



Full wwPDB X-ray Structure Validation Report ⓘ

May 18, 2020 – 11:51 pm BST

PDB ID : 5VXH
Title : Crystal structure of Xanthomonas campestris OleA E117D
Authors : Jensen, M.R.; Wilmot, C.M.
Deposited on : 2017-05-23
Resolution : 1.84 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 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 : 2.11
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) : 2.11

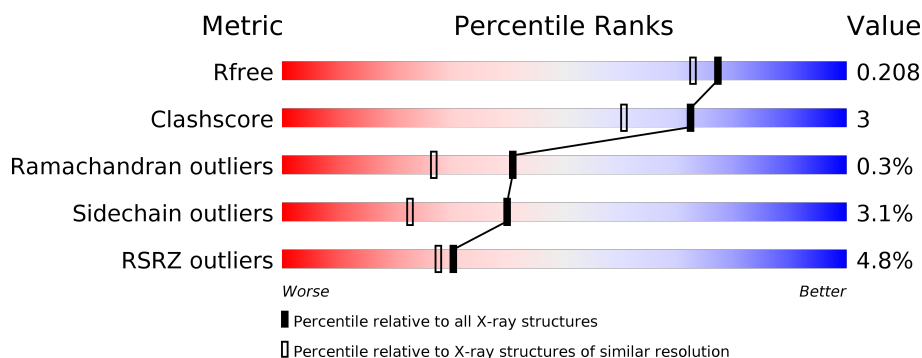
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.84 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}	130704	4003 (1.86-1.82)
Clashscore	141614	4233 (1.86-1.82)
Ramachandran outliers	138981	4185 (1.86-1.82)
Sidechain outliers	138945	4186 (1.86-1.82)
RSRZ outliers	127900	3957 (1.86-1.82)

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 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	358	<div> <div> <div></div> <div>84%</div> <div>11%</div> <div>• •</div> </div> </div>
1	B	358	<div> <div>8%</div> <div>75%</div> <div>14%</div> <div>• 9%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5419 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 3-oxoacyl-[ACP] synthase III.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	345	Total	C	N	O	S	0	5	0
			2657	1669	467	506	15			
1	B	326	Total	C	N	O	S	0	4	0
			2507	1580	437	476	14			

There are 42 discrepancies between the modelled and reference sequences:

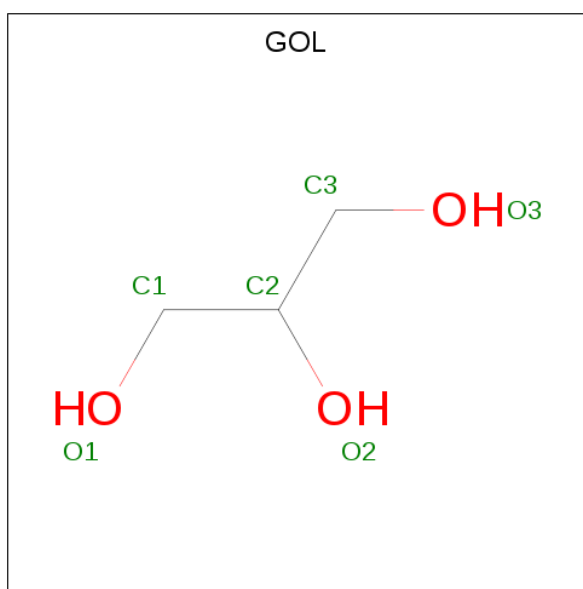
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q8PDX2
A	2	GLY	-	expression tag	UNP Q8PDX2
A	3	SER	-	expression tag	UNP Q8PDX2
A	4	SER	-	expression tag	UNP Q8PDX2
A	5	HIS	-	expression tag	UNP Q8PDX2
A	6	HIS	-	expression tag	UNP Q8PDX2
A	7	HIS	-	expression tag	UNP Q8PDX2
A	8	HIS	-	expression tag	UNP Q8PDX2
A	9	HIS	-	expression tag	UNP Q8PDX2
A	10	HIS	-	expression tag	UNP Q8PDX2
A	11	SER	-	expression tag	UNP Q8PDX2
A	12	SER	-	expression tag	UNP Q8PDX2
A	13	GLY	-	expression tag	UNP Q8PDX2
A	14	LEU	-	expression tag	UNP Q8PDX2
A	15	VAL	-	expression tag	UNP Q8PDX2
A	16	PRO	-	expression tag	UNP Q8PDX2
A	17	ARG	-	expression tag	UNP Q8PDX2
A	18	GLY	-	expression tag	UNP Q8PDX2
A	19	SER	-	expression tag	UNP Q8PDX2
A	20	HIS	-	expression tag	UNP Q8PDX2
A	117	ASP	GLU	engineered mutation	UNP Q8PDX2
B	1	MET	-	initiating methionine	UNP Q8PDX2
B	2	GLY	-	expression tag	UNP Q8PDX2
B	3	SER	-	expression tag	UNP Q8PDX2
B	4	SER	-	expression tag	UNP Q8PDX2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	5	HIS	-	expression tag	UNP Q8PDX2
B	6	HIS	-	expression tag	UNP Q8PDX2
B	7	HIS	-	expression tag	UNP Q8PDX2
B	8	HIS	-	expression tag	UNP Q8PDX2
B	9	HIS	-	expression tag	UNP Q8PDX2
B	10	HIS	-	expression tag	UNP Q8PDX2
B	11	SER	-	expression tag	UNP Q8PDX2
B	12	SER	-	expression tag	UNP Q8PDX2
B	13	GLY	-	expression tag	UNP Q8PDX2
B	14	LEU	-	expression tag	UNP Q8PDX2
B	15	VAL	-	expression tag	UNP Q8PDX2
B	16	PRO	-	expression tag	UNP Q8PDX2
B	17	ARG	-	expression tag	UNP Q8PDX2
B	18	GLY	-	expression tag	UNP Q8PDX2
B	19	SER	-	expression tag	UNP Q8PDX2
B	20	HIS	-	expression tag	UNP Q8PDX2
B	117	ASP	GLU	engineered mutation	UNP Q8PDX2

