



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 6PFN  
Title : Succinyl-CoA synthase from *Francisella tularensis*  
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Center for Structural Genomics of Infectious Diseases (CSGID)  
Deposited on : 2019-06-21  
Resolution : 1.76 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](mailto: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>.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
buster-report : 1.1.7 (2018)  
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) : 2.35.1

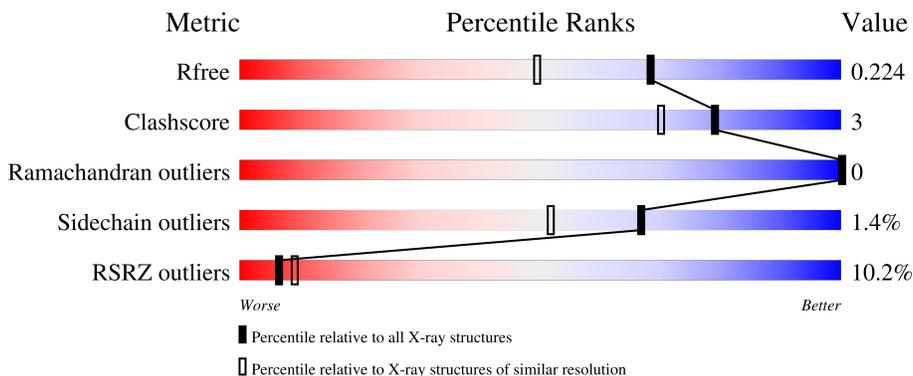
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.76 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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	296	 96%
1	C	296	 95%
2	B	387	 76% 8% 16%
2	D	387	 78% 8% 13%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 10365 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 Succinate–CoA ligase [ADP-forming] subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	295	2177	1389	362	417	9	0	3	0
1	C	293	2158	1373	362	414	9	0	4	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	85	VAL	ALA	engineered mutation	UNP A0A454XSD0
A	291	GLU	-	expression tag	UNP A0A454XSD0
A	292	ASN	-	expression tag	UNP A0A454XSD0
A	293	LEU	-	expression tag	UNP A0A454XSD0
A	294	TYR	-	expression tag	UNP A0A454XSD0
A	295	PHE	-	expression tag	UNP A0A454XSD0
A	296	GLN	-	expression tag	UNP A0A454XSD0
C	85	VAL	ALA	engineered mutation	UNP A0A454XSD0
C	291	GLU	-	expression tag	UNP A0A454XSD0
C	292	ASN	-	expression tag	UNP A0A454XSD0
C	293	LEU	-	expression tag	UNP A0A454XSD0
C	294	TYR	-	expression tag	UNP A0A454XSD0
C	295	PHE	-	expression tag	UNP A0A454XSD0
C	296	GLN	-	expression tag	UNP A0A454XSD0

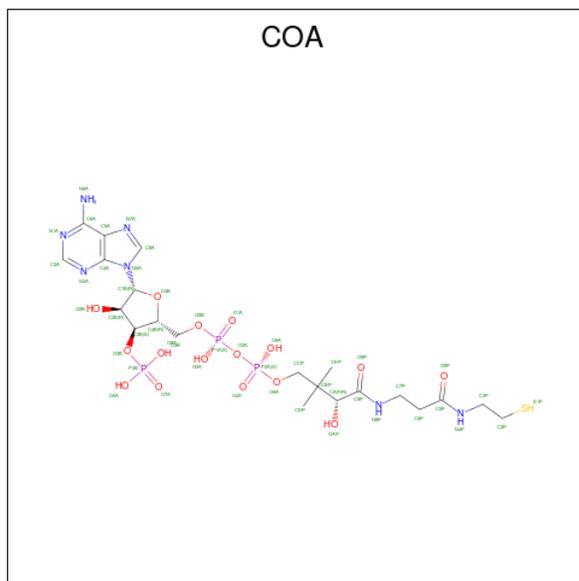
- Molecule 2 is a protein called Succinate–CoA ligase [ADP-forming] subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	326	2512	1599	428	474	11	0	7	0
2	D	336	2612	1663	442	497	10	0	8	0

