



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 24, 2024 – 10:53 PM EDT

PDB ID : 6LIV
Title : Crystal structure of Tyrosine decarboxylase in complex with PLP
Authors : Wang, H.; Yu, J.; Yao, M.
Deposited on : 2019-12-13
Resolution : 2.31 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	:	2.37.1
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)	:	2.37.1

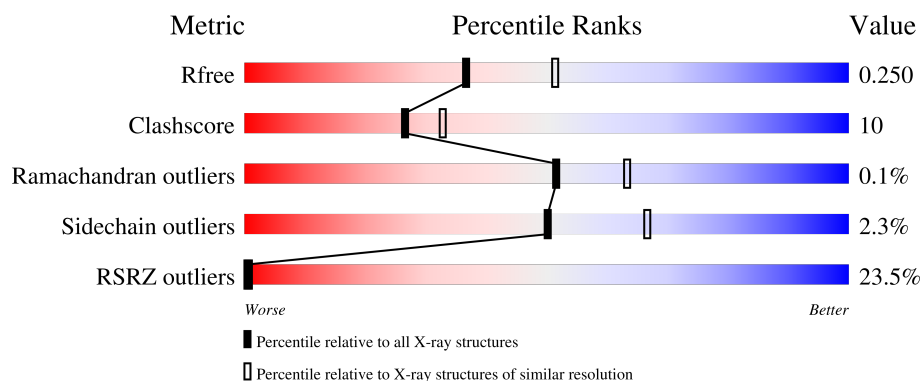
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 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}	130704	5974 (2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855 (2.34-2.30)

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	531	<div> <div>5%</div> <div>81% 9% 9%</div> </div>
1	B	531	<div> <div>4%</div> <div>82% 9% 9%</div> </div>
1	C	531	<div> <div>6%</div> <div>80% 11% 9%</div> </div>
1	D	531	<div> <div>2%</div> <div>81% 9% 9%</div> </div>
1	E	531	<div> <div>57%</div> <div>55% 34% 10%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	531	<div> <div>52%</div> <div>51%36%10%</div> </div>

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	GOL	C	601	-	-	X	-
2	GOL	C	602	-	-	-	X
2	GOL	D	601	-	-	X	-
2	GOL	D	602	-	-	X	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 23982 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 Tyrosine/DOPA decarboxylase 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	485	Total	C	N	O	P	S	0	0	0
			3840	2464	643	708	1	24			
1	B	483	Total	C	N	O	P	S	0	0	0
			3823	2454	639	705	1	24			
1	C	485	Total	C	N	O	P	S	0	0	0
			3840	2464	643	708	1	24			
1	D	483	Total	C	N	O	P	S	0	0	0
			3823	2454	639	705	1	24			
1	E	479	Total	C	N	O	P	S	0	0	0
			3802	2442	635	700	1	24			
1	F	477	Total	C	N	O	P	S	0	0	0
			3782	2429	633	695	1	24			

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



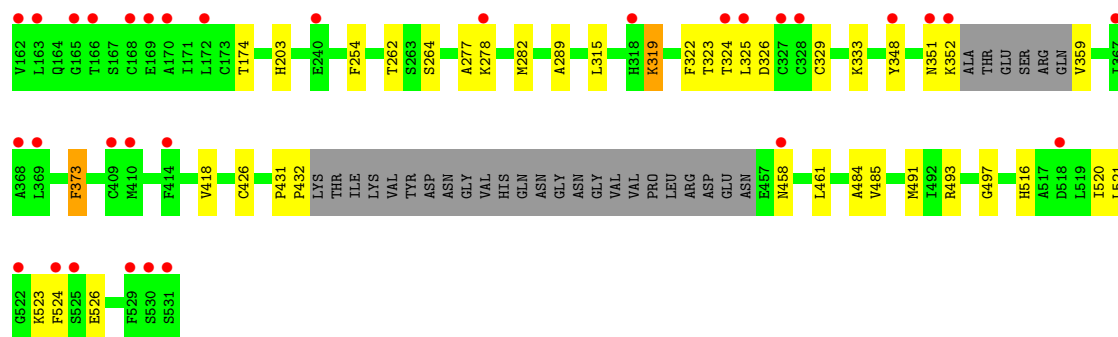
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 6	C 3	O 3	0	0
2	B	1	Total 6	C 3	O 3	0	0
2	B	1	Total 6	C 3	O 3	0	0
2	B	1	Total 6	C 3	O 3	0	0
2	C	1	Total 6	C 3	O 3	0	0
2	C	1	Total 6	C 3	O 3	0	0
2	C	1	Total 6	C 3	O 3	0	0
2	D	1	Total 6	C 3	O 3	0	0
2	D	1	Total 6	C 3	O 3	0	0

- Molecule 3 is water.