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



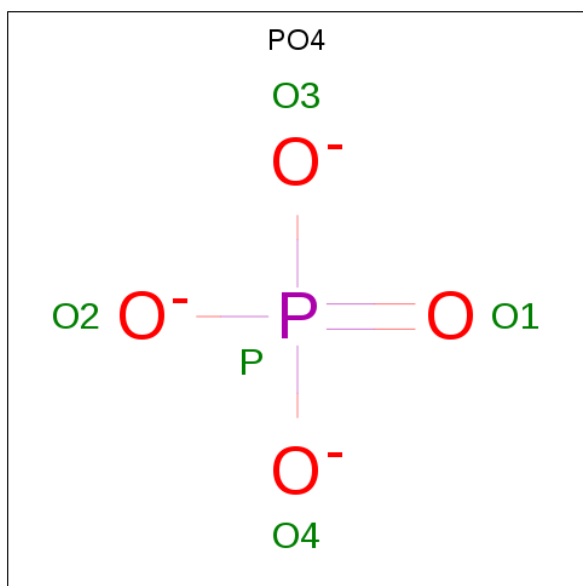
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		

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

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		

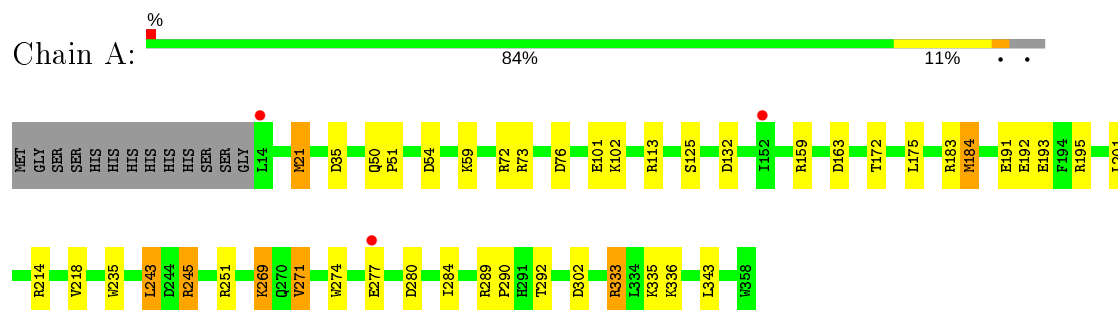
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	138	Total	O	0	0
			138	138		
4	B	88	Total	O	0	0
			88	88		

