



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 03:18 PM UTC

PDB ID : 5DWZ / pdb_00005dwz
Title : Structural and functional characterization of PqsBC, a condensing enzyme in the biosynthesis of the Pseudomonas aeruginosa quinolone signal
Authors : Drees, S.L.; Li, C.; Prasetya, F.; Saleem, M.; Dreveny, I.; Hennecke, U.; Williams, P.; Emsley, J.; Fetzner, S.
Deposited on : 2015-09-23
Resolution : 2.04 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

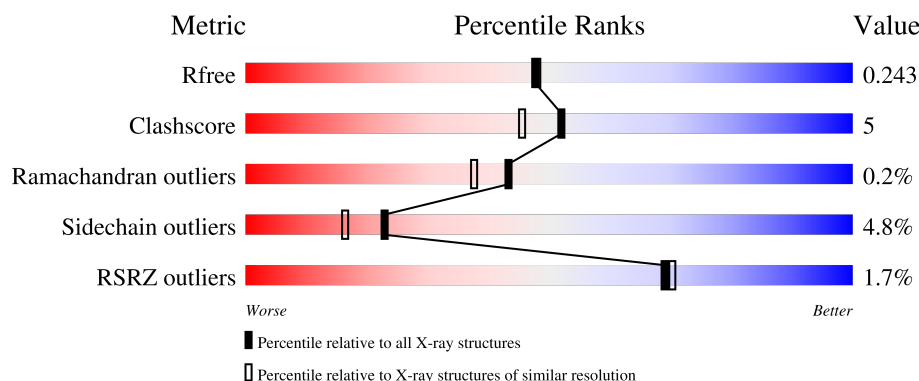
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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}	180053	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	C	350	86% 9% ..
1	D	350	2% 85% 11% ..
1	F	350	2% 83% 13% ..
1	H	350	3% 83% 12% ..
2	A	283	91% 7% .

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Mol	Chain	Length	Quality of chain
2	B	283	 88% 10% ..
2	E	283	 87% 10% ..
2	G	283	 88% 9% ..

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
3	PO4	D	404	-	X	-	-
3	PO4	F	403	-	X	-	-
3	PO4	H	402	-	X	-	-

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 20303 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-[acyl-carrier-protein] synthase 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	340	Total	C	N	O	S	1	1	0
			2625	1663	453	491	18			
1	D	340	Total	C	N	O	S	2	3	0
			2637	1672	454	493	18			
1	F	340	Total	C	N	O	S	12	0	0
			2622	1661	454	490	17			
1	H	341	Total	C	N	O	S	3	1	0
			2633	1667	455	493	18			

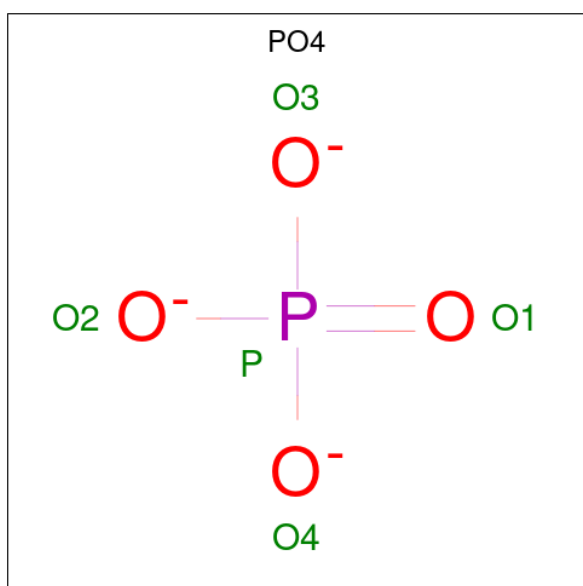
There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	SER	-	expression tag	UNP A0A0C6EZ24
C	0	ALA	-	expression tag	UNP A0A0C6EZ24
C	1	GLY	-	expression tag	UNP A0A0C6EZ24
C	129	ALA	CYS	engineered mutation	UNP A0A0C6EZ24
D	-1	SER	-	expression tag	UNP A0A0C6EZ24
D	0	ALA	-	expression tag	UNP A0A0C6EZ24
D	1	GLY	-	expression tag	UNP A0A0C6EZ24
D	129	ALA	CYS	engineered mutation	UNP A0A0C6EZ24
F	-1	SER	-	expression tag	UNP A0A0C6EZ24
F	0	ALA	-	expression tag	UNP A0A0C6EZ24
F	1	GLY	-	expression tag	UNP A0A0C6EZ24
F	129	ALA	CYS	engineered mutation	UNP A0A0C6EZ24
H	-1	SER	-	expression tag	UNP A0A0C6EZ24
H	0	ALA	-	expression tag	UNP A0A0C6EZ24
H	1	GLY	-	expression tag	UNP A0A0C6EZ24
H	129	ALA	CYS	engineered mutation	UNP A0A0C6EZ24