There are 2 discrepancies between the modelled and reference sequences:

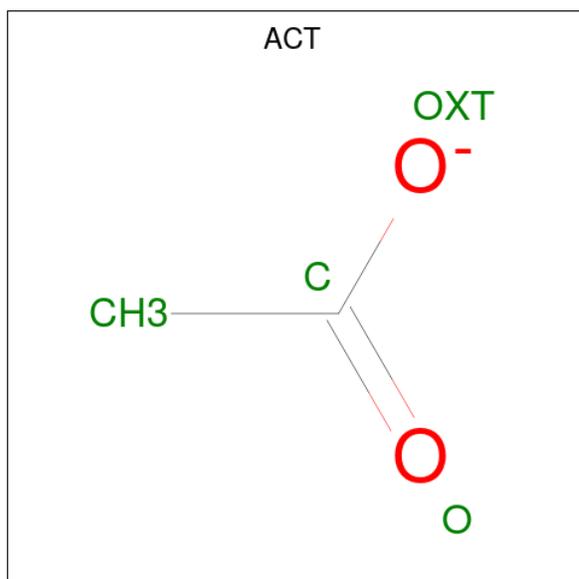
Chain	Residue	Modelled	Actual	Comment	Reference
B	69	THR	ALA	engineered mutation	UNP Q5NHF3
D	69	THR	ALA	engineered mutation	UNP Q5NHF3

- Molecule 3 is COENZYME A (three-letter code: COA) (formula:  $C_{21}H_{36}N_7O_{16}P_3S$ ).



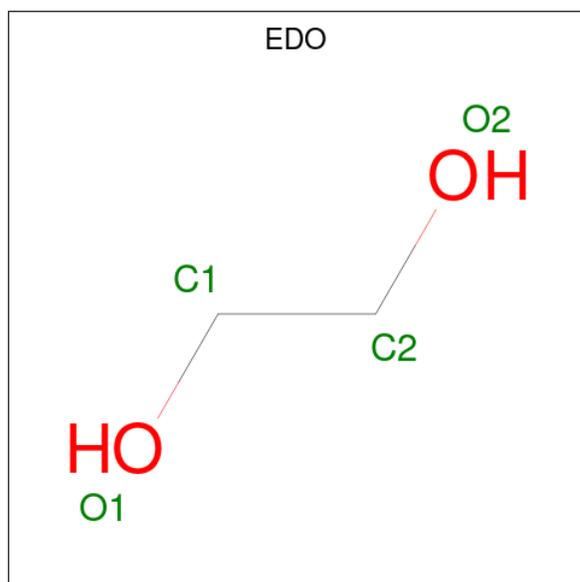
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			S
3	A	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
3	C	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	253	Total	O	0	0
			253	253		
6	B	187	Total	O	0	1
			187	187		
6	C	180	Total	O	0	0
			180	180		
6	D	182	Total	O	0	1
			182	182		



G282	G283	P284	A285	N286	V289	GLY	GLY	GLY	ALA	THR	LYS	E287	R298	V299	I300	E301	A302	F303	R304	L305	I306	L307	D308	D309	E310	N311	V312	K313	A314	I315	L316	I317	N318	I319	F320	G321	GLY	ILE	VAL	ARG	CYS	ASP	MET	ILE	ALA	GLU	ALA	ILE	ILE	E335	A336	V337	K338	E339	VAL	ASN	VAL	THR
VAL	F345	V346	V347	V348	R349	L350	GLU	GLY	ASN	ASN	ALA	GLU	LYS	GLY	ALA	LYS	ILE	LEU	ALA	ASP	SER	GLY	LEU	LYS	LEU	ILE	PRO	ALA	ASP	G374	L375	A376	D377	A378	A379	D380	K381	V382	V383	LYS	SER	LEU	GLY															

