



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 05:41 AM GMT

PDB ID : 2W0U  
Title : CRYSTAL STRUCTURE OF HUMAN GLYCOLATE OXIDASE IN COMPLEX WITH THE INHIBITOR 5-[(4-CHLOROPHENYL)SULFANYL]-1,2,3-THIADIAZOLE-4-CARBOXYLATE.  
Authors : Bourhis, J.M.; Lindqvist, Y.  
Deposited on : 2008-10-10  
Resolution : 2.84 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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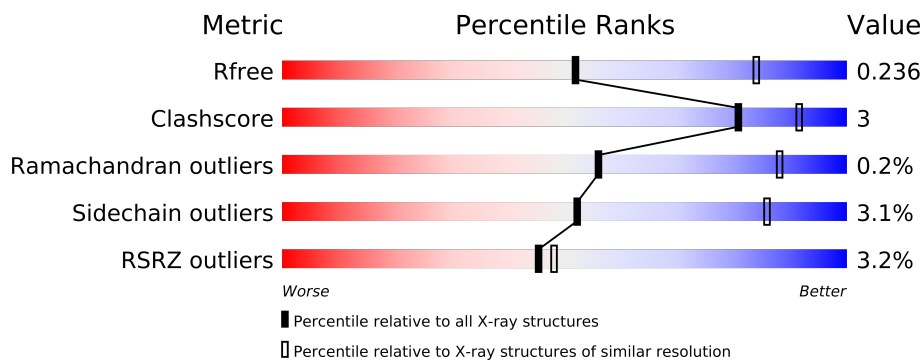
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.84 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))
$R_{free}$	66092	2270 (2.88-2.80)
Clashscore	79885	2848 (2.88-2.80)
Ramachandran outliers	78287	2786 (2.88-2.80)
Sidechain outliers	78261	2789 (2.88-2.80)
RSRZ outliers	66119	2274 (2.88-2.80)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	370	
1	B	370	
1	C	370	
1	D	370	

## 2 Entry composition i

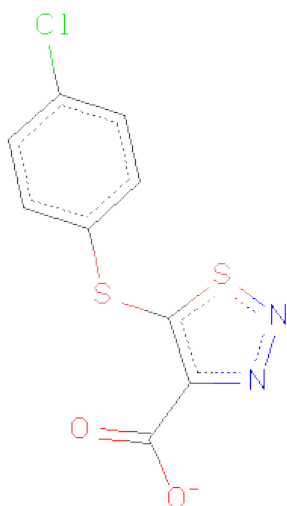
There are 4 unique types of molecules in this entry. The entry contains 10565 atoms, of which 0 are hydrogen and 0 are deuterium.

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 HYDROXYACID OXIDASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	334	Total	C	N	O	S	0	0	0
			2590	1645	456	477	12			
1	B	333	Total	C	N	O	S	0	0	0
			2583	1640	455	476	12			
1	C	332	Total	C	N	O	S	0	0	0
			2577	1634	456	475	12			
1	D	334	Total	C	N	O	S	0	0	0
			2594	1646	459	477	12			

- Molecule 2 is 5-[(4-CHLOROPHENYL)SULFANYL]-1,2,3-THIADIAZOLE-4-CARBOXYLATE (three-letter code: C7C) (formula: C<sub>9</sub>H<sub>4</sub>ClN<sub>2</sub>O<sub>2</sub>S<sub>2</sub>).



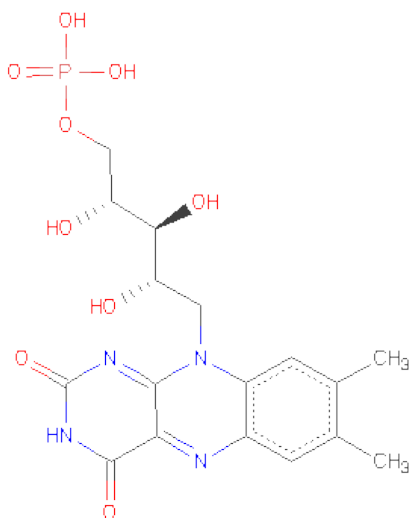
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	S	0
			16	9	1	2	2	2	
2	B	1	Total	C	Cl	N	O	S	0
			16	9	1	2	2	2	