- Molecule 2 is a protein called 3-oxoacyl-(Acyl carrier protein) synthase III.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	278	Total	C	N	O	S	1	0	0
			2113	1333	377	395	8			
2	A	278	Total	C	N	O	S	7	0	0
			2113	1333	377	395	8			
2	E	279	Total	C	N	O	S	4	0	0
			2117	1335	378	396	8			
2	G	278	Total	C	N	O	S	9	0	0
			2112	1332	377	395	8			

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



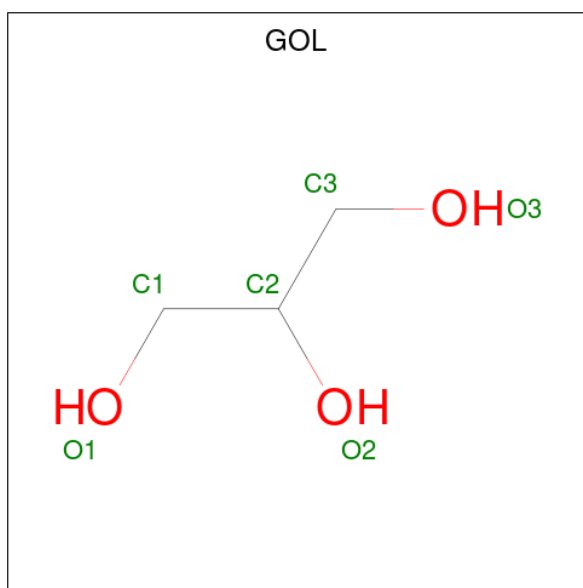
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	O	P	0	0
			5	4	1		
3	C	1	Total	O	P	0	0
			5	4	1		
3	C	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		
3	A	1	Total	O	P	0	0
			5	4	1		

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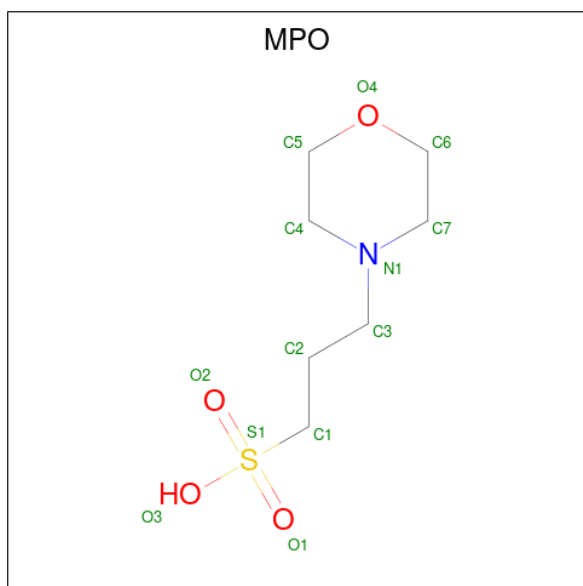
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	F	1	Total	O	P	0	0
			5	4	1		
3	F	1	Total	O	P	0	0
			5	4	1		
3	F	1	Total	O	P	0	0
			5	4	1		
3	F	1	Total	O	P	0	0
			5	4	1		
3	F	1	Total	O	P	0	0
			5	4	1		
3	E	1	Total	O	P	0	0
			5	4	1		
3	H	1	Total	O	P	0	0
			5	4	1		
3	H	1	Total	O	P	0	0
			5	4	1		
3	H	1	Total	O	P	0	0
			5	4	1		
3	H	1	Total	O	P	0	0
			5	4	1		
3	H	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



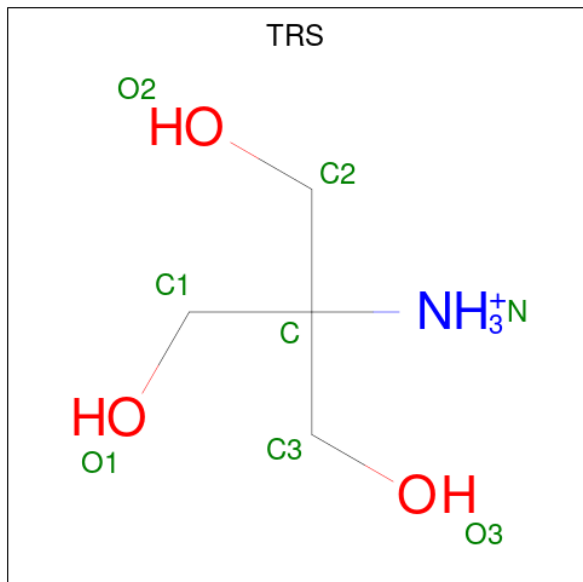
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is 3[N-MORPHOLINO]PROPANE SULFONIC ACID (CCD ID: MPO) (formula: $C_7H_{15}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	C	1	Total	C	N	O	S	0	0
			13	7	1	4	1		
5	C	1	Total	C	N	O	S	0	0
			13	7	1	4	1		
5	D	1	Total	C	N	O	S	0	0
			13	7	1	4	1		
5	H	1	Total	C	N	O	S	1	0
			13	7	1	4	1		

