



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 2, 2024 – 02:58 PM EST

PDB ID : 2WJ4
Title : CRYSTAL STRUCTURE OF THE COFACTOR-DEVOID 1-H-3-HYDROXY-4- OXOQUINALDINE 2,4-DIOXYGENASE (HOD) FROM ARTHROBACTER NITROGUAJACOLICUS RU61A ANAEROBICALLY COMPLEXED WITH ITS NATURAL SUBSTRATE 1-H-3-HYDROXY-4-OXOQUINALDINE
Authors : Steiner, R.A.
Deposited on : 2009-05-20
Resolution : 2.10 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<https://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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)

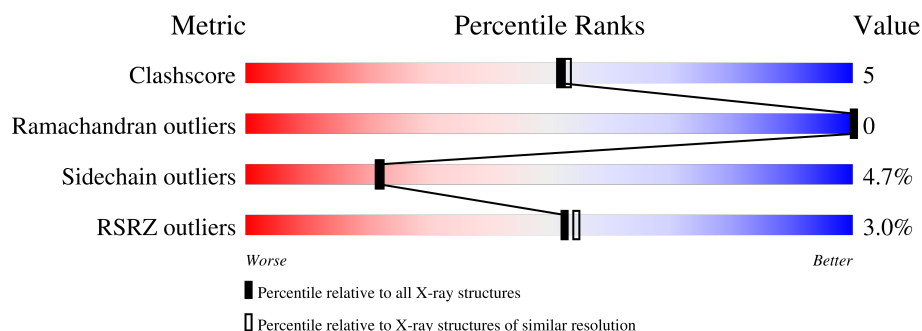
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



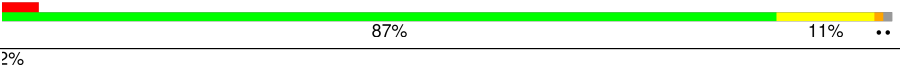

The reported resolution of this entry is 2.10 Å.

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))
Clashscore	180529	6893 (2.10-2.10)
Ramachandran outliers	177936	6839 (2.10-2.10)
Sidechain outliers	177891	6840 (2.10-2.10)
RSRZ outliers	164620	6234 (2.10-2.10)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	276	 4% 88% 11% ..
1	B	276	 2% 85% 13% ..
1	C	276	 4% 87% 11% ..
1	D	276	 2% 87% 12% ..

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.

Validation Pipeline (wwPDB-VP) : 2.40

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GOL	D	1275	-	-	X	-
2	GOL	D	1276	-	-	X	-
5	SRT	A	1284	-	X	-	-
5	SRT	B	1280	-	X	-	-
5	SRT	D	1279	-	X	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9483 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 1H-3-HYDROXY-4-OXOQUINALDINE 2,4-DIOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	274	Total	C	N	O	S	0	0	0
			2234	1426	391	409	8			
1	B	273	Total	C	N	O	S	0	0	0
			2227	1422	390	407	8			
1	C	273	Total	C	N	O	S	0	1	0
			2236	1428	391	409	8			
1	D	273	Total	C	N	O	S	0	0	0
			2230	1424	390	408	8			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	69	SER	CYS	engineered mutation	UNP A4V8M9
B	69	SER	CYS	engineered mutation	UNP A4V8M9
C	69	SER	CYS	engineered mutation	UNP A4V8M9
D	69	SER	CYS	engineered mutation	UNP A4V8M9

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



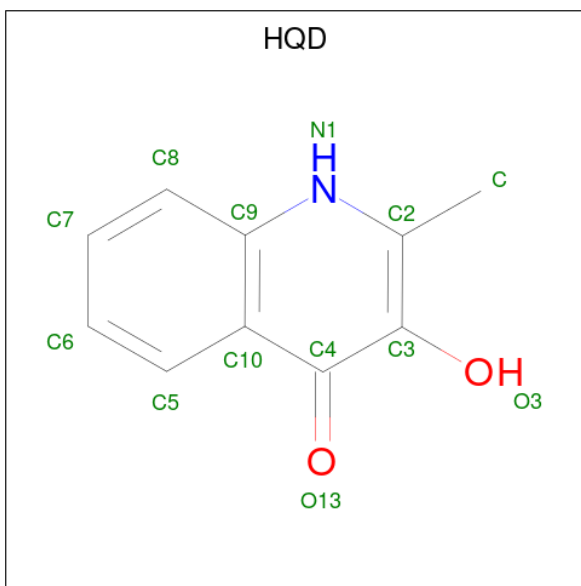
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