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.07Å 158.74Å 73.02Å 90.00° 113.11° 90.00°	Depositor
Resolution (Å)	49.65 – 1.76 49.60 – 1.76	Depositor EDS
% Data completeness (in resolution range)	97.6 (49.65-1.76) 97.7 (49.60-1.76)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.59 (at 1.76Å)	Xtrriage
Refinement program	REFMAC 5.8.0238	Depositor
R, $R_{free}$	0.186 , 0.218 0.194 , 0.224	Depositor DCC
$R_{free}$ test set	6906 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.2	Xtrriage
Anisotropy	0.367	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 44.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	10365	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.64% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical 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: ACT, EDO, COA

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	0.78	1/2225 (0.0%)	0.84	1/3016 (0.0%)
1	C	0.74	0/2207	0.79	0/2990
2	B	0.76	0/2566	0.85	0/3456
2	D	0.73	0/2669	0.81	0/3593
All	All	0.75	1/9667 (0.0%)	0.82	1/13055 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	260	GLU	CD-OE1	5.64	1.31	1.25

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	260	GLU	OE1-CD-OE2	5.23	129.57	123.30

There are no chirality outliers.

There are no planarity outliers.

### 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	A	2177	0	2237	7	0
1	C	2158	0	2222	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2512	0	2576	19	0
2	D	2612	0	2672	26	0
3	A	48	0	32	0	0
3	C	48	0	32	0	0
4	D	4	0	3	1	0
5	D	4	0	6	0	0
6	A	253	0	0	2	0
6	B	187	0	0	1	0
6	C	180	0	0	1	0
6	D	182	0	0	1	0
All	All	10365	0	9780	55	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.

The worst 5 of 55 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:D:315:ILE:HD11	2:D:346:VAL:HG23	1.81	0.62
1:A:137:ILE:HD12	2:B:323:ILE:HB	1.83	0.60
1:A:156:THR:HA	1:A:159:TYR:CD2	2.37	0.59
1:C:240:PRO:HD3	2:D:256:LEU:HD21	1.84	0.57
2:B:262:CYS:HA	2:B:316:LEU:O	2.06	0.56

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	296/296 (100%)	290 (98%)	6 (2%)	0	100	100
1	C	295/296 (100%)	286 (97%)	9 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	324/387 (84%)	315 (97%)	9 (3%)	0	100	100
2	D	334/387 (86%)	329 (98%)	5 (2%)	0	100	100
All	All	1249/1366 (91%)	1220 (98%)	29 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	230/228 (101%)	230 (100%)	0	100	100
1	C	228/228 (100%)	224 (98%)	4 (2%)	59	40
2	B	269/308 (87%)	265 (98%)	4 (2%)	65	49
2	D	280/308 (91%)	272 (97%)	8 (3%)	42	19
All	All	1007/1072 (94%)	991 (98%)	16 (2%)	67	45

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	278	GLN
2	D	277	ILE
2	D	136	GLU
2	D	259	ASN
1	C	256[B]	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	200	GLN
1	A	296	GLN
1	C	200	GLN
2	D	33	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 monosaccharides 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
3	COA	C	500	-	41,50,50	0.89	2 (4%)	52,75,75	1.00	2 (3%)
5	EDO	D	502	-	3,3,3	0.17	0	2,2,2	0.31	0
3	COA	A	500	-	41,50,50	0.69	1 (2%)	52,75,75	0.84	2 (3%)
4	ACT	D	501	-	3,3,3	1.96	1 (33%)	3,3,3	0.63	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
3	COA	C	500	-	-	1/44/64/64	0/3/3/3
3	COA	A	500	-	-	1/44/64/64	0/3/3/3
5	EDO	D	502	-	-	1/1/1/1	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	500	COA	P3B-O3B	2.67	1.64	1.59
4	D	501	ACT	OXT-C	-2.66	1.18	1.30
3	C	500	COA	P3B-O3B	2.49	1.64	1.59
3	C	500	COA	P3B-O9A	-2.07	1.46	1.54

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	500	COA	O4B-C1B-C2B	-2.58	103.16	106.93
3	C	500	COA	O2B-C2B-C3B	2.21	117.45	111.17
3	A	500	COA	O4B-C1B-C2B	-2.07	103.91	106.93
3	A	500	COA	C5A-C6A-N6A	2.00	123.39	120.35

There are no chirality outliers.