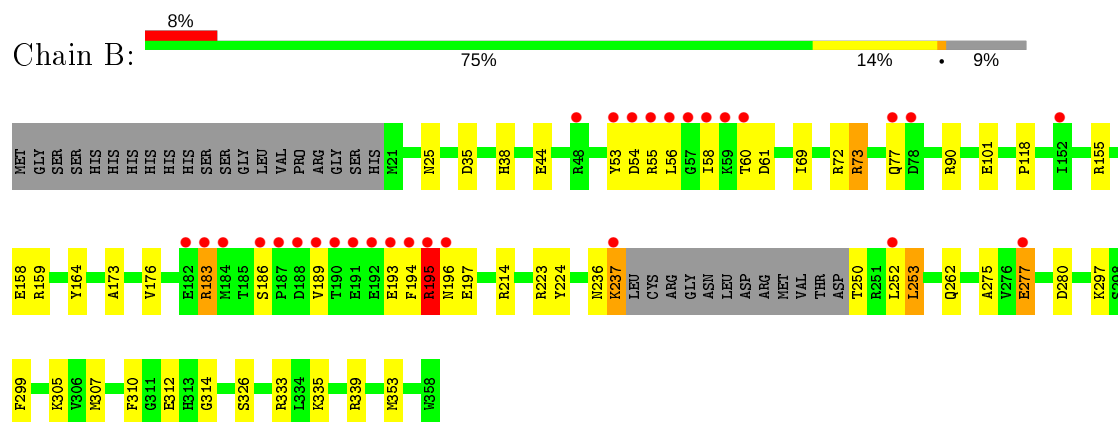
3 Residue-property plots [i](#)

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: 3-oxoacyl-[ACP] synthase III



- Molecule 1: 3-oxoacyl-[ACP] synthase III



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.88Å 85.41Å 102.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.84 39.44 – 1.84	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-1.84) 99.9 (39.44-1.84)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 1.84Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.158 , 0.198 0.171 , 0.208	Depositor DCC
R_{free} test set	3170 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	23.9	Xtriage
Anisotropy	0.284	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 46.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.019 for k,h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5419	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.92% 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: GOL, PO4

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	1.31	8/2700 (0.3%)	1.31	22/3657 (0.6%)
1	B	1.34	8/2545 (0.3%)	1.33	21/3445 (0.6%)
All	All	1.32	16/5245 (0.3%)	1.32	43/7102 (0.6%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	101	GLU	CD-OE1	11.28	1.38	1.25
1	B	44	GLU	CD-OE2	6.53	1.32	1.25
1	A	125	SER	CA-CB	6.18	1.62	1.52
1	A	191[A]	GLU	CD-OE1	-6.16	1.18	1.25
1	A	191[B]	GLU	CD-OE1	-6.16	1.18	1.25
1	B	326	SER	CB-OG	5.92	1.50	1.42
1	A	101	GLU	CD-OE1	5.80	1.32	1.25
1	B	312	GLU	CG-CD	5.63	1.60	1.51
1	B	164	TYR	CE1-CZ	-5.55	1.31	1.38
1	A	192	GLU	CD-OE1	-5.51	1.19	1.25
1	B	224	TYR	CZ-OH	5.28	1.46	1.37
1	A	235	TRP	CB-CG	5.22	1.59	1.50
1	B	25	ASN	CG-OD1	5.20	1.35	1.24
1	B	158	GLU	CD-OE1	5.13	1.31	1.25
1	A	193	GLU	CD-OE1	5.03	1.31	1.25
1	A	277	GLU	CD-OE2	5.02	1.31	1.25

