



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 08:38 am BST

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 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
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)	:	2.11

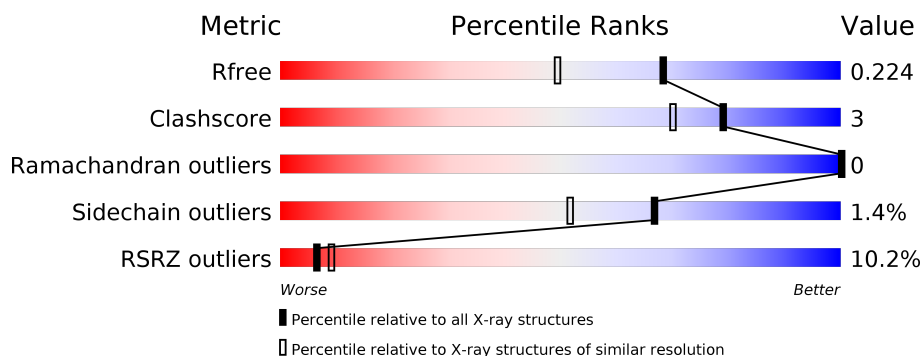
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.76 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 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	296	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="width: 96%; height: 10px; background-color: green;"></div> <div style="width: 96%; text-align: right;">96%</div> <div style="width: 100%; height: 10px; background-color: yellow;"></div> <div style="width: 100%; height: 10px; background-color: orange;"></div> <div style="width: 100%; height: 10px; background-color: grey;"></div> </div>
1	C	296	<div> <div style="width: 4%; height: 10px; background-color: red;"></div> <div style="width: 95%; height: 10px; background-color: green;"></div> <div style="width: 95%; text-align: right;">95%</div> <div style="width: 100%; height: 10px; background-color: yellow;"></div> <div style="width: 100%; height: 10px; background-color: orange;"></div> <div style="width: 100%; height: 10px; background-color: grey;"></div> </div>
2	B	387	<div> <div style="width: 12%; height: 10px; background-color: red;"></div> <div style="width: 76%; height: 10px; background-color: green;"></div> <div style="width: 76%; text-align: right;">76%</div> <div style="width: 8%; height: 10px; background-color: yellow;"></div> <div style="width: 8%; text-align: right;">8%</div> <div style="width: 16%; height: 10px; background-color: orange;"></div> <div style="width: 16%; text-align: right;">16%</div> <div style="width: 100%; height: 10px; background-color: grey;"></div> </div>
2	D	387	<div> <div style="width: 17%; height: 10px; background-color: red;"></div> <div style="width: 78%; height: 10px; background-color: green;"></div> <div style="width: 78%; text-align: right;">78%</div> <div style="width: 8%; height: 10px; background-color: yellow;"></div> <div style="width: 8%; text-align: right;">8%</div> <div style="width: 13%; height: 10px; background-color: orange;"></div> <div style="width: 13%; text-align: right;">13%</div> <div style="width: 100%; height: 10px; background-color: grey;"></div> </div>

2 Entry composition

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
1	A	295	Total	C	N	O	S	0	3	0
			2177	1389	362	417	9			
1	C	293	Total	C	N	O	S	0	4	0
			2158	1373	362	414	9			

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

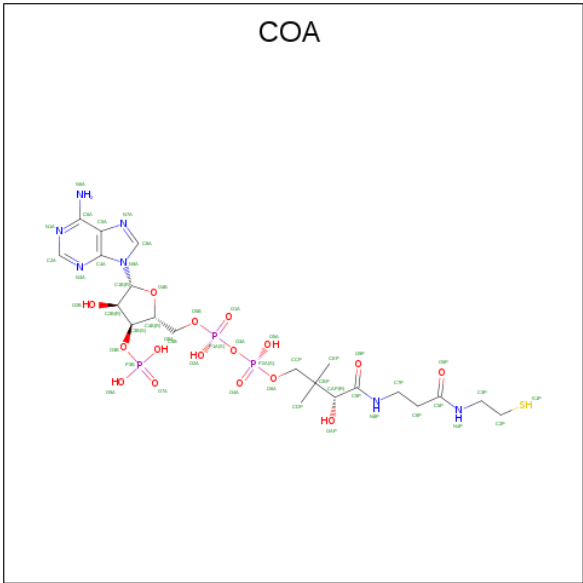
- Molecule 2 is a protein called Succinate–CoA ligase [ADP-forming] subunit beta.