- Molecule 6 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: $C_4H_{12}NO_3$).

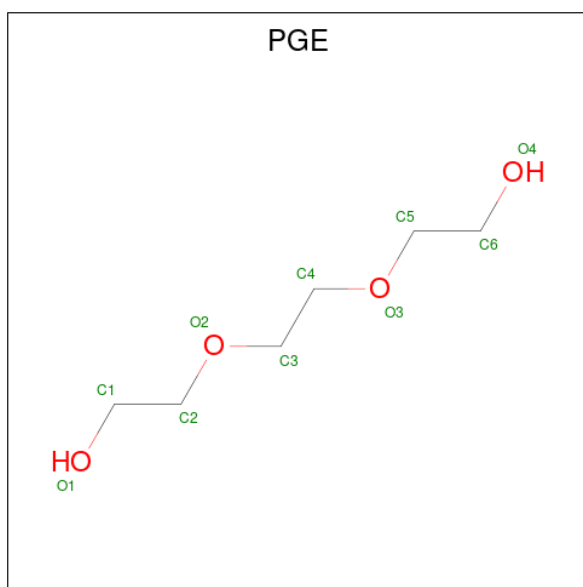


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	C	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

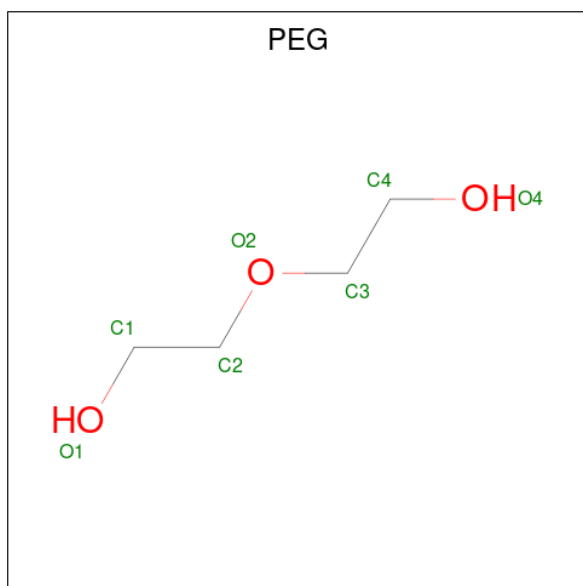
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	1	Total	Cl	0	0
			1	1		
7	D	1	Total	Cl	0	0
			1	1		

- Molecule 8 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 9 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	D	1	Total	C	O	0	0
			7	4	3		
9	D	1	Total	C	O	0	0
			7	4	3		
9	H	1	Total	C	O	0	0
			7	4	3		

- Molecule 10 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	E	1	Total	Na	0	0
			1	1		

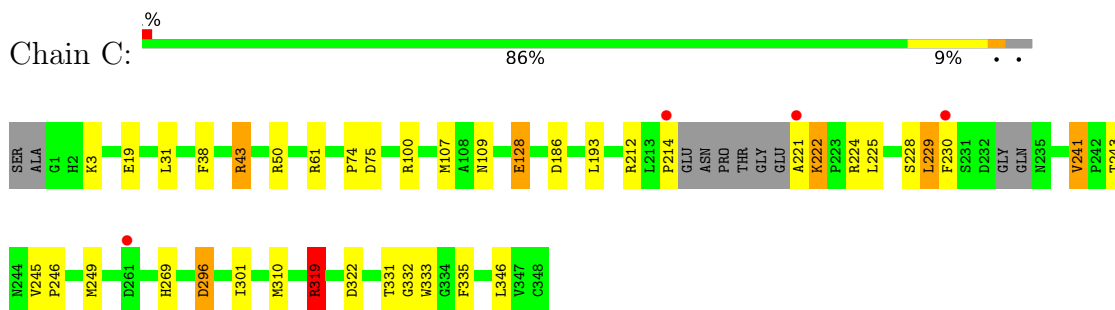
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	C	184	Total	O	0	0
			184	184		
11	B	167	Total	O	0	0
			167	167		
11	D	158	Total	O	0	0
			158	158		
11	A	141	Total	O	0	0
			141	141		
11	F	94	Total	O	0	0
			94	94		
11	E	140	Total	O	0	0
			140	140		
11	H	112	Total	O	0	0
			112	112		
11	G	99	Total	O	0	0
			99	99		

