



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 07:09 am BST

PDB ID : 5VXF
Title : Crystal structure of Xanthomonas campestris OleA E117Q
Authors : Jensen, M.R.; Wilmot, C.M.
Deposited on : 2017-05-23
Resolution : 1.75 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

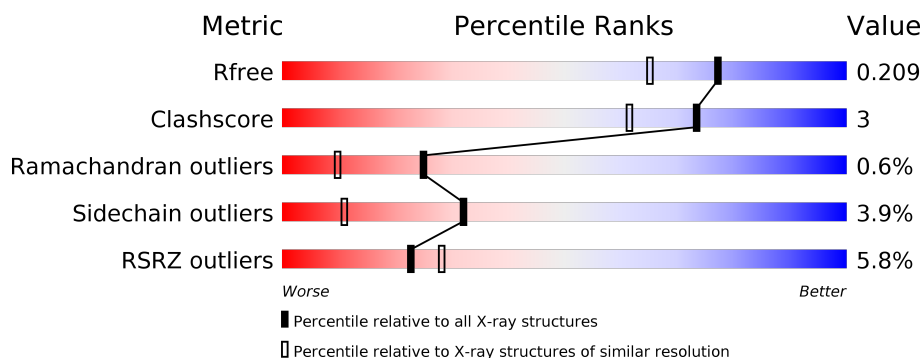
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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 style="width: 100%; height: 10px; background-color: red;"></div> <div style="width: 100%; height: 10px; background-color: green;"></div> <div style="width: 100%; height: 10px; background-color: yellow;"></div> <div style="width: 100%; height: 10px; background-color: grey;"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 81% 14% • • </div> </div>
1	B	358	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="width: 100%; height: 10px; background-color: green;"></div> <div style="width: 100%; height: 10px; background-color: yellow;"></div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="width: 100%; height: 10px; background-color: grey;"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 10% 75% 14% • • 8% </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5475 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	9	0
			2697	1697	473	510	17			
1	B	328	Total	C	N	O	S	0	6	0
			2539	1597	445	483	14			

There are 42 discrepancies between the modelled and reference sequences:

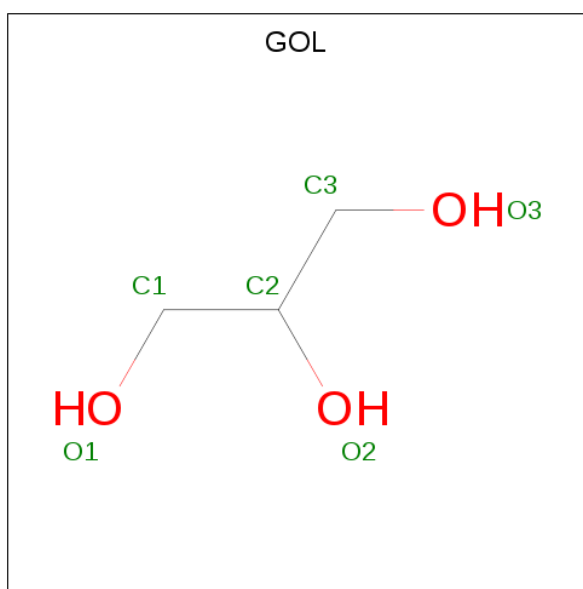
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q8PDX2
A	2	GLY	-	expression tag	UNP Q8PDX2
A	3	SER	-	expression tag	UNP Q8PDX2
A	4	SER	-	expression tag	UNP Q8PDX2
A	5	HIS	-	expression tag	UNP Q8PDX2
A	6	HIS	-	expression tag	UNP Q8PDX2
A	7	HIS	-	expression tag	UNP Q8PDX2
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	GLN	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	GLN	GLU	engineered mutation	UNP Q8PDX2

- 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	B	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		

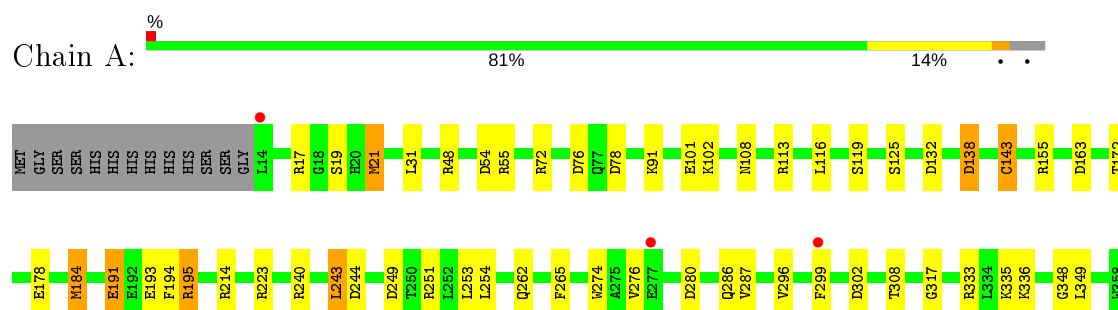
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	132	Total	O	0	1
			132	132		
3	B	83	Total	O	0	0
			83	83		