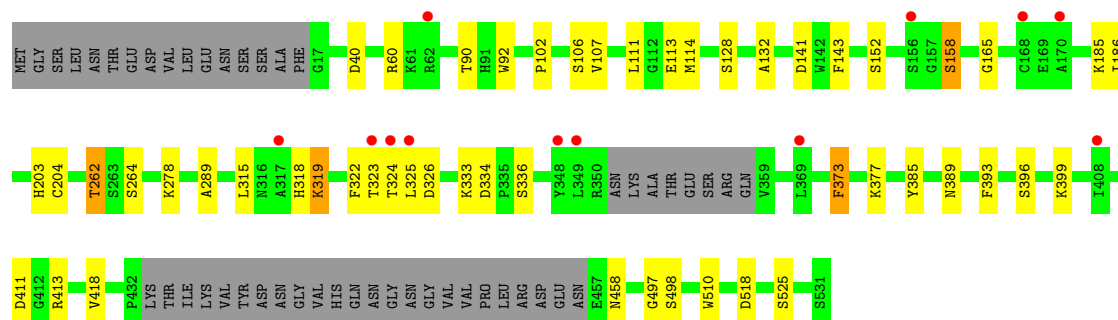
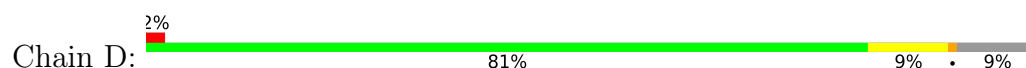
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	213	Total 213	O 213	0	0
3	B	262	Total 262	O 262	0	0
3	C	204	Total 204	O 204	0	0
3	D	269	Total 269	O 269	0	0
3	E	29	Total 29	O 29	0	0
3	F	41	Total 41	O 41	0	0

● Molecule 1: Tyrosine/DOPA decarboxylase 2

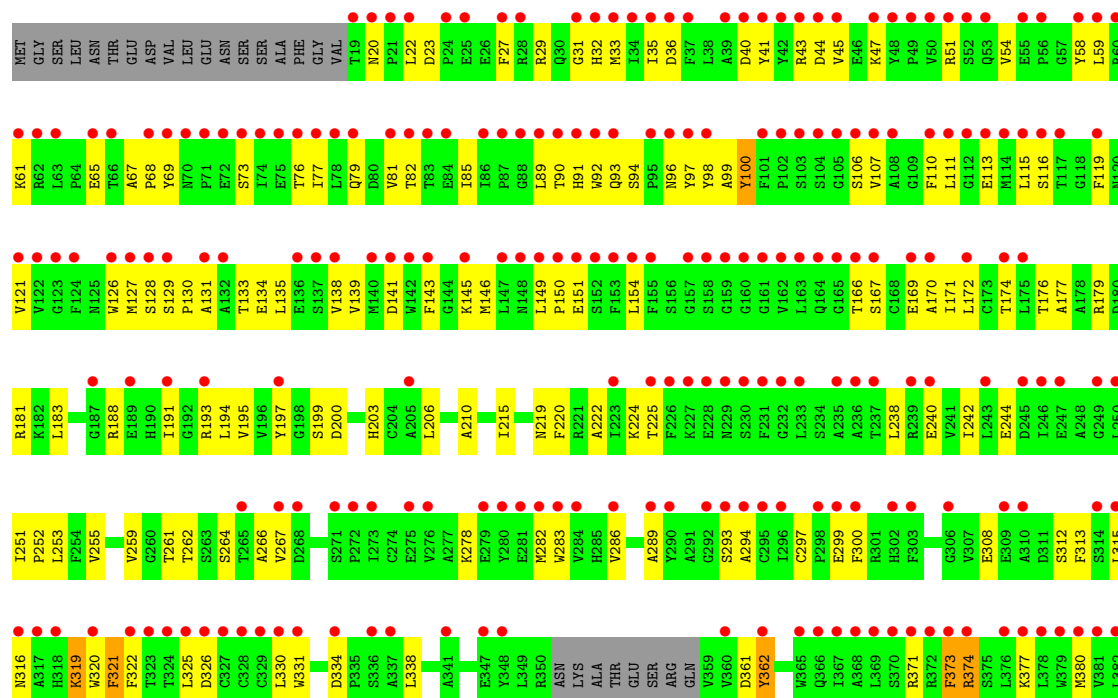




• Molecule 1: Tyrosine/DOPA decarboxylase 2



• Molecule 1: Tyrosine/DOPA decarboxylase 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	117.91Å 180.41Å 218.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.84 – 2.31 49.84 – 2.31	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.84-2.31) 99.7 (49.84-2.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.55 (at 2.32Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.227 , 0.250 0.227 , 0.250	Depositor DCC
R_{free} test set	10115 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.144	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 47.3	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	0.93	EDS
Total number of atoms	23982	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.97 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.6058e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: GOL, LLP