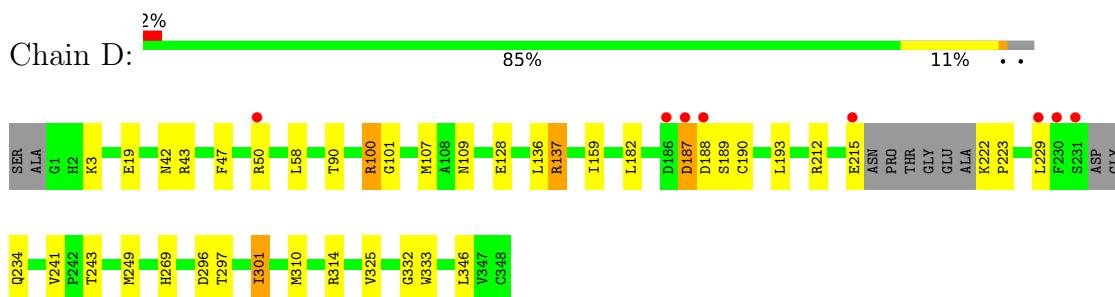
3 Residue-property plots

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 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.

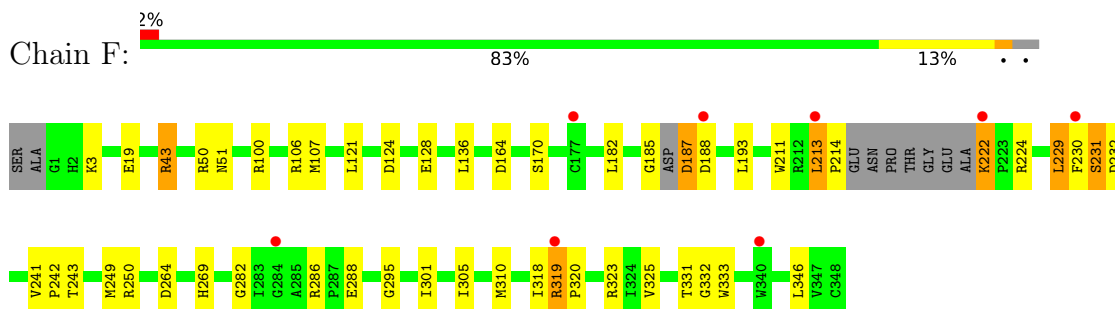
- Molecule 1: 3-oxoacyl-[acyl-carrier-protein] synthase 3



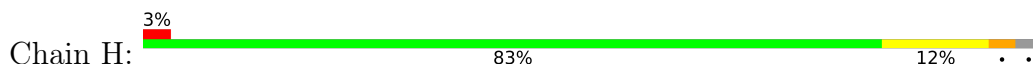
- Molecule 1: 3-oxoacyl-[acyl-carrier-protein] synthase 3

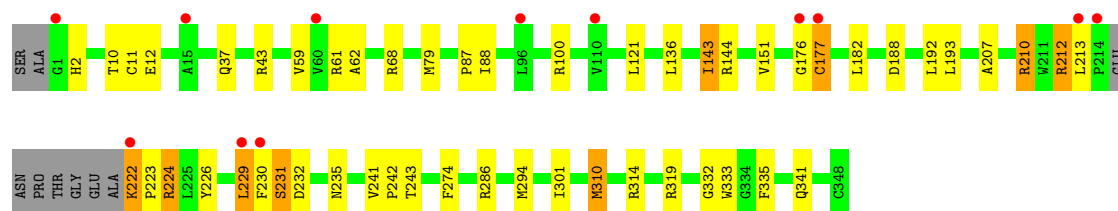


- Molecule 1: 3-oxoacyl-[acyl-carrier-protein] synthase 3



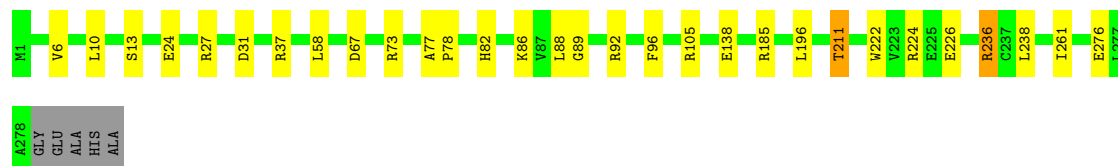
- Molecule 1: 3-oxoacyl-[acyl-carrier-protein] synthase 3





- Molecule 2: 3-oxoacyl-(Acyl carrier protein) synthase III

Chain B: 88% 10% ..