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	C	1	Total	C	Cl	N	O	S	0	0
			16	9	1	2	2	2		
2	D	1	Total	C	Cl	N	O	S	0	0
			16	9	1	2	2	2		

- Molecule 3 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C<sub>17</sub>H<sub>21</sub>N<sub>4</sub>O<sub>9</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
3	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
3	C	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
3	D	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	6	Total	O	0	0
			6	6		
4	B	12	Total	O	0	0
			12	12		
4	C	8	Total	O	0	0
			8	8		

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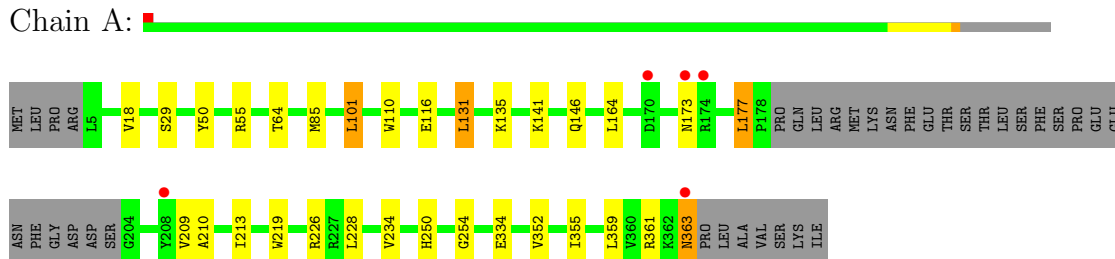
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	7	Total	O	0	0
			7	7		

### 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.

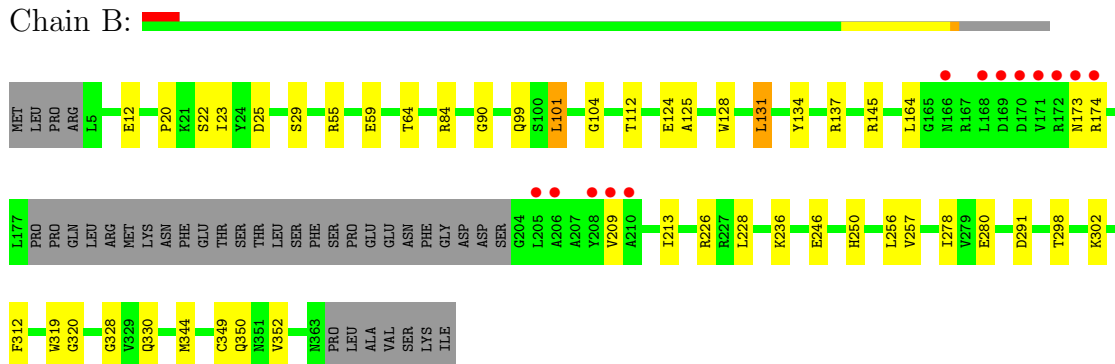
#### • Molecule 1: HYDROXYACID OXIDASE 1

Chain A:



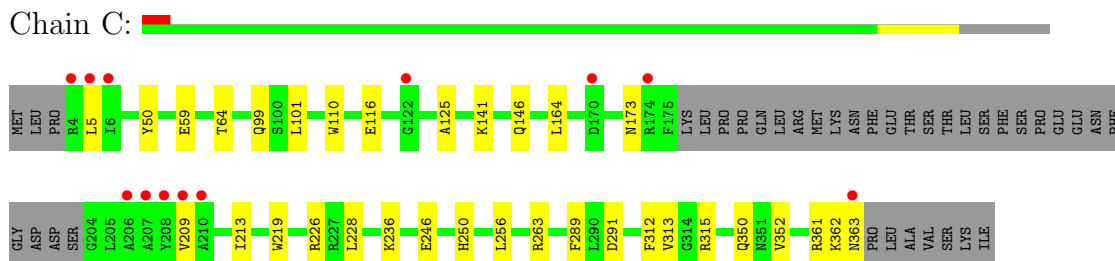
#### • Molecule 1: HYDROXYACID OXIDASE 1