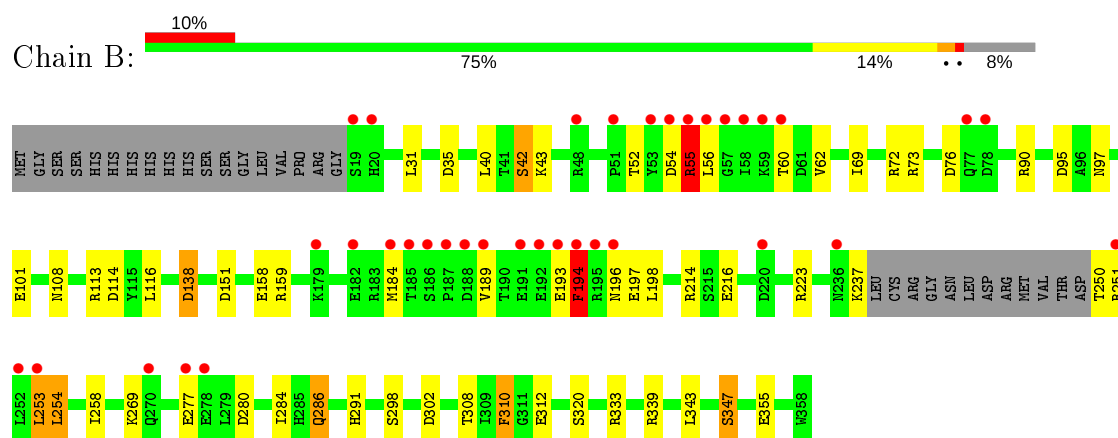
3 Residue-property plots [i](#)

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	82.24Å 85.86Å 102.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.75 44.15 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.6 (50.00-1.75) 99.7 (44.15-1.75)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.76 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.161 , 0.197 0.173 , 0.209	Depositor DCC
R_{free} test set	3718 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	25.5	Xtriage
Anisotropy	0.106	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.7	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	0.97	EDS
Total number of atoms	5475	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% 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

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	1.47	16/2739 (0.6%)	1.39	31/3708 (0.8%)
1	B	1.45	11/2577 (0.4%)	1.35	27/3488 (0.8%)
All	All	1.46	27/5316 (0.5%)	1.37	58/7196 (0.8%)

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	A	0	1
1	B	0	2
All	All	0	3

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	101	GLU	CD-OE1	10.61	1.37	1.25
1	A	333	ARG	CZ-NH1	10.18	1.46	1.33
1	B	310	PHE	CB-CG	-8.23	1.37	1.51
1	A	125	SER	CA-CB	7.76	1.64	1.52
1	A	101	GLU	CD-OE1	7.05	1.33	1.25
1	B	158	GLU	CD-OE1	6.66	1.32	1.25
1	B	347	SER	CB-OG	-6.63	1.33	1.42
1	B	138	ASP	CG-OD2	6.26	1.39	1.25
1	A	193	GLU	CD-OE2	6.25	1.32	1.25
1	A	274	TRP	CE3-CZ3	-6.13	1.28	1.38
1	A	287	VAL	CB-CG2	-5.97	1.40	1.52
1	A	333	ARG	NE-CZ	5.96	1.40	1.33
1	B	355	GLU	CD-OE1	-5.87	1.19	1.25
1	B	42	SER	CB-OG	-5.67	1.34	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	191	GLU	CB-CG	-5.67	1.41	1.52
1	A	138	ASP	CG-OD2	5.62	1.38	1.25
1	A	240	ARG	CD-NE	-5.59	1.36	1.46
1	B	216	GLU	CD-OE1	5.55	1.31	1.25
1	B	312	GLU	CG-CD	5.47	1.60	1.51
1	A	223	ARG	CD-NE	5.47	1.55	1.46
1	A	178	GLU	CD-OE2	5.43	1.31	1.25
1	A	274	TRP	CG-CD1	-5.33	1.29	1.36
1	A	296	VAL	CB-CG1	-5.31	1.41	1.52
1	A	19	SER	CB-OG	5.31	1.49	1.42
1	B	320	SER	CB-OG	5.18	1.49	1.42
1	B	159	ARG	CZ-NH1	-5.18	1.26	1.33
1	A	55	ARG	CZ-NH2	-5.09	1.26	1.33