All (3) torsion outliers are listed below:

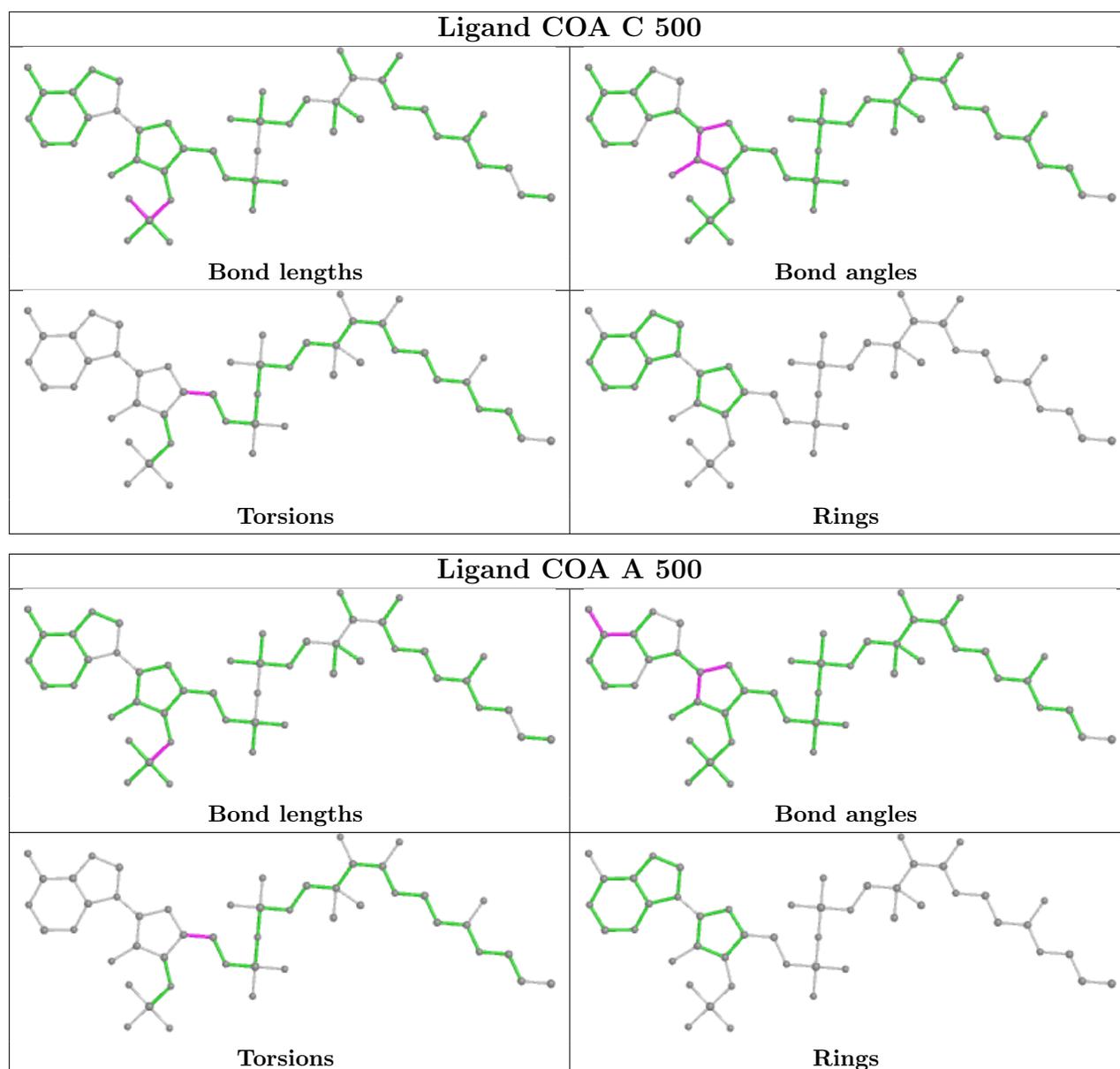
Mol	Chain	Res	Type	Atoms
5	D	502	EDO	O1-C1-C2-O2
3	A	500	COA	O4B-C4B-C5B-O5B
3	C	500	COA	O4B-C4B-C5B-O5B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	501	ACT	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	295/296 (99%)	0.03	4 (1%) 75 82	16, 24, 49, 75	0
1	C	293/296 (98%)	0.22	11 (3%) 40 47	17, 32, 57, 82	0
2	B	326/387 (84%)	0.63	46 (14%) 2 4	17, 36, 65, 78	0
2	D	336/387 (86%)	0.86	67 (19%) 1 1	16, 36, 79, 89	0
All	All	1250/1366 (91%)	0.45	128 (10%) 6 9	16, 31, 68, 89	0