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

There are 2 discrepancies between the modelled and reference sequences:

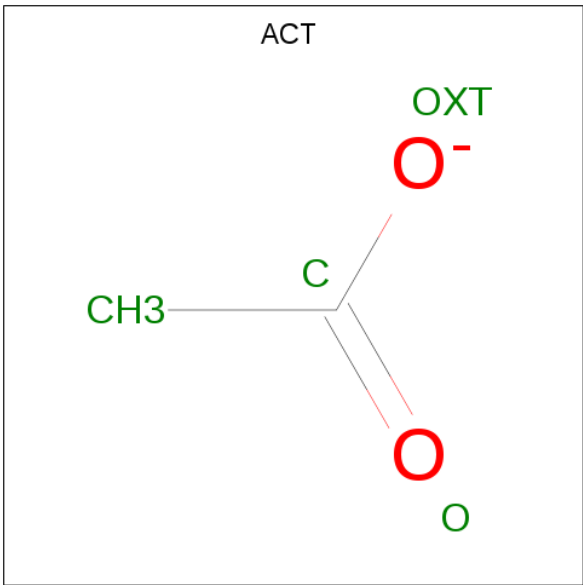
Chain	Residue	Modelled	Actual	Comment	Reference
B	69	THR	ALA	engineered mutation	UNP Q5NHF3
D	69	THR	ALA	engineered mutation	UNP Q5NHF3

- Molecule 3 is COENZYME A (three-letter code: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
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: C₂H₃O₂).



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: $C_2H_6O_2$).



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		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

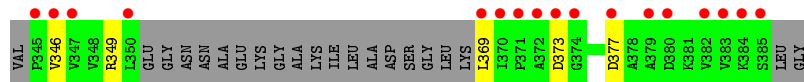
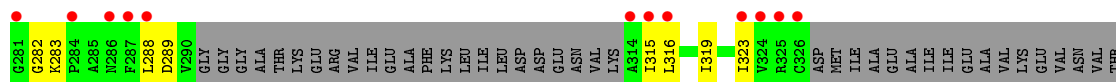
- Molecule 1: Succinate-CoA ligase [ADP-forming] subunit alpha



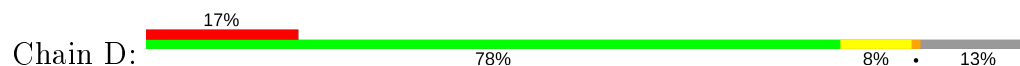
- Molecule 1: Succinate-CoA ligase [ADP-forming] subunit alpha

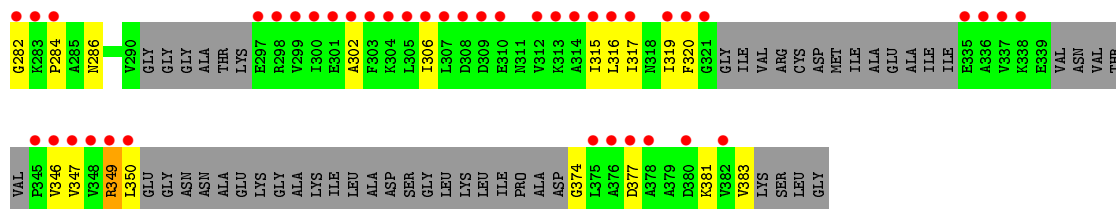


- Molecule 2: Succinate-CoA ligase [ADP-forming] subunit beta



- Molecule 2: Succinate-CoA ligase [ADP-forming] subunit beta





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	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
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 1.76Å)	Xtriage
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 ²)	24.2	Xtriage
Anisotropy	0.367	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10365	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage'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.*

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: COA, EDO, ACT

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.