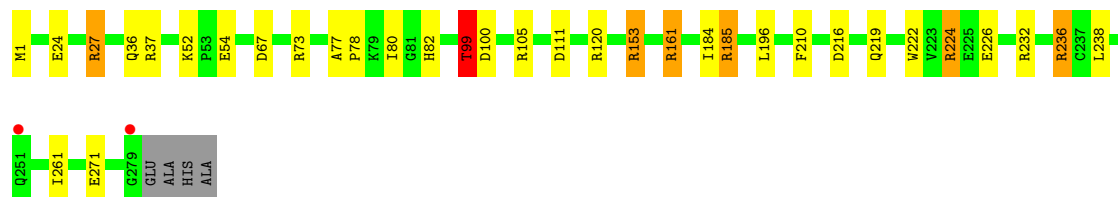
- Molecule 2: 3-oxoacyl-(Acyl carrier protein) synthase III

Chain A: 91% 7% .



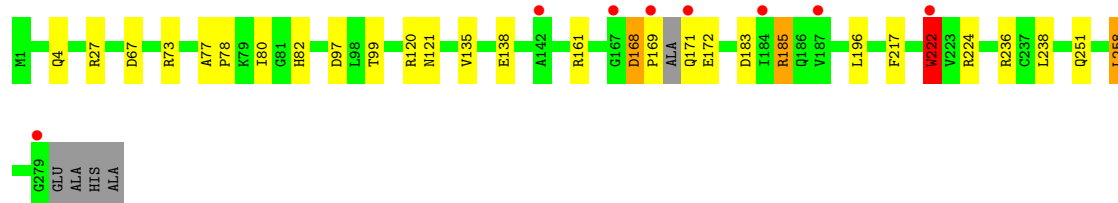
- Molecule 2: 3-oxoacyl-(Acyl carrier protein) synthase III

Chain E: 87% 10% ..



- Molecule 2: 3-oxoacyl-(Acyl carrier protein) synthase III

Chain G: 88% 9% 3% ..



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	78.49Å 114.96Å 289.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	144.84 – 2.04 144.84 – 2.04	Depositor EDS
% Data completeness (in resolution range)	99.1 (144.84-2.04) 99.3 (144.84-2.04)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 2.04Å)	Xtriage
Refinement program	REFMAC 5.8.0107	Depositor
R, R_{free}	0.190 , 0.237 0.199 , 0.243	Depositor DCC
R_{free} test set	8364 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	34.0	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 38.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	20303	wwPDB-VP
Average B, all atoms (Å ²)	38.0	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 20.32 % 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 8.9095e-03.*

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: TRS, NA, PGE, PO4, MPO, PEG, CL, 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	C	1.15	2/2684 (0.1%)	1.08	9/3640 (0.2%)
1	D	1.14	1/2702 (0.0%)	1.10	10/3664 (0.3%)
1	F	1.10	1/2678 (0.0%)	1.07	9/3631 (0.2%)
1	H	1.18	1/2693 (0.0%)	1.15	17/3653 (0.5%)
2	A	1.12	0/2154	1.01	2/2927 (0.1%)
2	B	1.19	4/2154 (0.2%)	1.03	3/2927 (0.1%)
2	E	1.15	5/2158 (0.2%)	1.03	3/2932 (0.1%)
2	G	1.12	3/2152 (0.1%)	1.05	2/2922 (0.1%)
All	All	1.14	17/19375 (0.1%)	1.07	55/26296 (0.2%)

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	C	0	1

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	82	HIS	C-O	-8.03	1.17	1.24
2	E	99	THR	C-O	-7.72	1.17	1.24
2	B	82	HIS	C-O	-7.72	1.17	1.24
2	E	153	ARG	C-O	-7.01	1.19	1.25
2	E	82	HIS	C-O	-6.58	1.18	1.24

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	243	THR	N-CA-C	10.72	125.88	113.01
1	D	107	MET	N-CA-C	10.28	122.56	111.36
1	H	241	VAL	N-CA-C	-9.85	99.86	109.02
1	C	100	ARG	N-CA-C	9.06	123.44	108.48
1	C	269	HIS	N-CA-C	-8.46	99.36	110.53