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	0.36	0/3909	0.42	0/5307
1	B	0.38	0/3892	0.44	0/5285
1	C	0.39	0/3909	0.42	0/5307
1	D	0.28	0/3892	0.42	0/5285
1	E	0.33	0/3870	0.47	0/5254
1	F	0.37	0/3850	0.52	0/5225
All	All	0.36	0/23322	0.45	0/31663

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	3840	0	3782	36	0
1	B	3823	0	3763	30	0
1	C	3840	0	3782	50	0
1	D	3823	0	3763	40	0
1	E	3802	0	3742	150	0
1	F	3782	0	3721	210	0
2	A	6	0	8	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	18	0	24	3	0
2	C	18	0	24	11	0
2	D	12	0	16	7	0
3	A	213	0	0	2	0
3	B	262	0	0	1	0
3	C	204	0	0	3	0
3	D	269	0	0	3	0
3	E	29	0	0	1	0
3	F	41	0	0	3	0
All	All	23982	0	22625	470	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 10.

The worst 5 of 470 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:319:LLP:H4'1	2:C:601:GOL:H11	1.23	1.14
1:C:203:HIS:NE2	2:C:601:GOL:H12	1.67	1.08
1:C:203:HIS:HE2	2:C:601:GOL:H12	1.00	1.07
1:F:385:TYR:HB3	1:F:390:LEU:HD21	1.44	0.99
1:F:131:ALA:O	1:F:135:LEU:HD12	1.61	0.98

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	478/531 (90%)	466 (98%)	11 (2%)	1 (0%)	47 58
1	B	476/531 (90%)	465 (98%)	11 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	478/531 (90%)	465 (97%)	13 (3%)	0	100	100
1	D	476/531 (90%)	465 (98%)	11 (2%)	0	100	100
1	E	470/531 (88%)	454 (97%)	15 (3%)	1 (0%)	47	58
1	F	468/531 (88%)	443 (95%)	25 (5%)	0	100	100
All	All	2846/3186 (89%)	2758 (97%)	86 (3%)	2 (0%)	51	63

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	100	TYR
1	A	324	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	415/455 (91%)	410 (99%)	5 (1%)	71	83
1	B	413/455 (91%)	405 (98%)	8 (2%)	57	73
1	C	415/455 (91%)	410 (99%)	5 (1%)	71	83
1	D	413/455 (91%)	405 (98%)	8 (2%)	57	73
1	E	411/455 (90%)	401 (98%)	10 (2%)	49	65
1	F	408/455 (90%)	388 (95%)	20 (5%)	25	34
All	All	2475/2730 (91%)	2419 (98%)	56 (2%)	50	66

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	143	PHE
1	F	480	TYR
1	E	420	ARG
1	F	458	ASN
1	F	362	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	392	ASN
1	F	30	GLN
1	F	120	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 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	LLP	E	319	1	23,24,25	2.59	6 (26%)	25,32,34	1.40	3 (12%)
1	LLP	F	319	1	23,24,25	2.59	6 (26%)	25,32,34	1.39	4 (16%)
1	LLP	D	319	1	23,24,25	2.61	6 (26%)	25,32,34	1.33	4 (16%)
1	LLP	A	319	1	23,24,25	2.59	6 (26%)	25,32,34	1.34	4 (16%)
1	LLP	C	319	1	23,24,25	2.60	6 (26%)	25,32,34	1.36	4 (16%)
1	LLP	B	319	1	23,24,25	2.60	5 (21%)	25,32,34	1.32	4 (16%)

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	LLP	E	319	1	-	5/16/17/19	0/1/1/1
1	LLP	F	319	1	-	5/16/17/19	0/1/1/1
1	LLP	D	319	1	-	2/16/17/19	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	LLP	A	319	1	-	2/16/17/19	0/1/1/1
1	LLP	C	319	1	-	2/16/17/19	0/1/1/1
1	LLP	B	319	1	-	2/16/17/19	0/1/1/1

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	319	LLP	C4-C4'	8.10	1.62	1.46
1	D	319	LLP	C4-C4'	8.07	1.62	1.46
1	B	319	LLP	C4-C4'	8.02	1.61	1.46
1	F	319	LLP	C4-C4'	8.01	1.61	1.46
1	A	319	LLP	C4-C4'	8.00	1.61	1.46

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	319	LLP	C4-C4'-NZ	-3.77	107.01	124.31
1	F	319	LLP	C4-C4'-NZ	-3.53	108.11	124.31
1	B	319	LLP	C4-C4'-NZ	-3.52	108.15	124.31
1	C	319	LLP	C4-C4'-NZ	-3.52	108.15	124.31
1	A	319	LLP	C4-C4'-NZ	-3.49	108.29	124.31

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	319	LLP	C-CA-CB-CG
1	B	319	LLP	C-CA-CB-CG
1	C	319	LLP	C-CA-CB-CG
1	D	319	LLP	C4-C4'-NZ-CE
1	D	319	LLP	C-CA-CB-CG

There are no ring outliers.