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

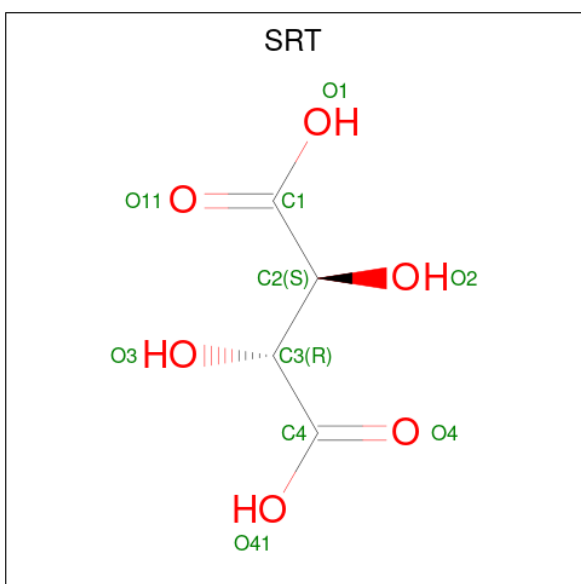
- Molecule 4 is 3-HYDROXY-2-METHYLQUINOLIN-4(1H)-ONE (three-letter code: HQD)

(formula: $C_{10}H_9NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			13	10	1	2		
4	B	1	Total	C	N	O	0	0
			13	10	1	2		
4	C	1	Total	C	N	O	0	0
			13	10	1	2		
4	D	1	Total	C	N	O	0	0
			13	10	1	2		

- Molecule 5 is S,R MESO-TARTARIC ACID (three-letter code: SRT) (formula: $C_4H_6O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 10 4 6	0	0
5	A	1	Total C O 10 4 6	0	0
5	A	1	Total C O 10 4 6	0	0
5	B	1	Total C O 10 4 6	0	0
5	B	1	Total C O 10 4 6	0	0
5	C	1	Total C O 10 4 6	0	0
5	D	1	Total C O 10 4 6	0	0

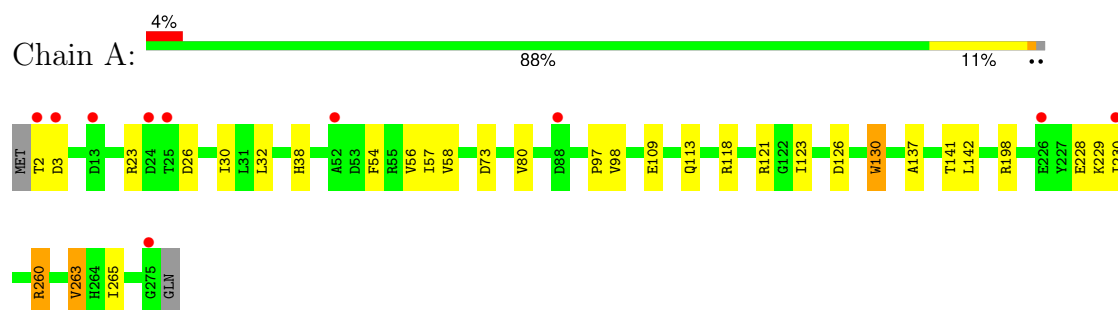
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	101	Total O 101 101	0	0
6	B	99	Total O 99 99	0	0
6	C	108	Total O 108 108	0	0
6	D	79	Total O 79 79	0	0

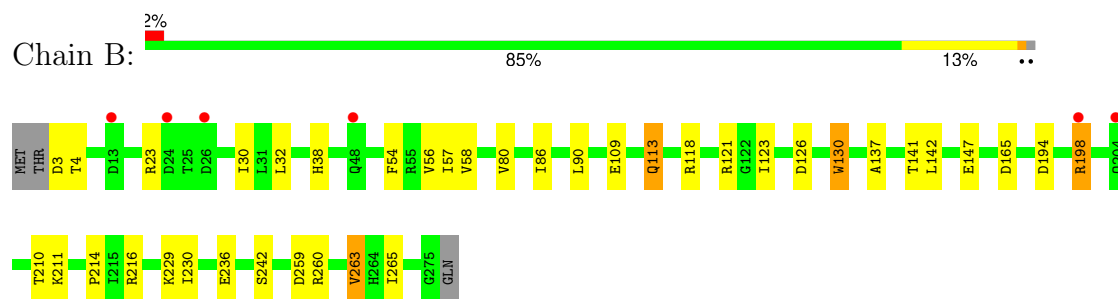
3 Residue-property plots [i](#)

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. 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. 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.