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	319	ARG	Sidechain

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	C	2625	0	2600	28	0
1	D	2637	0	2619	29	0
1	F	2622	0	2597	35	0
1	H	2633	0	2607	38	0
2	A	2113	0	2123	7	0
2	B	2113	0	2123	15	0
2	E	2117	0	2126	34	0
2	G	2112	0	2120	25	0
3	A	5	0	0	0	0
3	C	15	0	0	0	0
3	D	20	0	0	0	0
3	E	5	0	0	0	0
3	F	30	0	0	0	0
3	H	25	0	0	0	0
4	B	24	0	32	3	0
4	C	12	0	16	2	0
4	D	6	0	8	0	0
5	C	26	0	29	5	0
5	D	13	0	14	1	0
5	H	13	0	14	3	0
6	C	8	0	12	3	0
7	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	D	1	0	0	1	0
8	B	10	0	14	3	0
9	D	14	0	20	0	0
9	H	7	0	10	0	0
10	E	1	0	0	0	0
11	A	141	0	0	2	0
11	B	167	0	0	0	1
11	C	184	0	0	4	1
11	D	158	0	0	3	0
11	E	140	0	0	1	0
11	F	94	0	0	2	0
11	G	99	0	0	1	0
11	H	112	0	0	1	0
All	All	20303	0	19084	196	1

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 196 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)
2:E:99:THR:CG2	2:E:100:ASP:H	1.49	1.15
1:F:319:ARG:HA	1:F:319:ARG:HE	1.13	1.10
2:E:99:THR:HG22	2:E:100:ASP:H	0.98	1.06
1:D:43:ARG:HG2	1:D:43:ARG:HH11	1.22	1.04
2:G:169:PRO:HA	2:G:171:GLN:HB2	1.37	1.03

All (1) 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)
11:C:546:HOH:O	11:B:744:HOH:O[4_565]	2.01	0.19

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	C	335/350 (96%)	326 (97%)	8 (2%)	1 (0%)	36	30
1	D	337/350 (96%)	329 (98%)	7 (2%)	1 (0%)	36	30
1	F	334/350 (95%)	325 (97%)	8 (2%)	1 (0%)	36	30
1	H	338/350 (97%)	328 (97%)	9 (3%)	1 (0%)	36	30
2	A	276/283 (98%)	273 (99%)	3 (1%)	0	100	100
2	B	276/283 (98%)	273 (99%)	3 (1%)	0	100	100
2	E	277/283 (98%)	272 (98%)	5 (2%)	0	100	100
2	G	274/283 (97%)	268 (98%)	6 (2%)	0	100	100
All	All	2447/2532 (97%)	2394 (98%)	49 (2%)	4 (0%)	43	37

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	301	ILE
1	F	301	ILE
1	H	301	ILE
1	C	301	ILE

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	C	279/285 (98%)	264 (95%)	15 (5%)	20	12
1	D	282/285 (99%)	274 (97%)	8 (3%)	38	34
1	F	278/285 (98%)	259 (93%)	19 (7%)	14	8
1	H	280/285 (98%)	266 (95%)	14 (5%)	22	15
2	A	221/223 (99%)	210 (95%)	11 (5%)	22	15
2	B	221/223 (99%)	213 (96%)	8 (4%)	31	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	221/223 (99%)	211 (96%)	10 (4%)	24	18
2	G	221/223 (99%)	210 (95%)	11 (5%)	22	15
All	All	2003/2032 (99%)	1907 (95%)	96 (5%)	23	16