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	113	ARG	NE-CZ-NH2	-11.87	114.36	120.30
1	A	76	ASP	CB-CG-OD2	-11.73	107.74	118.30
1	A	113	ARG	NE-CZ-NH1	10.34	125.47	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	333	ARG	NE-CZ-NH2	-10.03	115.28	120.30
1	B	90	ARG	NE-CZ-NH1	9.99	125.30	120.30
1	A	163	ASP	CB-CG-OD1	9.13	126.52	118.30
1	B	35	ASP	CB-CG-OD1	8.83	126.25	118.30
1	A	302	ASP	CB-CG-OD1	8.83	126.24	118.30
1	A	271	VAL	CG1-CB-CG2	8.81	125.00	110.90
1	B	183	ARG	NE-CZ-NH1	8.69	124.65	120.30
1	A	184	MET	CG-SD-CE	-8.08	87.27	100.20
1	A	132	ASP	CB-CG-OD1	7.89	125.40	118.30
1	B	61	ASP	CB-CG-OD2	-7.19	111.83	118.30
1	B	305	LYS	CD-CE-NZ	-7.17	95.22	111.70
1	A	183	ARG	NE-CZ-NH2	6.72	123.66	120.30
1	A	159	ARG	NE-CZ-NH2	-6.67	116.96	120.30
1	A	195	ARG	NE-CZ-NH2	-6.55	117.03	120.30
1	A	243	LEU	CB-CG-CD2	-6.48	99.99	111.00
1	B	339	ARG	NE-CZ-NH1	-6.46	117.07	120.30
1	B	223	ARG	NE-CZ-NH2	-6.45	117.08	120.30
1	A	251	ARG	NE-CZ-NH2	-6.43	117.08	120.30
1	B	307	MET	CG-SD-CE	-6.35	90.04	100.20
1	A	302	ASP	CB-CG-OD2	-6.30	112.63	118.30
1	B	339	ARG	NE-CZ-NH2	6.21	123.41	120.30
1	A	245	ARG	NE-CZ-NH2	6.17	123.39	120.30
1	B	333	ARG	NE-CZ-NH1	6.13	123.36	120.30
1	B	253	LEU	CA-CB-CG	6.05	129.23	115.30
1	B	73	ARG	NE-CZ-NH1	5.87	123.23	120.30
1	B	195	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	B	101	GLU	CG-CD-OE2	-5.79	106.71	118.30
1	A	35	ASP	CB-CG-OD1	5.79	123.51	118.30
1	A	59	LYS	CD-CE-NZ	-5.74	98.49	111.70
1	B	223	ARG	CG-CD-NE	-5.68	99.87	111.80
1	B	280	ASP	CB-CG-OD2	5.64	123.37	118.30
1	A	73	ARG	NE-CZ-NH1	5.63	123.11	120.30
1	B	214	ARG	NE-CZ-NH1	5.61	123.11	120.30
1	A	54	ASP	CB-CG-OD1	5.40	123.16	118.30
1	A	214	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	B	159	ARG	NE-CZ-NH1	5.25	122.92	120.30
1	B	155	ARG	NE-CZ-NH1	5.21	122.90	120.30
1	B	353	MET	CG-SD-CE	-5.14	91.98	100.20
1	A	76	ASP	CB-CG-OD1	5.13	122.92	118.30
1	A	280	ASP	CB-CG-OD1	-5.04	113.77	118.30

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	2657	0	2693	18	0
1	B	2507	0	2536	18	0
2	A	18	0	24	1	0
2	B	6	0	8	0	0
3	A	5	0	0	0	0
4	A	138	0	0	2	0
4	B	88	0	0	0	0
All	All	5419	0	5261	36	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 3.

All (36) 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:A:175:LEU:HD23	1:A:243:LEU:HG	1.62	0.82
1:B:262:GLN:HG2	1:B:299:PHE:HE1	1.46	0.79
1:A:284[B]:ILE:HG13	1:A:284[B]:ILE:O	1.87	0.74
1:A:333:ARG:NH1	4:A:501:HOH:O	2.19	0.73
1:B:194:PHE:O	1:B:195:ARG:O	2.12	0.67
1:A:284[B]:ILE:CG1	1:A:284[B]:ILE:O	2.42	0.66
1:B:262:GLN:HG2	1:B:299:PHE:CE1	2.30	0.66
1:B:54:ASP:C	1:B:55:ARG:O	2.40	0.58
1:A:284[B]:ILE:HD11	1:A:292:THR:HG23	1.87	0.57
1:B:69:ILE:HB	1:B:310[A]:PHE:CE2	2.39	0.57
1:B:277:GLU:CD	1:B:277:GLU:H	2.10	0.55
1:B:262:GLN:CG	1:B:299:PHE:CE1	2.91	0.54
1:B:183:ARG:HG2	1:B:193:GLU:OE1	2.09	0.53
1:B:69:ILE:HD12	1:B:314:GLY:HA2	1.92	0.52
1:A:184:MET:CE	1:A:201:LEU:HD11	2.41	0.49
1:B:186:SER:HB2	1:B:189:VAL:HG23	1.94	0.49
1:B:252:LEU:HD23	1:B:253:LEU:H	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:LYS:HE3	1:A:274:TRP:O	2.15	0.47
1:B:173:ALA:O	1:B:176:VAL:HG12	2.15	0.46
1:A:269:LYS:HG2	1:A:274:TRP:O	2.15	0.46
1:B:195:ARG:O	1:B:196:ASN:C	2.54	0.45
1:A:172:THR:HB	4:A:504:HOH:O	2.16	0.45
1:A:102:LYS:HD3	1:A:102:LYS:HA	1.66	0.45
1:A:218:VAL:HG23	1:A:218:VAL:O	2.17	0.44
1:B:55:ARG:NH1	1:B:56:LEU:HD21	2.32	0.43
1:A:284[B]:ILE:HG22	1:A:343:LEU:HD13	2.00	0.43
1:A:184:MET:HB3	1:A:184:MET:HE3	1.62	0.42
1:B:275:ALA:HB1	1:B:277:GLU:OE2	2.20	0.41
1:A:289:ARG:HB3	1:A:290:PRO:HD3	2.03	0.41
1:A:184:MET:HE1	1:A:201:LEU:HD11	2.01	0.41
1:A:245:ARG:HH11	1:A:245:ARG:HD3	1.73	0.41
1:B:236:ASN:HD21	1:B:237:LYS:HE2	1.86	0.41
1:B:53:TYR:HD1	1:B:58:ILE:HB	1.86	0.41
1:A:50:GLN:HB3	1:A:51:PRO:HD3	2.02	0.41
1:B:38:HIS:O	1:B:73:ARG:HA	2.22	0.40
1:A:21:MET:HG3	2:A:402:GOL:H32	2.03	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	348/358 (97%)	338 (97%)	10 (3%)	0	100	100
1	B	326/358 (91%)	311 (95%)	13 (4%)	2 (1%)	25	12
All	All	674/716 (94%)	649 (96%)	23 (3%)	2 (0%)	41	27

