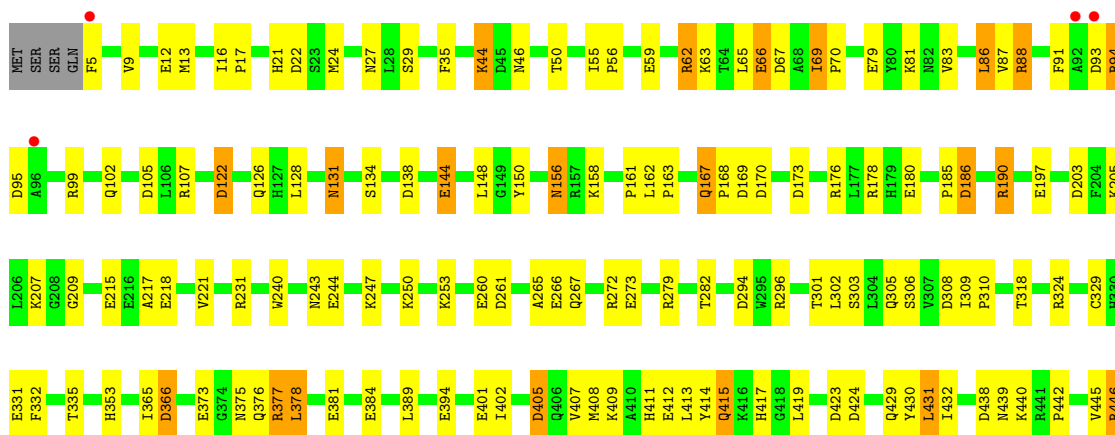




- Molecule 1: GLUCARATE DEHYDRATASE



- Molecule 1: GLUCARATE DEHYDRATASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	71.09Å 84.61Å 98.86Å 103.42° 93.99° 113.06°	Depositor
Resolution (Å)	30.00 – 1.90 29.65 – 1.70	Depositor EDS
% Data completeness (in resolution range)	95.0 (30.00-1.90) 94.4 (29.65-1.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.69 (at 1.70Å)	Xtrriage
Refinement program	TNT 5E	Depositor
R, R_{free}	0.196 , (Not available) 0.179 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	16.7	Xtrriage
Anisotropy	0.161	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 92.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14943	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.94% 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, IPA, GLR

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	1.10	20/3498 (0.6%)	1.29	43/4741 (0.9%)
1	B	1.05	21/3487 (0.6%)	1.27	43/4728 (0.9%)
1	C	1.11	23/3486 (0.7%)	1.28	43/4728 (0.9%)
1	D	1.08	17/3482 (0.5%)	1.30	48/4722 (1.0%)
All	All	1.09	81/13953 (0.6%)	1.29	177/18919 (0.9%)

The worst 5 of 81 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	412	GLU	CD-OE2	8.27	1.34	1.25
1	C	79	GLU	CD-OE2	8.20	1.34	1.25
1	A	214	GLU	CD-OE2	7.90	1.34	1.25
1	B	54	GLU	CD-OE2	7.60	1.34	1.25
1	C	215	GLU	CD-OE2	7.41	1.33	1.25

The worst 5 of 177 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	377	ARG	NE-CZ-NH1	10.00	125.30	120.30
1	A	324	ARG	NE-CZ-NH1	9.13	124.86	120.30
1	A	424	ASP	CB-CG-OD1	8.85	126.26	118.30
1	C	294	ASP	CB-CG-OD2	-8.83	110.35	118.30
1	A	203	ASP	CB-CG-OD2	-8.82	110.37	118.30

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	3419	0	3345	89	0
1	B	3408	0	3327	93	0
1	C	3407	0	3324	65	0
1	D	3403	0	3312	99	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	13	0	6	0	0
3	B	13	0	6	0	0
3	C	13	0	6	2	0
3	D	13	0	6	0	0
4	A	8	0	16	4	0
4	D	8	0	16	7	0
5	A	342	0	0	9	0
5	B	259	0	0	4	0
5	C	344	0	0	3	0
5	D	289	0	0	10	0
All	All	14943	0	13364	334	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 12.