Chain B:



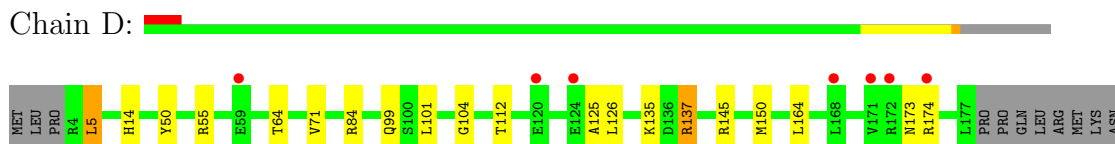
#### • Molecule 1: HYDROXYACID OXIDASE 1

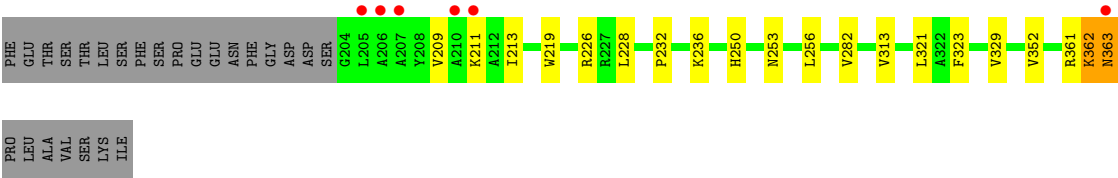
Chain C:



#### • Molecule 1: HYDROXYACID OXIDASE 1

Chain D:





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	138.69Å 138.69Å 186.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.73 – 2.84 47.43 – 2.84	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.73-2.84) 99.6 (47.43-2.84)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.80 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.205 , 0.250 0.195 , 0.236	Depositor DCC
$R_{free}$ test set	2179 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	44.5	Xtriage
Anisotropy	0.002	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 9.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	1 of 43574 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	10565	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.92% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FMN, C7C

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	0.42	1/2632 (0.0%)	0.57	1/3559 (0.0%)
1	B	0.40	0/2624	0.58	1/3547 (0.0%)
1	C	0.48	1/2618 (0.0%)	0.55	0/3539
1	D	0.52	2/2635 (0.1%)	0.59	2/3561 (0.1%)
All	All	0.46	4/10509 (0.0%)	0.57	4/14206 (0.0%)

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	D	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	363	ASN	C-O	11.22	1.44	1.23
1	C	363	ASN	C-O	9.52	1.41	1.23
1	D	363	ASN	N-CA	6.54	1.59	1.46
1	A	363	ASN	C-O	5.46	1.33	1.23

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	363	ASN	CA-C-O	-7.47	104.42	120.10
1	D	363	ASN	N-CA-C	6.81	129.39	111.00
1	B	131	LEU	CA-CB-CG	6.48	130.21	115.30
1	A	131	LEU	CA-CB-CG	5.92	128.92	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	362	LYS	Peptide

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2590	0	2659	15	0
1	B	2583	0	2652	21	0
1	C	2577	0	2641	15	0
1	D	2594	0	2665	18	0
2	A	16	0	4	2	0
2	B	16	0	4	0	0
2	C	16	0	4	2	0
2	D	16	0	4	0	0
3	A	31	0	19	0	0
3	B	31	0	19	1	0
3	C	31	0	19	0	0
3	D	31	0	19	0	0
4	A	6	0	0	0	0
4	B	12	0	0	0	0
4	C	8	0	0	0	0
4	D	7	0	0	0	0
All	All	10565	0	10709	70	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 3.