All (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
2:D:6:TYR:CD1	2:D:24:VAL:HG21	2.39	0.56
2:D:278:GLN:HA	2:D:282:GLY:O	2.07	0.55
1:A:73[B]:VAL:CG1	1:A:77:PHE:HB2	2.37	0.54
4:D:501:ACT:H2	6:D:689:HOH:O	2.08	0.53
1:C:130:PRO:HG2	1:C:172:GLN:HB2	1.92	0.52
2:D:315:ILE:CD1	2:D:346:VAL:HG23	2.40	0.51
1:A:145:LYS:HE2	6:A:619:HOH:O	2.11	0.50
1:C:156:THR:HA	1:C:159:TYR:CD2	2.47	0.50
2:D:265[A]:ASN:OD1	2:D:319:ILE:HA	2.11	0.50
2:D:278:GLN:HG3	2:D:284:PRO:HD3	1.94	0.49
2:D:277:ILE:HD11	2:D:316:LEU:HD23	1.92	0.49
2:B:106:THR:HB	2:B:107:ARG:HG3	1.94	0.48
2:D:315:ILE:HD11	2:D:346:VAL:CG2	2.44	0.48
2:B:258:GLY:HA3	2:B:283:LYS:O	2.15	0.47
2:D:374:GLY:O	2:D:377:ASP:HB3	2.14	0.47
2:D:277:ILE:HD11	2:D:316:LEU:CD2	2.44	0.47
1:A:113:LYS:HG2	6:A:774:HOH:O	2.15	0.47
2:D:347:VAL:HG13	2:D:381:LYS:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:260:ILE:HD12	2:D:383:VAL:HG22	1.96	0.47
2:B:277:ILE:O	2:B:280:TYR:N	2.40	0.46
2:D:262:CYS:HA	2:D:316:LEU:O	2.16	0.46
2:B:315:ILE:HG12	2:B:346:VAL:HG22	1.98	0.46
2:B:278:GLN:HA	2:B:282:GLY:O	2.16	0.45
1:C:159:TYR:HB3	2:D:320:PHE:CE1	2.51	0.45
2:D:349:ARG:HD3	2:D:350:LEU:N	2.31	0.45
1:C:19:LYS:NZ	6:C:605:HOH:O	2.49	0.45
2:D:173[B]:LYS:HD3	2:D:173[B]:LYS:HA	1.75	0.45
2:D:317:ILE:CG2	2:D:319:ILE:CD1	2.95	0.45
2:D:200:ASN:HA	2:D:201:PRO:HA	1.83	0.43
1:A:76:PRO:HB3	2:B:225:TYR:CE1	2.53	0.43
2:B:33:GLN:HG3	6:B:486:HOH:O	2.18	0.43
2:B:315:ILE:CD1	2:B:346:VAL:HG22	2.48	0.43
2:B:150:VAL:HG11	2:B:186:TYR:CE1	2.54	0.43
2:D:261:GLY:O	2:D:315:ILE:HA	2.19	0.42
2:B:31:ALA:HB1	2:B:69:THR:HG22	2.01	0.42
2:D:199:ILE:HD13	2:D:212:CYS:SG	2.59	0.42
2:D:260:ILE:CD1	2:D:383:VAL:HG22	2.49	0.42
1:A:245:MET:O	2:B:267:ALA:HB1	2.19	0.42
2:B:121:LYS:HD2	2:B:152:PRO:HD3	2.01	0.42
2:B:265:ASN:OD1	2:B:319:ILE:HA	2.19	0.41
1:C:73:VAL:CG1	1:C:77:PHE:HB2	2.51	0.41
2:B:196:LEU:HG	2:B:218:ASN:HB3	2.02	0.41
2:B:346:VAL:HB	2:B:369:LEU:HD13	2.01	0.41
2:D:319:ILE:N	2:D:319:ILE:HD12	2.35	0.41
2:B:373:ASP:HB3	2:B:377:ASP:OD2	2.21	0.41
2:D:302:ALA:O	2:D:306:ILE:HG13	2.21	0.41
2:D:317:ILE:HG22	2:D:319:ILE:CD1	2.51	0.41
1:C:193:LYS:HG2	1:C:221:TYR:OH	2.22	0.40
2:D:261:GLY:HA2	2:D:286:ASN:OD1	2.21	0.40
2:B:288:LEU:HD12	2:B:289:ASP:H	1.86	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	296/296 (100%)	290 (98%)	6 (2%)	0	100	100
1	C	295/296 (100%)	286 (97%)	9 (3%)	0	100	100
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 ⓘ

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

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	106	THR
2	B	206	GLU
2	B	278	GLN
2	B	349	ARG
1	C	134	LYS
1	C	244	ARG
1	C	256[A]	LYS
1	C	256[B]	LYS