The worst 5 of 128 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	314	ALA	9.0
2	D	300	ILE	8.9
2	B	383	VAL	8.8
2	B	369	LEU	8.7
2	D	299	VAL	7.7

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [i](#)

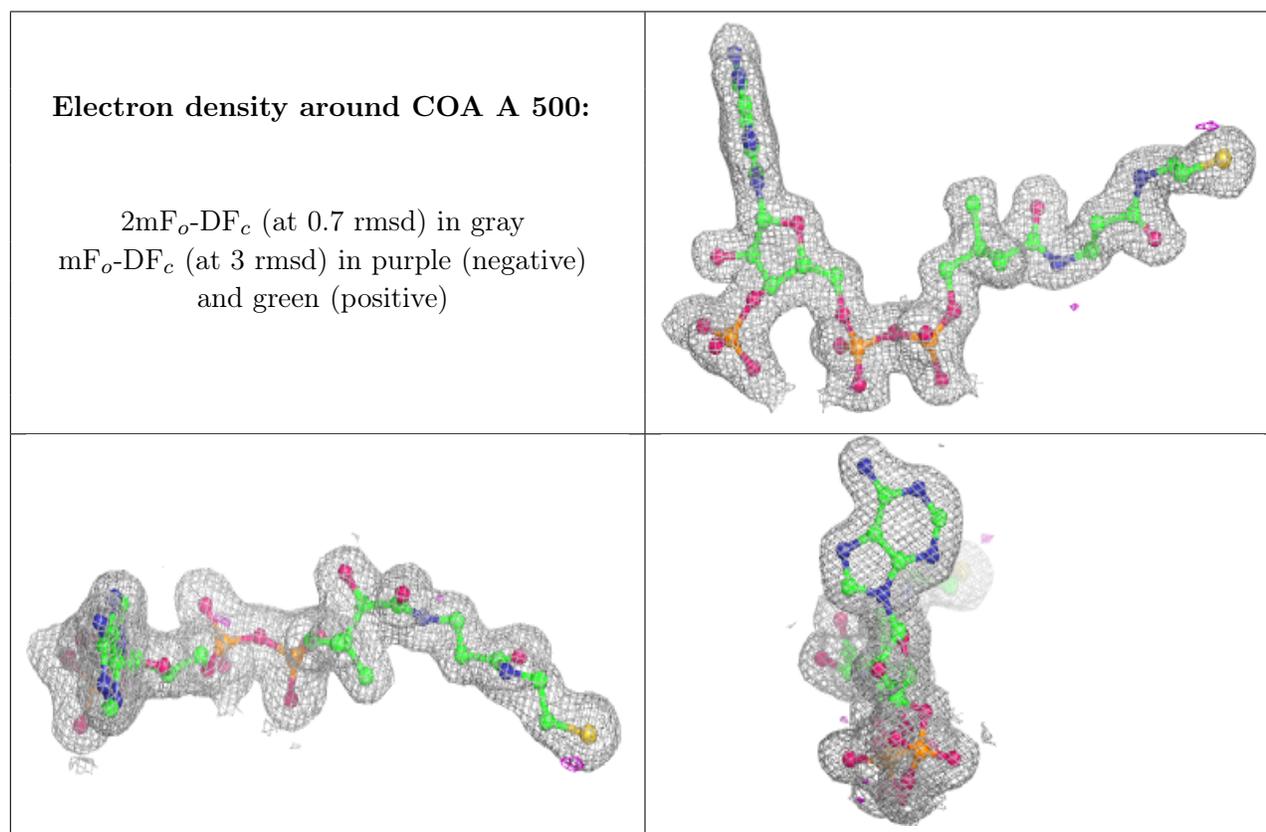
There are no monosaccharides in this entry.