All (70) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:209:VAL:HG13	1:A:213:ILE:HD12	1.51	0.92
1:C:164:LEU:HD13	1:C:209:VAL:HG21	1.58	0.83
1:D:137:ARG:HH11	1:D:137:ARG:HG2	1.49	0.77
1:B:164:LEU:HD13	1:B:209:VAL:HG21	1.70	0.74

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:145:ARG:NH2	1:B:228:LEU:O	2.22	0.72
1:C:59:GLU:O	1:C:350:GLN:NE2	2.25	0.68
1:A:116:GLU:OE2	1:A:146:GLN:NE2	2.29	0.66
1:D:209:VAL:HG13	1:D:213:ILE:HD12	1.78	0.63
1:A:110:TRP:NE1	2:A:1364:C7C:CL	2.69	0.62
1:D:164:LEU:HD13	1:D:209:VAL:HG21	1.81	0.62
1:A:219:TRP:HB3	1:A:250:HIS:CE1	2.35	0.61
1:D:14:HIS:CD2	1:D:323:PHE:HD1	2.20	0.60
1:C:64:THR:HB	1:C:352:VAL:HG21	1.83	0.59
1:A:141:LYS:HG3	1:A:228:LEU:HD11	1.83	0.59
1:D:362:LYS:HG2	1:D:363:ASN:C	2.23	0.58
1:B:101:LEU:HD11	1:B:330:GLN:HG3	1.87	0.57
1:B:209:VAL:HG13	1:B:213:ILE:HD12	1.85	0.57
1:A:164:LEU:HD13	1:A:209:VAL:HG21	1.89	0.55
1:C:219:TRP:HB3	1:C:250:HIS:CE1	2.42	0.54
1:A:135:LYS:NZ	1:A:210:ALA:O	2.41	0.54
1:B:246:GLU:O	1:B:250:HIS:HD2	1.91	0.53
1:A:355:ILE:HG23	1:A:359:LEU:HD12	1.92	0.52
1:A:101:LEU:HD21	1:A:334:GLU:HG3	1.90	0.52
1:C:116:GLU:OE2	1:C:146:GLN:HG2	2.09	0.51
1:C:209:VAL:HG13	1:C:213:ILE:HD12	1.92	0.51
1:C:256:LEU:HD13	1:C:289:PHE:HB2	1.91	0.51
1:D:84:ARG:HD2	1:D:112:THR:O	2.11	0.50
1:D:232:PRO:HA	1:D:253:ASN:OD1	2.13	0.49
1:C:50:TYR:CE2	1:C:361:ARG:HB2	2.48	0.48
1:B:344:MET:HG2	1:B:349:CYS:HB2	1.95	0.48
1:D:219:TRP:HB3	1:D:250:HIS:CE1	2.49	0.48
1:D:137:ARG:NH1	1:D:137:ARG:HG2	2.24	0.48
1:D:99:GLN:HB2	1:D:125:ALA:HB2	1.96	0.48
1:C:236:LYS:HA	1:C:256:LEU:HB3	1.96	0.47
1:D:321:LEU:HD13	1:D:329:VAL:HG21	1.96	0.47
1:C:141:LYS:HG3	1:C:228:LEU:HD11	1.97	0.47
1:B:59:GLU:O	1:B:350:GLN:NE2	2.46	0.46
1:B:257:VAL:HG22	1:B:278:ILE:HD13	1.98	0.46
1:C:246:GLU:O	1:C:250:HIS:HD2	1.98	0.46
1:B:12:GLU:HG3	1:B:319:TRP:CE2	2.51	0.46
1:D:145:ARG:NH2	1:D:228:LEU:O	2.49	0.46
1:D:50:TYR:CE2	1:D:361:ARG:HB2	2.51	0.46
1:B:320:GLY:O	1:B:328:GLY:HA3	2.17	0.45
1:A:64:THR:HB	1:A:352:VAL:HG21	1.97	0.45
1:D:64:THR:HB	1:D:352:VAL:HG21	1.98	0.45
1:B:25:ASP:O	1:B:29:SER:OG	2.23	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:137:ARG:HH11	1:D:137:ARG:CG	2.25	0.45
1:B:298:THR:O	1:B:302:LYS:HG3	2.17	0.45
1:C:110:TRP:NE1	2:C:1364:C7C:CL	2.87	0.45
1:A:85:MET:HG2	1:A:177:LEU:HD13	1.99	0.44
1:A:234:VAL:HG13	1:A:254:GLY:C	2.37	0.44
1:A:110:TRP:CD1	2:A:1364:C7C:CL	3.08	0.44
1:C:291:ASP:HB3	1:C:312:PHE:HB2	1.99	0.43
1:B:20:PRO:HG2	1:B:23:ILE:HD12	2.00	0.43
1:B:84:ARG:HG3	1:B:90:GLY:HA3	2.01	0.43
1:B:236:LYS:HA	1:B:256:LEU:HB3	2.01	0.42
1:A:18:VAL:O	1:B:20:PRO:HB3	2.19	0.42
1:B:134:TYR:O	1:B:137:ARG:NH1	2.53	0.41
1:D:104:GLY:HA2	1:D:126:LEU:O	2.20	0.41
1:B:104:GLY:HA3	1:B:128:TRP:CH2	2.55	0.41
2:C:1364:C7C:O15	2:C:1364:C7C:S8	2.79	0.41
1:B:99:GLN:HB2	1:B:125:ALA:HB2	2.03	0.41
1:D:236:LYS:HA	1:D:256:LEU:HB3	2.03	0.41
1:A:50:TYR:CE2	1:A:361:ARG:HB2	2.55	0.41
1:B:64:THR:HB	1:B:352:VAL:HG21	2.03	0.41
1:C:263:ARG:HD2	1:C:315:ARG:NH2	2.37	0.41
3:B:1365:FMN:H9	3:B:1365:FMN:H1'2	1.84	0.40
1:D:135:LYS:HD2	1:D:211:LYS:O	2.22	0.40
1:B:291:ASP:HB3	1:B:312:PHE:HB2	2.03	0.40
1:C:99:GLN:HB2	1:C:125:ALA:HB2	2.04	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	330/370 (89%)	321 (97%)	9 (3%)	0	100	100
1	B	329/370 (89%)	315 (96%)	14 (4%)	0	100	100
1	C	328/370 (89%)	311 (95%)	16 (5%)	1 (0%)	50	83