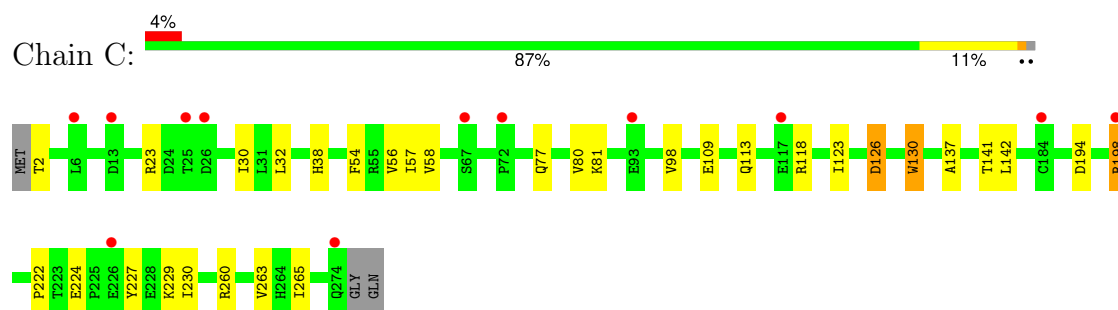
• Molecule 1: 1H-3-HYDROXY-4-OXOQUINALDINE 2,4-DIOXYGENASE



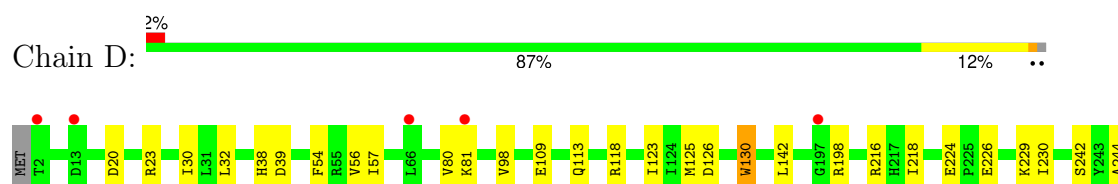
• Molecule 1: 1H-3-HYDROXY-4-OXOQUINALDINE 2,4-DIOXYGENASE



• Molecule 1: 1H-3-HYDROXY-4-OXOQUINALDINE 2,4-DIOXYGENASE



• Molecule 1: 1H-3-HYDROXY-4-OXOQUINALDINE 2,4-DIOXYGENASE



P253	D256	R260	V263	H264	I265	G274	GLY	GLN
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	44.81Å 167.20Å 167.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.84 – 2.10 38.84 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.2 (38.84-2.10) 93.5 (38.84-2.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.17 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0070	Depositor
R, R_{free}	0.176 , 0.204 0.219 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	32.4	Xtriage
Anisotropy	0.384	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 40.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.138 for -h,l,k	Xtriage
Reported twinning fraction	0.577 for H, K, L 0.423 for -H, L, K	Depositor
Outliers	3 of 70128 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9483	wwPDB-VP
Average B, all atoms (Å ²)	30.0	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 23.51 % 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 4.5991e-03. 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SRT, HQD, GOL, K

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	0.88	2/2305 (0.1%)	1.05	4/3137 (0.1%)
1	B	0.90	4/2298 (0.2%)	1.09	6/3127 (0.2%)
1	C	0.89	1/2310 (0.0%)	0.83	5/3144 (0.2%)
1	D	0.90	0/2301	0.88	4/3132 (0.1%)
All	All	0.89	7/9214 (0.1%)	0.96	19/12540 (0.2%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	263	VAL	CB-CG1	-11.32	1.29	1.52
1	B	263	VAL	CB-CG2	-8.72	1.34	1.52
1	A	113	GLN	CG-CD	-7.13	1.34	1.51
1	C	263	VAL	CB-CG2	-6.85	1.38	1.52
1	B	113	GLN	CD-OE1	-6.63	1.09	1.24

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	260	ARG	NE-CZ-NH2	28.88	134.74	120.30
1	B	260	ARG	NE-CZ-NH1	-27.34	106.63	120.30
1	A	260	ARG	NE-CZ-NH1	-27.09	106.76	120.30
1	A	260	ARG	NE-CZ-NH2	26.62	133.61	120.30
1	B	260	ARG	CD-NE-CZ	15.21	144.90	123.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	2234	0	2125	14	0
1	B	2227	0	2118	23	0
1	C	2236	0	2130	18	0
1	D	2230	0	2122	22	0
2	A	18	0	22	2	0
2	B	6	0	8	0	0
2	C	6	0	8	0	0
2	D	12	0	16	11	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	13	0	9	0	0
4	B	13	0	8	0	0
4	C	13	0	8	0	0
4	D	13	0	9	0	0
5	A	30	0	11	0	0
5	B	20	0	7	2	0
5	C	10	0	4	0	0
5	D	10	0	4	0	0
6	A	101	0	0	0	1
6	B	99	0	0	5	1
6	C	108	0	0	4	1
6	D	79	0	0	4	1
All	All	9483	0	8609	89	2

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 5.