The worst 5 of 334 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:D:402:ILE:HD11	1:D:407:VAL:HG21	1.42	1.01
1:D:408:MET:HA	1:D:408:MET:HE2	1.45	0.97
1:A:407:VAL:HG12	1:A:408:MET:CE	1.96	0.96
1:D:250:LYS:HA	1:D:253:LYS:HG3	1.50	0.91
1:D:415:GLN:HA	1:D:415:GLN:NE2	1.87	0.90

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	440/446 (99%)	425 (97%)	15 (3%)	0	100	100
1	B	440/446 (99%)	425 (97%)	15 (3%)	0	100	100
1	C	440/446 (99%)	425 (97%)	15 (3%)	0	100	100
1	D	440/446 (99%)	424 (96%)	15 (3%)	1 (0%)	47	38
All	All	1760/1784 (99%)	1699 (96%)	60 (3%)	1 (0%)	51	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	46	ASN

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	356/362 (98%)	337 (95%)	19 (5%)	22	13
1	B	353/362 (98%)	341 (97%)	12 (3%)	37	28
1	C	354/362 (98%)	341 (96%)	13 (4%)	34	25
1	D	351/362 (97%)	335 (95%)	16 (5%)	27	17
All	All	1414/1448 (98%)	1354 (96%)	60 (4%)	30	20

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	339	HIS
1	D	377	ARG
1	C	160	THR
1	D	207	LYS
1	D	439	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	417	HIS
1	D	156	ASN
1	C	439	ASN
1	D	131	ASN
1	D	267	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](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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
4	IPA	A	603	-	3,3,3	0.52	0	3,3,3	0.35	0
3	GLR	C	501	2	11,12,12	2.29	3 (27%)	10,16,16	1.09	0
4	IPA	D	602	-	3,3,3	0.67	0	3,3,3	0.48	0
4	IPA	A	601	-	3,3,3	0.59	0	3,3,3	0.18	0
3	GLR	D	502	2	11,12,12	1.86	2 (18%)	10,16,16	1.34	1 (10%)
4	IPA	D	604	-	3,3,3	0.54	0	3,3,3	0.31	0
3	GLR	A	499	2	11,12,12	1.55	2 (18%)	10,16,16	1.49	3 (30%)
3	GLR	B	500	2	11,12,12	2.13	2 (18%)	10,16,16	1.79	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	GLR	A	499	2	-	0/16/16/16	-
3	GLR	D	502	2	-	0/16/16/16	-
3	GLR	B	500	2	-	0/16/16/16	-
3	GLR	C	501	2	-	0/16/16/16	-

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	500	GLR	C5-C6	-5.83	1.45	1.53
3	C	501	GLR	C5-C6	-5.54	1.46	1.53
3	D	502	GLR	C5-C6	-4.29	1.47	1.53
3	C	501	GLR	C2-C1	-3.10	1.48	1.52
3	A	499	GLR	C5-C6	-2.57	1.50	1.53

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	500	GLR	O6A-C6-C5	-3.18	117.48	121.72
3	A	499	GLR	O5-C5-C6	2.84	123.54	119.43
3	D	502	GLR	O1A-C1-C2	2.54	120.13	113.27
3	B	500	GLR	O6B-C6-C5	2.44	120.64	113.97
3	A	499	GLR	O6A-C6-C5	-2.36	118.57	121.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	603	IPA	4	0
3	C	501	GLR	2	0
4	D	602	IPA	4	0
4	D	604	IPA	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	442/446 (99%)	-0.36	1 (0%) 95 95	11, 21, 44, 86	0
1	B	442/446 (99%)	-0.16	5 (1%) 80 82	10, 27, 55, 85	0
1	C	442/446 (99%)	-0.41	4 (0%) 84 85	9, 20, 42, 86	0
1	D	442/446 (99%)	-0.29	4 (0%) 84 85	9, 22, 54, 85	0
All	All	1768/1784 (99%)	-0.30	14 (0%) 86 87	9, 22, 50, 86	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	5	PHE	4.8
1	D	5	PHE	3.7
1	C	96	ALA	3.7
1	B	6	THR	3.6
1	A	5	PHE	3.1

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 monosaccharides 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(\AA^2)	Q<0.9
4	IPA	A	603	4/4	0.91	0.23	14,28,39,82	0
4	IPA	D	604	4/4	0.92	0.13	11,17,28,29	0
4	IPA	D	602	4/4	0.94	0.17	10,32,34,40	0
4	IPA	A	601	4/4	0.94	0.17	5,23,36,40	0
3	GLR	A	499	13/13	0.95	0.11	10,18,34,84	0
2	MG	D	498	1/1	0.96	0.05	15,15,15,15	0
2	MG	A	498	1/1	0.96	0.05	15,15,15,15	0
3	GLR	C	501	13/13	0.96	0.12	14,20,35,43	0
3	GLR	D	502	13/13	0.96	0.12	12,19,34,100	0
2	MG	B	498	1/1	0.97	0.05	17,17,17,17	0
3	GLR	B	500	13/13	0.97	0.10	12,22,39,42	0
2	MG	C	498	1/1	0.99	0.05	13,13,13,13	0

6.5 Other polymers [i](#)

There are no such residues in this entry.