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	D	330/370 (89%)	310 (94%)	19 (6%)	1 (0%)	50 83
All	All	1317/1480 (89%)	1257 (95%)	58 (4%)	2 (0%)	56 88

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	5	LEU
1	C	5	LEU

### 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	274/308 (89%)	266 (97%)	8 (3%)	55 87
1	B	273/308 (89%)	263 (96%)	10 (4%)	45 81
1	C	272/308 (88%)	267 (98%)	5 (2%)	71 94
1	D	274/308 (89%)	263 (96%)	11 (4%)	42 78
All	All	1093/1232 (89%)	1059 (97%)	34 (3%)	52 86

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	SER
1	A	55	ARG
1	A	101	LEU
1	A	131	LEU
1	A	173	ASN
1	A	177	LEU
1	A	226	ARG
1	A	363	ASN
1	B	22	SER
1	B	55	ARG
1	B	101	LEU
1	B	112	THR
1	B	124	GLU

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Mol	Chain	Res	Type
1	B	131	LEU
1	B	173	ASN
1	B	174	ARG
1	B	226	ARG
1	B	280	GLU
1	C	101	LEU
1	C	173	ASN
1	C	226	ARG
1	C	313	VAL
1	C	362	LYS
1	D	5	LEU
1	D	55	ARG
1	D	71	VAL
1	D	101	LEU
1	D	137	ARG
1	D	150	MET
1	D	173	ASN
1	D	174	ARG
1	D	226	ARG
1	D	282	VAL
1	D	313	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	HIS
1	A	146	GLN
1	A	250	HIS
1	B	250	HIS
1	C	250	HIS
1	C	324	GLN
1	D	69	GLN
1	D	250	HIS
1	D	324	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

8 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	C7C	A	1364	-	13,17,17	2.12	4 (30%)	13,23,23	4.31	3 (23%)
3	FMN	A	1365	-	33,33,33	0.95	1 (3%)	46,50,50	1.45	6 (13%)
2	C7C	B	1364	-	13,17,17	2.13	4 (30%)	13,23,23	4.30	3 (23%)
3	FMN	B	1365	-	33,33,33	0.92	1 (3%)	46,50,50	1.43	5 (10%)
2	C7C	C	1364	-	13,17,17	2.14	4 (30%)	13,23,23	4.28	3 (23%)
3	FMN	C	1365	-	33,33,33	1.07	2 (6%)	46,50,50	1.57	7 (15%)
2	C7C	D	1364	-	13,17,17	2.13	4 (30%)	13,23,23	4.30	3 (23%)
3	FMN	D	1365	-	33,33,33	1.03	2 (6%)	46,50,50	1.64	7 (15%)