The worst 5 of 89 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:224:GLU:OE2	6:C:2090:HOH:O	1.97	0.81
1:D:226:GLU:HB2	6:D:2063:HOH:O	1.90	0.70
2:D:1275:GOL:C2	2:D:1276:GOL:H32	2.22	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1275:GOL:H2	2:D:1276:GOL:H32	1.76	0.66
2:D:1275:GOL:C2	2:D:1276:GOL:C3	2.73	0.66

All (2) 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)
6:B:2088:HOH:O	6:C:2053:HOH:O[4_456]	2.04	0.16
6:A:2098:HOH:O	6:D:2045:HOH:O[4_456]	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	272/276 (99%)	265 (97%)	7 (3%)	0	100	100
1	B	271/276 (98%)	265 (98%)	6 (2%)	0	100	100
1	C	272/276 (99%)	266 (98%)	6 (2%)	0	100	100
1	D	271/276 (98%)	263 (97%)	8 (3%)	0	100	100
All	All	1086/1104 (98%)	1059 (98%)	27 (2%)	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	236/238 (99%)	223 (94%)	13 (6%)	18	16
1	B	235/238 (99%)	224 (95%)	11 (5%)	22	22
1	C	237/238 (100%)	227 (96%)	10 (4%)	25	26
1	D	236/238 (99%)	226 (96%)	10 (4%)	25	26
All	All	944/952 (99%)	900 (95%)	44 (5%)	22	22

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	118	ARG
1	D	38	HIS
1	C	126	ASP
1	C	198	ARG
1	D	113	GLN

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

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 23 ligands modelled in this entry, 5 are monoatomic - leaving 18 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	$\# Z > 2$
2	GOL	A	1277	3	5,5,5	0.29	0	5,5,5	1.82	1 (20%)
2	GOL	C	1275	3	5,5,5	0.25	0	5,5,5	0.70	0
2	GOL	D	1275	-	5,5,5	0.35	0	5,5,5	1.26	0
4	HQD	B	1278	-	14,14,14	2.95	7 (50%)	18,20,20	1.47	2 (11%)
4	HQD	A	1281	-	14,14,14	2.79	5 (35%)	18,20,20	1.45	2 (11%)
5	SRT	C	1278	-	9,9,9	1.25	1 (11%)	12,12,12	2.03	4 (33%)
2	GOL	B	1276	3	5,5,5	0.81	0	5,5,5	0.68	0
4	HQD	C	1277	-	14,14,14	3.67	5 (35%)	18,20,20	1.46	2 (11%)
5	SRT	D	1279	-	9,9,9	1.23	1 (11%)	12,12,12	2.65	5 (41%)
2	GOL	A	1276	3	5,5,5	0.67	0	5,5,5	1.05	0
4	HQD	D	1278	-	14,14,14	3.59	6 (42%)	18,20,20	1.45	2 (11%)
5	SRT	B	1279	-	9,9,9	1.44	2 (22%)	12,12,12	1.56	3 (25%)
5	SRT	A	1283	3	9,9,9	1.45	1 (11%)	12,12,12	1.93	6 (50%)
2	GOL	D	1276	-	5,5,5	0.64	0	5,5,5	0.96	0
2	GOL	A	1278	-	5,5,5	0.41	0	5,5,5	0.86	0
5	SRT	B	1280	-	9,9,9	1.93	3 (33%)	12,12,12	4.33	9 (75%)
5	SRT	A	1284	-	9,9,9	1.16	0	12,12,12	2.24	8 (66%)
5	SRT	A	1282	-	9,9,9	1.53	2 (22%)	12,12,12	1.12	2 (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
2	GOL	A	1277	3	-	1/4/4/4	-
2	GOL	C	1275	3	-	0/4/4/4	-
2	GOL	D	1275	-	-	2/4/4/4	-
4	HQD	B	1278	-	-	-	0/2/2/2
4	HQD	A	1281	-	-	-	0/2/2/2
5	SRT	C	1278	-	-	8/12/12/12	-
2	GOL	B	1276	3	-	2/4/4/4	-
5	SRT	D	1279	-	-	10/12/12/12	-
4	HQD	C	1277	-	-	-	0/2/2/2
2	GOL	A	1276	3	-	2/4/4/4	-
4	HQD	D	1278	-	-	-	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	SRT	B	1279	-	-	5/12/12/12	-
5	SRT	A	1283	3	-	4/12/12/12	-
2	GOL	D	1276	-	-	4/4/4/4	-
2	GOL	A	1278	-	-	3/4/4/4	-
5	SRT	B	1280	-	-	9/12/12/12	-
5	SRT	A	1284	-	-	8/12/12/12	-
5	SRT	A	1282	-	-	5/12/12/12	-