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	195	ARG
1	B	197	GLU

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	284/290 (98%)	277 (98%)	7 (2%)	47	31
1	B	266/290 (92%)	256 (96%)	10 (4%)	33	15
All	All	550/580 (95%)	533 (97%)	17 (3%)	40	23

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	MET
1	A	72	ARG
1	A	269	LYS
1	A	271	VAL
1	A	333	ARG
1	A	335	LYS
1	A	336	LYS
1	B	60	THR
1	B	72	ARG
1	B	77	GLN
1	B	118	PRO
1	B	195	ARG
1	B	237	LYS
1	B	250	THR
1	B	277	GLU
1	B	297	LYS
1	B	335	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	236	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

5 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	$\# Z > 2$
3	PO4	A	404	-	4,4,4	0.79	0	6,6,6	0.83	0
2	GOL	A	403	-	5,5,5	0.37	0	5,5,5	0.71	0
2	GOL	A	401	-	5,5,5	0.31	0	5,5,5	1.34	0
2	GOL	A	402	-	5,5,5	0.67	0	5,5,5	0.80	0
2	GOL	B	401	-	5,5,5	0.96	0	5,5,5	0.97	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	A	403	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	A	401	-	-	0/4/4/4	-
2	GOL	A	402	-	-	0/4/4/4	-
2	GOL	B	401	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	GOL	O1-C1-C2-C3
2	B	401	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	402	GOL	1	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 ⓘ

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, 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	345/358 (96%)	-0.28	3 (0%) 84 84	17, 23, 39, 58	0
1	B	326/358 (91%)	0.20	29 (8%) 9 8	15, 26, 59, 79	0
All	All	671/716 (93%)	-0.05	32 (4%) 30 28	15, 24, 53, 79	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	189	VAL	5.2
1	B	187	PRO	5.0
1	B	186	SER	4.7
1	B	191	GLU	4.2
1	A	14	LEU	4.1
1	B	58	ILE	4.1
1	B	53	TYR	4.0
1	B	193	GLU	3.9
1	B	59	LYS	3.6
1	B	192	GLU	3.6
1	B	56	LEU	3.5
1	B	77	GLN	3.4
1	B	195	ARG	3.0
1	B	196	ASN	3.0
1	B	78	ASP	2.8
1	B	252	LEU	2.8
1	B	194	PHE	2.8
1	B	60	THR	2.6
1	A	152	ILE	2.5
1	B	182	GLU	2.5
1	B	57	GLY	2.4
1	B	237	LYS	2.4
1	A	277	GLU	2.4
1	B	48	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	55	ARG	2.3
1	B	184	MET	2.3
1	B	188	ASP	2.3
1	B	54	ASP	2.2
1	B	190	THR	2.1
1	B	277	GLU	2.1
1	B	152	ILE	2.0
1	B	183	ARG	2.0

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. 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
3	PO4	A	404	5/5	0.82	0.20	61,73,79,85	0
2	GOL	A	401	6/6	0.91	0.14	34,38,39,39	0
2	GOL	A	403	6/6	0.93	0.15	33,39,44,47	0
2	GOL	B	401	6/6	0.94	0.15	28,30,31,34	0
2	GOL	A	402	6/6	0.96	0.09	25,33,36,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.