6 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	E	319	LLP	1	0
1	F	319	LLP	1	0
1	D	319	LLP	4	0
1	A	319	LLP	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	319	LLP	2	0
1	B	319	LLP	2	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

9 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	GOL	B	603	-	5,5,5	0.71	0	5,5,5	1.05	0
2	GOL	C	601	-	5,5,5	0.14	0	5,5,5	0.72	0
2	GOL	C	603	-	5,5,5	0.61	0	5,5,5	1.19	1 (20%)
2	GOL	D	601	-	5,5,5	0.60	0	5,5,5	0.45	0
2	GOL	D	602	-	5,5,5	0.43	0	5,5,5	0.64	0
2	GOL	C	602	-	5,5,5	0.24	0	5,5,5	0.56	0
2	GOL	A	601	-	5,5,5	0.27	0	5,5,5	0.99	0
2	GOL	B	601	-	5,5,5	0.42	0	5,5,5	0.67	0
2	GOL	B	602	-	5,5,5	0.31	0	5,5,5	0.61	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
2	GOL	B	603	-	-	2/4/4/4	-
2	GOL	C	601	-	-	4/4/4/4	-
2	GOL	C	603	-	-	2/4/4/4	-
2	GOL	D	601	-	-	4/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	D	602	-	-	2/4/4/4	-
2	GOL	C	602	-	-	2/4/4/4	-
2	GOL	A	601	-	-	4/4/4/4	-
2	GOL	B	601	-	-	2/4/4/4	-
2	GOL	B	602	-	-	0/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	603	GOL	O3-C3-C2	2.13	120.42	110.20

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	GOL	O1-C1-C2-C3
2	B	601	GOL	O1-C1-C2-C3
2	C	601	GOL	C1-C2-C3-O3
2	C	602	GOL	C1-C2-C3-O3
2	C	603	GOL	O1-C1-C2-C3

There are no ring outliers.

7 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	601	GOL	6	0
2	C	603	GOL	2	0
2	D	601	GOL	4	0
2	D	602	GOL	4	0
2	C	602	GOL	3	0
2	A	601	GOL	3	0
2	B	601	GOL	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	484/531 (91%)	0.47	28 (5%) 23 29	21, 30, 47, 74	0
1	B	482/531 (90%)	0.31	22 (4%) 32 40	21, 28, 43, 86	0
1	C	484/531 (91%)	0.47	34 (7%) 16 22	20, 30, 51, 83	0
1	D	482/531 (90%)	0.27	12 (2%) 57 64	20, 28, 43, 77	0
1	E	478/531 (90%)	2.87	303 (63%) 0 0	52, 76, 91, 101	0
1	F	476/531 (89%)	2.86	278 (58%) 0 0	43, 74, 96, 104	0
All	All	2886/3186 (90%)	1.20	677 (23%) 0 1	20, 33, 89, 104	0

The worst 5 of 677 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	22	LEU	18.8
1	F	379	TRP	13.4
1	F	48	TYR	12.0
1	F	33	MET	11.9
1	F	387	VAL	11.7

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	LLP	E	319	24/25	0.79	0.25	60,68,78,81	0
1	LLP	F	319	24/25	0.90	0.28	44,56,72,76	0
1	LLP	C	319	24/25	0.93	0.23	21,28,31,34	0
1	LLP	D	319	24/25	0.93	0.23	19,23,28,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	LLP	A	319	24/25	0.94	0.22	19,24,30,31	0
1	LLP	B	319	24/25	0.94	0.22	19,25,29,30	0

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
2	GOL	C	602	6/6	0.76	0.42	29,38,40,43	6
2	GOL	B	603	6/6	0.79	0.36	18,26,28,31	6
2	GOL	C	601	6/6	0.84	0.49	26,35,37,38	6
2	GOL	B	602	6/6	0.85	0.47	29,31,32,33	6
2	GOL	C	603	6/6	0.86	0.23	28,35,38,39	6
2	GOL	D	601	6/6	0.86	0.49	23,28,34,34	6
2	GOL	D	602	6/6	0.87	0.50	30,32,32,36	6
2	GOL	B	601	6/6	0.90	0.48	24,30,32,35	6
2	GOL	A	601	6/6	0.90	0.45	27,31,32,35	6

6.5 Other polymers [i](#)

There are no such residues in this entry.