All (58) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	333	ARG	NE-CZ-NH1	16.68	128.64	120.30
1	B	90	ARG	NE-CZ-NH1	13.51	127.05	120.30
1	A	184[A]	MET	CG-SD-CE	-9.89	84.38	100.20
1	A	184[B]	MET	CG-SD-CE	-9.89	84.38	100.20
1	A	333	ARG	NE-CZ-NH2	-9.69	115.46	120.30
1	A	251	ARG	NE-CZ-NH2	-9.27	115.67	120.30
1	B	333	ARG	NE-CZ-NH1	-8.80	115.90	120.30
1	A	302	ASP	CB-CG-OD2	-8.21	110.91	118.30
1	B	95	ASP	CB-CG-OD2	8.11	125.60	118.30
1	A	132	ASP	CB-CG-OD1	7.82	125.34	118.30
1	A	195	ARG	NE-CZ-NH2	-7.38	116.61	120.30
1	B	90	ARG	NE-CZ-NH2	-7.32	116.64	120.30
1	B	151	ASP	CB-CG-OD2	-7.30	111.72	118.30
1	A	333	ARG	CB-CG-CD	7.04	129.91	111.60
1	A	155	ARG	NE-CZ-NH1	7.01	123.81	120.30
1	B	73	ARG	NE-CZ-NH1	6.94	123.77	120.30
1	B	214	ARG	NE-CZ-NH1	6.88	123.74	120.30
1	A	76	ASP	CB-CG-OD2	-6.82	112.17	118.30
1	A	155	ARG	NE-CZ-NH2	-6.74	116.93	120.30
1	A	138	ASP	CB-CG-OD1	-6.70	112.27	118.30
1	B	280	ASP	CB-CG-OD2	6.62	124.26	118.30
1	A	214	ARG	NE-CZ-NH1	6.62	123.61	120.30
1	B	95	ASP	CB-CG-OD1	-6.57	112.39	118.30
1	B	302	ASP	CB-CG-OD2	-6.54	112.41	118.30
1	A	54	ASP	CB-CG-OD1	6.29	123.97	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	253	LEU	CB-CG-CD2	6.20	121.54	111.00
1	B	101	GLU	CG-CD-OE1	6.17	130.64	118.30
1	B	35	ASP	CB-CG-OD1	6.16	123.84	118.30
1	A	244	ASP	CB-CG-OD1	6.13	123.82	118.30
1	A	48	ARG	NE-CZ-NH2	6.04	123.32	120.30
1	B	114	ASP	CB-CG-OD2	-5.94	112.95	118.30
1	A	78	ASP	CB-CG-OD2	5.89	123.60	118.30
1	A	163	ASP	CB-CG-OD2	-5.85	113.04	118.30
1	A	243	LEU	CB-CG-CD2	5.82	120.89	111.00
1	A	194	PHE	CB-CG-CD1	-5.76	116.77	120.80
1	A	76	ASP	CB-CG-OD1	5.60	123.34	118.30
1	B	101	GLU	CG-CD-OE2	-5.58	107.14	118.30
1	B	339	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	A	249	ASP	CB-CG-OD2	-5.56	113.30	118.30
1	B	223	ARG	NE-CZ-NH1	5.55	123.08	120.30
1	A	31	LEU	CA-CB-CG	5.50	127.96	115.30
1	A	48	ARG	NE-CZ-NH1	-5.48	117.56	120.30
1	A	172	THR	OG1-CB-CG2	-5.41	97.56	110.00
1	B	158	GLU	CG-CD-OE2	-5.41	107.49	118.30
1	B	339	ARG	NE-CZ-NH1	5.39	123.00	120.30
1	A	223	ARG	NE-CZ-NH1	-5.39	117.61	120.30
1	B	114	ASP	CB-CG-OD1	5.37	123.13	118.30
1	B	159	ARG	NE-CZ-NH1	5.35	122.98	120.30
1	B	31	LEU	CA-CB-CG	5.32	127.54	115.30
1	A	333	ARG	N-CA-CB	5.29	120.13	110.60
1	B	55	ARG	NE-CZ-NH1	5.25	122.93	120.30
1	A	280	ASP	CB-CG-OD2	5.24	123.01	118.30
1	A	302	ASP	CB-CG-OD1	5.20	122.98	118.30
1	B	158	GLU	CG-CD-OE1	5.12	128.54	118.30
1	B	40	LEU	CB-CG-CD1	5.09	119.65	111.00
1	B	113	ARG	NE-CZ-NH2	-5.05	117.77	120.30
1	A	163	ASP	CB-CG-OD1	5.03	122.82	118.30
1	B	253	LEU	CA-CB-CG	5.02	126.85	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	119	SER	Mainchain
1	B	250	THR	Peptide
1	B	251	ARG	Peptide