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	310	MET
1	H	37	GLN
1	F	323	ARG
2	E	161	ARG
1	H	188	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	126	GLN
1	H	244	ASN
2	G	121	ASN
1	H	341	GLN
1	F	51	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 39 ligands modelled in this entry, 3 are monoatomic - leaving 36 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$
4	GOL	C	404	-	5,5,5	0.52	0	5,5,5	0.64	0
3	PO4	H	401	-	4,4,4	1.87	1 (25%)	6,6,6	1.02	0
3	PO4	D	404	-	4,4,4	2.75	3 (75%)	6,6,6	1.42	1 (16%)
3	PO4	H	403	-	4,4,4	1.06	0	6,6,6	0.50	0
3	PO4	C	403	-	4,4,4	2.37	3 (75%)	6,6,6	0.51	0
3	PO4	F	404	-	4,4,4	1.29	1 (25%)	6,6,6	2.08	2 (33%)
9	PEG	D	408	-	6,6,6	0.72	0	5,5,5	0.67	0
5	MPO	C	406	-	13,13,13	2.92	2 (15%)	17,17,17	2.00	3 (17%)
3	PO4	C	402	-	4,4,4	1.96	2 (50%)	6,6,6	1.19	1 (16%)
5	MPO	C	407	-	13,13,13	2.52	2 (15%)	17,17,17	1.26	1 (5%)
3	PO4	A	401	-	4,4,4	0.97	0	6,6,6	0.47	0
5	MPO	H	406	-	13,13,13	4.08	2 (15%)	17,17,17	2.12	6 (35%)
3	PO4	H	402	-	4,4,4	2.32	3 (75%)	6,6,6	1.41	2 (33%)
3	PO4	F	403	-	4,4,4	2.08	2 (50%)	6,6,6	2.11	3 (50%)
3	PO4	F	401	-	4,4,4	1.61	1 (25%)	6,6,6	1.43	1 (16%)
4	GOL	B	501	-	5,5,5	0.26	0	5,5,5	0.31	0
4	GOL	C	405	-	5,5,5	0.42	0	5,5,5	2.87	2 (40%)
4	GOL	B	504	-	5,5,5	0.27	0	5,5,5	0.32	0
3	PO4	C	401	-	4,4,4	1.27	0	6,6,6	2.02	1 (16%)
9	PEG	D	407	-	6,6,6	0.24	0	5,5,5	0.55	0
3	PO4	F	406	-	4,4,4	1.96	2 (50%)	6,6,6	1.84	1 (16%)
4	GOL	B	502	-	5,5,5	0.26	0	5,5,5	0.31	0
5	MPO	D	406	-	13,13,13	3.20	4 (30%)	17,17,17	2.08	4 (23%)
9	PEG	H	407	-	6,6,6	0.68	0	5,5,5	0.61	0
3	PO4	F	405	-	4,4,4	3.34	3 (75%)	6,6,6	0.83	0
3	PO4	H	404	-	4,4,4	0.90	0	6,6,6	1.36	1 (16%)
4	GOL	D	405	-	5,5,5	0.29	0	5,5,5	0.48	0
4	GOL	B	503	-	5,5,5	0.26	0	5,5,5	0.32	0
3	PO4	D	401	-	4,4,4	2.09	1 (25%)	6,6,6	1.44	1 (16%)
3	PO4	D	403	-	4,4,4	1.46	1 (25%)	6,6,6	1.92	2 (33%)
3	PO4	H	405	-	4,4,4	1.41	0	6,6,6	1.87	1 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PO4	E	401	-	4,4,4	0.95	0	6,6,6	0.46	0
6	TRS	C	408	-	7,7,7	0.86	0	9,9,9	2.33	3 (33%)
3	PO4	F	402	-	4,4,4	1.83	2 (50%)	6,6,6	1.03	0
8	PGE	B	505	-	9,9,9	0.38	0	8,8,8	0.32	0
3	PO4	D	402	-	4,4,4	1.35	1 (25%)	6,6,6	1.84	1 (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
4	GOL	D	405	-	-	2/4/4/4	-
4	GOL	B	503	-	-	0/4/4/4	-
4	GOL	C	404	-	-	0/4/4/4	-
5	MPO	H	406	-	-	5/7/15/15	0/1/1/1
9	PEG	D	407	-	-	3/4/4/4	-
5	MPO	C	407	-	-	5/7/15/15	0/1/1/1
9	PEG	D	408	-	-	1/4/4/4	-
4	GOL	B	502	-	-	0/4/4/4	-
4	GOL	B	501	-	-	0/4/4/4	-
5	MPO	C	406	-	-	4/7/15/15	0/1/1/1
5	MPO	D	406	-	-	5/7/15/15	0/1/1/1
4	GOL	C	405	-	-	2/4/4/4	-
6	TRS	C	408	-	-	6/9/9/9	-
9	PEG	H	407	-	-	1/4/4/4	-
8	PGE	B	505	-	-	5/7/7/7	-
4	GOL	B	504	-	-	0/4/4/4	-

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	406	MPO	C1-S1	-13.23	1.59	1.77
5	D	406	MPO	C1-S1	-9.79	1.63	1.77
5	C	407	MPO	C1-S1	-7.82	1.66	1.77
5	C	406	MPO	C1-S1	-7.49	1.67	1.77
5	C	406	MPO	O1-S1	7.16	1.65	1.45

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	406	MPO	O1-S1-C1	5.41	114.91	106.73
4	C	405	GOL	C3-C2-C1	-4.95	93.64	111.80
5	D	406	MPO	O3-S1-C1	4.76	115.33	106.00
5	C	406	MPO	C6-C7-N1	4.34	116.72	110.12
6	C	408	TRS	C3-C-N	-4.21	97.42	108.17

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	405	GOL	C1-C2-C3-O3
5	C	406	MPO	C2-C1-S1-O1
5	C	406	MPO	C1-C2-C3-N1
5	C	407	MPO	C2-C1-S1-O1
5	C	407	MPO	C2-C1-S1-O2

There are no ring outliers.