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	C7C	A	1364	-	-	0/2/8/8	0/2/2/2
3	FMN	A	1365	-	-	0/18/18/18	0/0/3/3
2	C7C	B	1364	-	-	0/2/8/8	0/2/2/2
3	FMN	B	1365	-	-	0/18/18/18	0/0/3/3
2	C7C	C	1364	-	-	0/2/8/8	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FMN	C	1365	-	-	0/18/18/18	0/0/3/3
2	C7C	D	1364	-	-	0/2/8/8	0/2/2/2
3	FMN	D	1365	-	-	0/18/18/18	0/0/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1364	C7C	C4-S8	-4.95	1.70	1.77
2	B	1364	C7C	C4-S8	-4.94	1.70	1.77
2	C	1364	C7C	C4-S8	-4.93	1.70	1.77
2	A	1364	C7C	C4-S8	-4.90	1.70	1.77
2	C	1364	C7C	C13-C9	4.24	1.48	1.37
2	A	1364	C7C	C13-C9	4.23	1.48	1.37
2	B	1364	C7C	C13-C9	4.22	1.48	1.37
2	D	1364	C7C	C13-C9	4.22	1.48	1.37
3	C	1365	FMN	C1'-N10	3.26	1.51	1.48
3	D	1365	FMN	C1'-N10	3.16	1.51	1.48
2	C	1364	C7C	S10-N11	2.49	1.70	1.67
2	B	1364	C7C	S10-N11	2.46	1.70	1.67
2	D	1364	C7C	S10-N11	2.45	1.70	1.67
2	A	1364	C7C	S10-N11	2.43	1.70	1.67
2	B	1364	C7C	C1-CL	2.34	1.80	1.74
2	C	1364	C7C	C1-CL	2.32	1.79	1.74
2	D	1364	C7C	C1-CL	2.31	1.79	1.74
2	A	1364	C7C	C1-CL	2.30	1.79	1.74
3	D	1365	FMN	C5A-N5	2.25	1.38	1.35
3	A	1365	FMN	C5A-N5	2.14	1.38	1.35
3	B	1365	FMN	C5A-N5	2.12	1.38	1.35
3	C	1365	FMN	C5A-N5	2.11	1.38	1.35