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	2697	0	2724	18	0
1	B	2539	0	2566	18	0
2	A	12	0	16	1	0
2	B	12	0	16	3	0
3	A	132	0	0	1	0
3	B	83	0	0	0	0
All	All	5475	0	5322	35	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 (35) 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:253[B]:LEU:O	1:A:253[B]:LEU:HD13	1.67	0.93
1:A:253[B]:LEU:C	1:A:253[B]:LEU:HD13	2.01	0.79
1:A:253[B]:LEU:C	1:A:253[B]:LEU:CD1	2.62	0.68
1:B:62:VAL:HG11	1:B:198:LEU:HD13	1.80	0.62
1:B:284[B]:ILE:HG22	1:B:343:LEU:HG	1.83	0.59
1:B:286[B]:GLN:HE22	1:B:308:THR:HG22	1.66	0.59
1:A:113:ARG:CZ	1:A:116:LEU:HD23	2.35	0.57
1:A:265[B]:PHE:CZ	1:A:276:VAL:HG23	2.40	0.57
1:A:143[B]:CYS:SG	1:A:317:GLY:HA2	2.48	0.54
1:B:62:VAL:HG11	1:B:198:LEU:CD1	2.38	0.53
1:B:284[B]:ILE:CG1	1:B:286[B]:GLN:HE21	2.22	0.53
1:A:254:LEU:C	1:A:254:LEU:HD23	2.30	0.51
1:A:286:GLN:OE1	1:A:308[B]:THR:HB	2.11	0.50
1:B:286[B]:GLN:NE2	1:B:308:THR:HG22	2.27	0.50
1:B:52:THR:HG21	1:B:194:PHE:CE1	2.47	0.49
1:B:43:LYS:N	2:B:402:GOL:H31	2.27	0.49
1:B:55:ARG:NH2	1:B:189:VAL:O	2.43	0.48
1:B:284[B]:ILE:HG13	1:B:286[B]:GLN:HE21	1.80	0.46
1:A:243:LEU:HD23	1:B:116:LEU:HD11	1.96	0.46
1:A:108:ASN:HB3	1:A:138:ASP:OD1	2.17	0.45
1:A:191:GLU:HG2	1:A:195:ARG:CZ	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:42:SER:HB2	2:B:402:GOL:H31	1.99	0.44
1:A:262:GLN:HG2	1:A:299[A]:PHE:HE1	1.82	0.44
1:A:143[A]:CYS:HB3	3:A:623:HOH:O	2.17	0.44
1:A:348:GLY:N	1:A:349:LEU:HA	2.33	0.44
1:B:254:LEU:HB2	1:B:291:HIS:NE2	2.33	0.43
1:A:184[A]:MET:HB3	1:A:184[A]:MET:HE3	1.26	0.43
1:B:54:ASP:C	1:B:56:LEU:H	2.23	0.42
1:B:42:SER:HB2	2:B:402:GOL:C3	2.49	0.42
1:A:21:MET:HA	2:A:401:GOL:H32	2.01	0.41
1:B:184:MET:HE3	1:B:197:GLU:C	2.41	0.41
1:B:69:ILE:HB	1:B:310:PHE:CE2	2.55	0.41
1:A:253[B]:LEU:HD22	1:A:349:LEU:HD21	2.02	0.40
1:B:108:ASN:HB3	1:B:138:ASP:OD1	2.21	0.40
1:A:91:LYS:HE2	1:A:91:LYS:HB3	1.96	0.40

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	352/358 (98%)	343 (97%)	9 (3%)	0	100	100
1	B	330/358 (92%)	312 (94%)	14 (4%)	4 (1%)	13	3
All	All	682/716 (95%)	655 (96%)	23 (3%)	4 (1%)	25	10