9 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	406	MPO	2	0
5	C	407	MPO	3	0
5	H	406	MPO	3	0
4	B	501	GOL	2	0
4	C	405	GOL	2	0
4	B	502	GOL	1	0
5	D	406	MPO	1	0
6	C	408	TRS	3	0
8	B	505	PGE	3	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	C	340/350 (97%)	-0.14	4 (1%) 76 78	19, 31, 58, 77	3 (0%)
1	D	340/350 (97%)	0.16	8 (2%) 59 61	21, 35, 57, 76	6 (1%)
1	F	340/350 (97%)	0.47	8 (2%) 59 61	29, 42, 59, 85	10 (2%)
1	H	341/350 (97%)	0.58	12 (3%) 47 48	24, 41, 63, 93	3 (0%)
2	A	278/283 (98%)	-0.24	0 100 100	22, 30, 47, 70	2 (0%)
2	B	278/283 (98%)	-0.41	0 100 100	19, 27, 44, 68	1 (0%)
2	E	279/283 (98%)	-0.03	2 (0%) 84 85	25, 34, 49, 70	5 (1%)
2	G	278/283 (98%)	0.37	8 (2%) 53 55	27, 40, 63, 81	3 (1%)
All	All	2474/2532 (97%)	0.11	42 (1%) 69 70	19, 36, 58, 93	33 (1%)

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	230	PHE	4.9
1	D	215	GLU	3.7
2	G	279	GLY	3.6
1	D	231	SER	3.5
1	H	222	LYS	3.5

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 oligosaccharides 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. 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
3	PO4	E	401	5/5	0.68	0.17	65,68,93,98	0
4	GOL	B	502	6/6	0.76	0.21	59,60,66,66	0
8	PGE	B	505	10/10	0.79	0.15	37,62,64,66	0
7	CL	D	409	1/1	0.80	0.14	47,47,47,47	1
3	PO4	A	401	5/5	0.81	0.16	56,68,78,88	0
9	PEG	H	407	7/7	0.81	0.14	58,60,63,64	0
9	PEG	D	407	7/7	0.82	0.16	46,48,56,57	0
9	PEG	D	408	7/7	0.83	0.13	58,61,65,66	0
6	TRS	C	408	8/8	0.85	0.18	44,50,54,56	0
4	GOL	B	501	6/6	0.85	0.15	38,44,51,62	0
4	GOL	B	503	6/6	0.85	0.14	43,46,48,50	0
3	PO4	H	404	5/5	0.87	0.14	63,76,90,99	0
5	MPO	C	406	13/13	0.87	0.13	63,68,82,85	0
3	PO4	F	405	5/5	0.88	0.14	51,51,60,63	0
4	GOL	C	405	6/6	0.88	0.12	44,55,57,61	0
7	CL	C	409	1/1	0.89	0.13	46,46,46,46	0
4	GOL	C	404	6/6	0.89	0.12	39,47,49,49	0
4	GOL	D	405	6/6	0.89	0.10	38,53,56,57	0
5	MPO	D	406	13/13	0.92	0.13	44,53,57,59	2
3	PO4	C	402	5/5	0.92	0.11	42,45,53,55	0
3	PO4	C	401	5/5	0.94	0.09	50,55,65,66	0
5	MPO	C	407	13/13	0.94	0.15	28,35,60,62	0
3	PO4	H	401	5/5	0.95	0.07	42,46,51,52	0
3	PO4	H	403	5/5	0.95	0.10	50,50,53,55	0
4	GOL	B	504	6/6	0.95	0.07	23,26,30,34	0
3	PO4	F	404	5/5	0.95	0.09	47,47,50,59	0
3	PO4	D	402	5/5	0.95	0.09	47,51,65,67	0
3	PO4	F	406	5/5	0.95	0.09	41,42,44,46	0
3	PO4	F	401	5/5	0.95	0.09	45,46,55,58	0
5	MPO	H	406	13/13	0.96	0.12	29,38,63,67	1
3	PO4	C	403	5/5	0.96	0.08	33,34,35,40	0
3	PO4	H	405	5/5	0.96	0.08	41,46,48,51	0
3	PO4	F	403	5/5	0.96	0.07	33,35,37,43	0
3	PO4	D	403	5/5	0.97	0.06	39,41,43,47	0
3	PO4	D	404	5/5	0.97	0.06	27,31,32,33	0
3	PO4	F	402	5/5	0.97	0.06	39,39,41,42	0
10	NA	E	402	1/1	0.97	0.06	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	PO4	D	401	5/5	0.98	0.08	34,36,38,43	0
3	PO4	H	402	5/5	0.98	0.08	33,34,36,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.