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1277	HQD	C3-C2	10.75	1.51	1.37
4	D	1278	HQD	C3-C2	10.20	1.50	1.37
4	A	1281	HQD	C3-C2	7.11	1.46	1.37
4	B	1278	HQD	C3-C2	7.00	1.46	1.37
4	A	1281	HQD	C10-C4	-5.19	1.38	1.48

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1280	SRT	O3-C3-C2	8.34	127.14	110.17
5	B	1280	SRT	O3-C3-C4	-7.34	95.00	110.69
5	B	1280	SRT	O4-C4-C3	-5.19	107.79	121.62
5	D	1279	SRT	O3-C3-C2	-4.94	100.10	110.17
5	D	1279	SRT	C2-C3-C4	4.88	120.63	109.82

There are no chirality outliers.

5 of 63 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1276	GOL	C1-C2-C3-O3
2	B	1276	GOL	O1-C1-C2-C3
2	D	1275	GOL	O1-C1-C2-C3
2	D	1276	GOL	O1-C1-C2-O2
2	D	1276	GOL	O1-C1-C2-C3

There are no ring outliers.

4 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1275	GOL	8	0
2	A	1276	GOL	2	0
2	D	1276	GOL	10	0
5	B	1280	SRT	2	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](#)

Warning: The R factor obtained from EDS is 0.227, which does not match the depositor's R factor of 0.17602. Please interpret the results in this section carefully.

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	274/276 (99%)	0.57	10 (3%) 46 48	20, 30, 40, 49	0
1	B	273/276 (98%)	0.50	6 (2%) 62 64	20, 30, 40, 46	0
1	C	273/276 (98%)	0.57	12 (4%) 39 42	18, 30, 39, 50	1 (0%)
1	D	273/276 (98%)	0.60	5 (1%) 67 69	21, 30, 40, 52	0
All	All	1093/1104 (99%)	0.56	33 (3%) 52 54	18, 30, 40, 52	1 (0%)

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	25	THR	4.1
1	C	13	ASP	3.8
1	C	198	ARG	3.5
1	A	3	ASP	3.1
1	C	117	GLU	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(Å ²)	Q<0.9
2	GOL	B	1276	6/6	0.56	0.27	46,47,47,48	0
2	GOL	A	1278	6/6	0.75	0.15	52,53,53,53	0
5	SRT	B	1279	10/10	0.76	0.14	32,36,39,42	0
2	GOL	A	1277	6/6	0.81	0.15	24,29,31,33	0
5	SRT	C	1278	10/10	0.81	0.12	30,37,41,41	0
5	SRT	A	1283	10/10	0.83	0.11	22,32,38,38	0
2	GOL	D	1275	6/6	0.83	0.11	31,32,37,38	0
2	GOL	D	1276	6/6	0.83	0.14	15,20,27,28	0
5	SRT	D	1279	10/10	0.84	0.11	31,40,45,47	0
5	SRT	B	1280	10/10	0.85	0.12	18,35,39,40	0
2	GOL	C	1275	6/6	0.86	0.14	33,35,35,38	0
5	SRT	A	1282	10/10	0.87	0.09	24,30,37,37	0
2	GOL	A	1276	6/6	0.88	0.14	29,35,37,39	0
5	SRT	A	1284	10/10	0.88	0.11	15,34,38,39	0
4	HQD	D	1278	13/13	0.91	0.08	23,27,31,32	0
4	HQD	C	1277	13/13	0.91	0.09	19,24,27,28	0
4	HQD	B	1278	13/13	0.92	0.08	15,18,21,21	0
4	HQD	A	1281	13/13	0.93	0.07	14,19,22,23	0
3	K	A	1280	1/1	0.94	0.10	39,39,39,39	0
3	K	A	1279	1/1	0.94	0.13	38,38,38,38	0
3	K	C	1276	1/1	0.95	0.06	25,25,25,25	0
3	K	D	1277	1/1	0.97	0.06	33,33,33,33	0
3	K	B	1277	1/1	0.98	0.04	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.