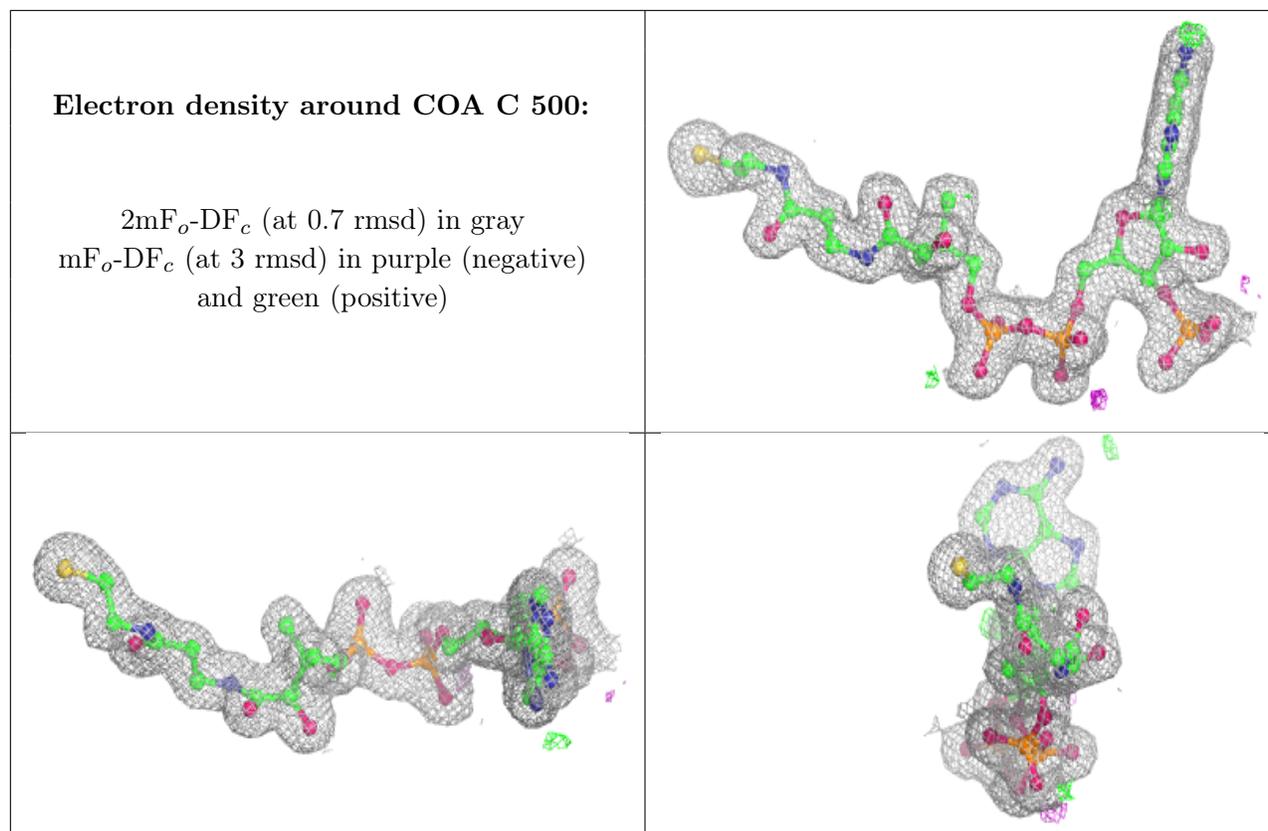
### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	EDO	D	502	4/4	0.89	0.15	35,38,41,45	0
4	ACT	D	501	4/4	0.91	0.14	32,38,39,40	0
3	COA	A	500	48/48	0.97	0.07	22,24,28,29	0
3	COA	C	500	48/48	0.98	0.07	18,21,27,31	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.