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Mol	Chain	Res	Type
2	D	136	GLU
2	D	173[A]	LYS
2	D	173[B]	LYS
2	D	198	GLU
2	D	259	ASN
2	D	277	ILE
2	D	278	GLN
2	D	349	ARG

Some 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 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
5	EDO	D	502	-	3,3,3	0.17	0	2,2,2	0.31	0
4	ACT	D	501	-	1,3,3	5.52	1 (100%)	0,3,3	0.00	-
3	COA	A	500	-	41,50,50	0.69	1 (2%)	52,75,75	0.84	2 (3%)
3	COA	C	500	-	41,50,50	0.89	2 (4%)	52,75,75	1.00	2 (3%)

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
5	EDO	D	502	-	-	1/1/1/1	-
3	COA	A	500	-	-	1/44/64/64	0/3/3/3
3	COA	C	500	-	-	1/44/64/64	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	501	ACT	CH3-C	5.52	1.55	1.48
3	A	500	COA	P3B-O3B	2.67	1.64	1.59
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:

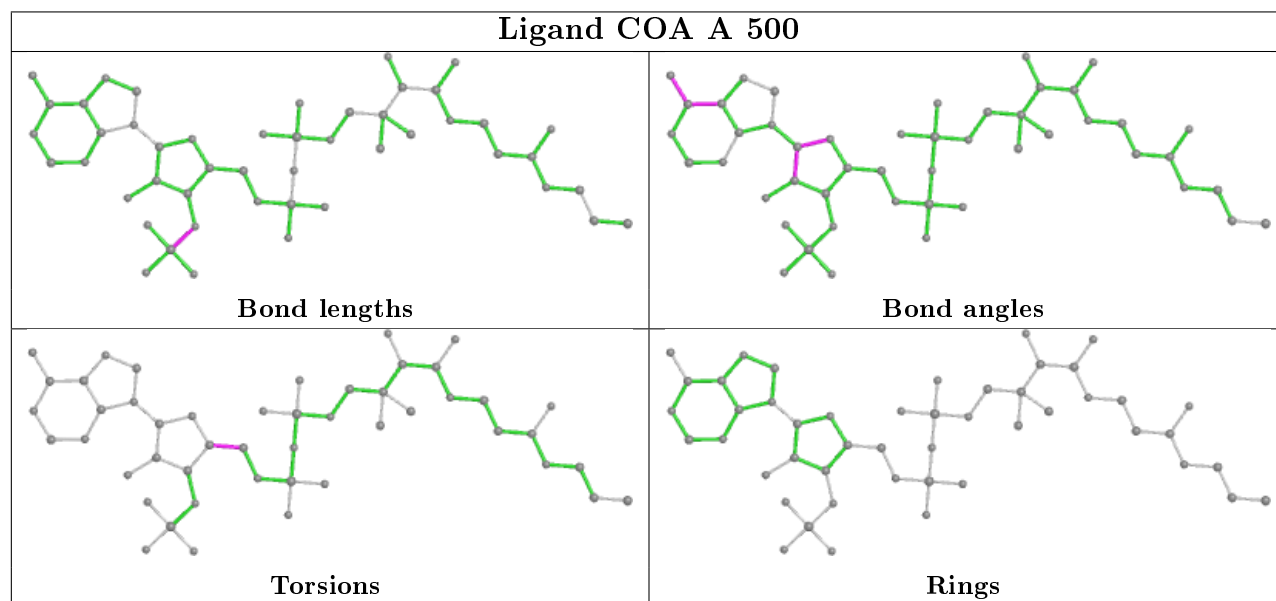
Mol	Chain	Res	Type	Atoms
5	D	502	EDO	O1-C1-C2-O2
3	A	500	COA	O4B-C4B-C5B-O5B
3	C	500	COA	O4B-C4B-C5B-O5B