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	55	ARG
1	B	76	ASP
1	B	193	GLU
1	B	194	PHE

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	288/290 (99%)	280 (97%)	8 (3%)	43	20
1	B	270/290 (93%)	255 (94%)	15 (6%)	21	5
All	All	558/580 (96%)	535 (96%)	23 (4%)	32	10

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ARG
1	A	21	MET
1	A	72	ARG
1	A	102	LYS
1	A	143[A]	CYS
1	A	143[B]	CYS
1	A	335	LYS
1	A	336	LYS
1	B	60	THR
1	B	72	ARG
1	B	97	ASN
1	B	194	PHE
1	B	196	ASN
1	B	237	LYS
1	B	253	LEU
1	B	254	LEU
1	B	258	ILE
1	B	269	LYS
1	B	277	GLU
1	B	286[A]	GLN
1	B	286[B]	GLN
1	B	298	SER
1	B	347	SER

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

Mol	Chain	Res	Type
1	A	24	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 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	A	402	-	5,5,5	0.11	0	5,5,5	1.47	1 (20%)
2	GOL	B	402	-	5,5,5	0.79	0	5,5,5	2.20	2 (40%)
2	GOL	B	401	-	5,5,5	0.35	0	5,5,5	1.33	1 (20%)
2	GOL	A	401	-	5,5,5	0.64	0	5,5,5	1.29	1 (20%)

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	402	-	-	3/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	B	402	-	-	3/4/4/4	-
2	GOL	B	401	-	-	4/4/4/4	-
2	GOL	A	401	-	-	0/4/4/4	-

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	402	GOL	O2-C2-C3	-3.63	93.12	109.12
2	B	402	GOL	O3-C3-C2	2.65	122.91	110.20
2	B	401	GOL	O1-C1-C2	-2.65	97.49	110.20
2	A	402	GOL	O2-C2-C3	2.36	119.50	109.12
2	A	401	GOL	O1-C1-C2	-2.23	99.53	110.20

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	402	GOL	O1-C1-C2-C3
2	B	402	GOL	C1-C2-C3-O3
2	B	401	GOL	O1-C1-C2-C3
2	B	401	GOL	C1-C2-C3-O3
2	A	402	GOL	O1-C1-C2-O2
2	B	402	GOL	O2-C2-C3-O3
2	B	401	GOL	O1-C1-C2-O2
2	B	401	GOL	O2-C2-C3-O3
2	A	402	GOL	O2-C2-C3-O3
2	B	402	GOL	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	402	GOL	3	0
2	A	401	GOL	1	0

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, 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%)	-0.19	3 (0%) 84 89	19, 26, 42, 58	0
1	B	328/358 (91%)	0.36	36 (10%) 5 7	19, 29, 67, 98	0
All	All	673/716 (93%)	0.08	39 (5%) 23 28	19, 27, 57, 98	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	57	GLY	5.8
1	B	187	PRO	5.7
1	B	189	VAL	5.3
1	B	53	TYR	5.1
1	B	191	GLU	4.7
1	B	194	PHE	4.2
1	B	58	ILE	4.2
1	B	20	HIS	4.2
1	B	19	SER	4.1
1	B	192	GLU	3.8
1	B	193	GLU	3.8
1	B	77	GLN	3.7
1	B	55	ARG	3.6
1	B	182	GLU	3.5
1	B	78	ASP	3.5
1	B	59	LYS	3.4
1	B	196	ASN	3.4
1	B	60	THR	3.3
1	A	14	LEU	3.3
1	B	56	LEU	3.2
1	B	186	SER	3.1
1	B	185	THR	3.0
1	B	48	ARG	2.8
1	B	54	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	252	LEU	2.8
1	B	184	MET	2.7
1	B	195	ARG	2.7
1	B	251	ARG	2.6
1	B	277	GLU	2.6
1	B	51	PRO	2.5
1	B	270	GLN	2.5
1	A	277	GLU	2.4
1	B	236	ASN	2.3
1	B	220	ASP	2.3
1	B	253	LEU	2.3
1	B	278	GLU	2.2
1	A	299[A]	PHE	2.1
1	B	188	ASP	2.1
1	B	179	LYS	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
2	GOL	B	402	6/6	0.84	0.25	26,37,41,45	6
2	GOL	A	402	6/6	0.87	0.15	34,42,45,45	0
2	GOL	B	401	6/6	0.93	0.12	32,36,42,48	0
2	GOL	A	401	6/6	0.94	0.10	28,35,36,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.