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1364	C7C	C13-N12-N11	14.71	115.75	106.43
2	D	1364	C7C	C13-N12-N11	14.67	115.73	106.43
2	B	1364	C7C	C13-N12-N11	14.67	115.72	106.43
2	C	1364	C7C	C13-N12-N11	14.63	115.70	106.43
3	D	1365	FMN	C2-N1-C10	6.27	121.30	114.98
3	B	1365	FMN	C2-N1-C10	5.84	120.86	114.98
3	C	1365	FMN	C2-N1-C10	5.71	120.73	114.98
3	A	1365	FMN	C2-N1-C10	5.46	120.48	114.98
2	A	1364	C7C	C9-S10-N11	3.67	94.25	90.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1364	C7C	C9-S10-N11	3.66	94.24	90.44
2	D	1364	C7C	C9-S10-N11	3.64	94.22	90.44
2	C	1364	C7C	C9-S10-N11	3.64	94.22	90.44
3	D	1365	FMN	C4A-C10-N1	-3.53	119.20	122.73
3	C	1365	FMN	C5A-C9A-N10	3.43	120.18	116.80
3	D	1365	FMN	C4A-N5-C5A	3.42	120.53	116.69
3	B	1365	FMN	C5A-C9A-N10	3.25	120.00	116.80
3	A	1365	FMN	C4A-C10-N1	-3.09	119.65	122.73
3	D	1365	FMN	C5A-C9A-N10	3.06	119.82	116.80
3	B	1365	FMN	C4A-C10-N1	-3.05	119.69	122.73
3	A	1365	FMN	C4A-N5-C5A	3.04	120.11	116.69
3	C	1365	FMN	C4A-C10-N1	-3.00	119.73	122.73
2	B	1364	C7C	C4-S8-C9	2.89	109.50	103.98
2	C	1364	C7C	C4-S8-C9	2.88	109.50	103.98
2	D	1364	C7C	C4-S8-C9	2.88	109.49	103.98
2	A	1364	C7C	C4-S8-C9	2.88	109.48	103.98
3	A	1365	FMN	C5A-C9A-N10	2.87	119.63	116.80
3	C	1365	FMN	C4A-N5-C5A	2.85	119.89	116.69
3	B	1365	FMN	C4-N3-C2	-2.71	119.82	125.39
3	C	1365	FMN	C2'-C1'-N10	-2.71	108.86	112.45
3	D	1365	FMN	C4-N3-C2	-2.59	120.08	125.39
3	A	1365	FMN	C4-N3-C2	-2.55	120.16	125.39
3	D	1365	FMN	C9A-N10-C10	-2.47	119.34	121.77
3	C	1365	FMN	C9A-N10-C10	-2.44	119.37	121.77
3	A	1365	FMN	C2'-C1'-N10	-2.44	109.21	112.45
3	B	1365	FMN	C4A-N5-C5A	2.43	119.42	116.69
3	D	1365	FMN	C2'-C1'-N10	-2.42	109.24	112.45
3	C	1365	FMN	C4-N3-C2	-2.16	120.96	125.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	334/370 (90%)	-0.20	5 (1%)	70 72	18, 31, 60, 86	1 (0%)
1	B	333/370 (90%)	-0.16	13 (3%)	37 39	19, 33, 61, 87	1 (0%)
1	C	332/370 (89%)	-0.04	12 (3%)	41 42	23, 38, 64, 86	1 (0%)
1	D	334/370 (90%)	-0.10	13 (3%)	37 39	24, 38, 67, 89	1 (0%)
All	All	1333/1480 (90%)	-0.12	43 (3%)	45 48	18, 35, 64, 89	4 (0%)

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	210	ALA	5.4
1	B	173	ASN	4.4
1	A	170	ASP	4.0
1	B	209	VAL	3.5
1	B	210	ALA	3.2
1	C	174	ARG	3.2
1	B	174	ARG	3.1
1	B	170	ASP	3.0
1	D	206	ALA	3.0
1	D	171	VAL	2.9
1	D	205	LEU	2.9
1	C	206	ALA	2.7
1	D	363	ASN	2.7
1	B	206	ALA	2.7
1	C	363	ASN	2.6
1	C	170	ASP	2.6
1	D	207	ALA	2.6
1	C	209	VAL	2.5
1	C	4	ARG	2.5
1	D	211	LYS	2.5
1	B	208	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	166	ASN	2.5
1	B	172	ARG	2.4
1	D	120	GLU	2.4
1	B	168	LEU	2.4
1	A	173	ASN	2.4
1	B	171	VAL	2.3
1	A	363	ASN	2.3
1	C	210	ALA	2.3
1	D	174	ARG	2.3
1	D	124	GLU	2.3
1	D	172	ARG	2.3
1	A	208	TYR	2.2
1	B	169	ASP	2.2
1	C	6	ILE	2.2
1	D	59	GLU	2.1
1	C	5	LEU	2.1
1	A	174	ARG	2.1
1	C	207	ALA	2.1
1	D	168	LEU	2.1
1	C	122	GLY	2.1
1	B	205	LEU	2.0
1	C	208	TYR	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	C7C	C	1364	16/16	0.25	0.18	58,60,64,66	0
2	C7C	D	1364	16/16	0.25	0.15	57,59,64,66	0
3	FMN	D	1365	31/31	0.15	-0.14	25,30,31,31	0
2	C7C	B	1364	16/16	0.22	-0.27	54,55,58,60	0
2	C7C	A	1364	16/16	0.20	-0.50	48,49,54,56	0
3	FMN	B	1365	31/31	0.14	-0.60	21,26,27,28	0
3	FMN	A	1365	31/31	0.14	-0.77	20,24,25,25	0
3	FMN	C	1365	31/31	0.13	-0.92	25,30,32,34	0

## 6.5 Other polymers

There are no such residues in this entry.