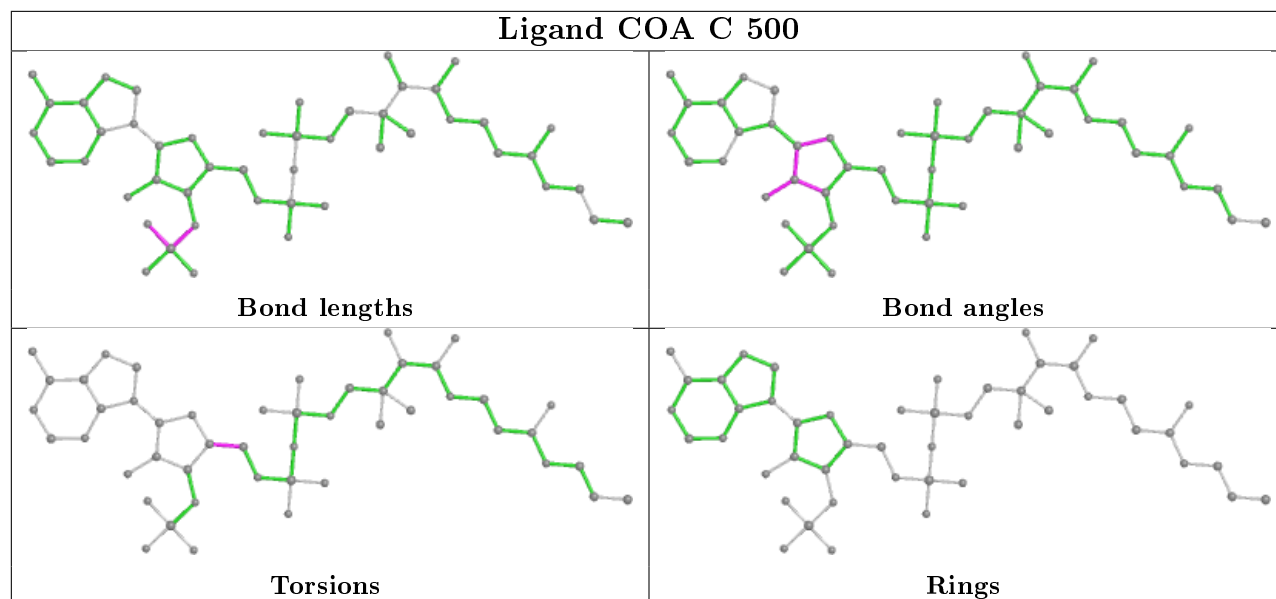
There are no ring outliers.

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 ⓘ

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	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

All (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
2	D	303	PHE	7.2
2	B	279	LEU	7.1
2	B	370	ILE	7.1
2	B	350[A]	LEU	7.0
2	D	337	VAL	6.7
2	D	346	VAL	6.7
1	A	254	GLY	6.7
2	D	336	ALA	6.5
2	D	313	LYS	6.2
2	B	346	VAL	6.1
1	C	254	GLY	5.7
2	D	350	LEU	5.6
2	D	281	GLY	5.6
2	B	372	ALA	5.3
2	D	306	ILE	5.0
2	D	256	LEU	4.8

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Mol	Chain	Res	Type	RSRZ
2	B	371	PRO	4.8
2	D	320	PHE	4.8
1	C	253	SER	4.6
2	D	307	LEU	4.5
2	B	379	ALA	4.5
2	D	375	LEU	4.5
2	B	103	TYR	4.5
2	D	280	TYR	4.4
2	D	257	GLU	4.3
2	D	345	PRO	4.3
2	B	347	VAL	4.2
2	D	298	ARG	4.1
2	D	382	VAL	4.1
2	D	284	PRO	4.1
2	D	338	LYS	4.0
2	B	385	SER	4.0
2	B	384	LYS	4.0
2	D	315	ILE	4.0
2	D	29	ASN	3.9
2	D	283	LYS	3.9
2	D	251	LEU	3.9
2	B	325	ARG	3.8
1	C	255	GLY	3.8
2	B	256	LEU	3.7
2	D	376	ALA	3.7
2	B	280	TYR	3.7
2	B	314	ALA	3.7
2	D	335	GLU	3.6
2	B	284	PRO	3.6
2	D	32	ALA	3.5
1	C	294	TYR	3.4
2	D	261	GLY	3.3
2	D	348	VAL	3.3
2	B	382	VAL	3.2
2	D	305	LEU	3.2
2	D	259	ASN	3.2
2	D	263	MET	3.2
2	B	105	VAL	3.2
2	D	319	ILE	3.2
2	B	374	GLY	3.2
1	A	236	GLY	3.1
2	B	260	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
2	B	380	ASP	3.1
2	B	281	GLY	3.1
2	D	377	ASP	3.0
2	B	250	GLU	3.0
2	D	302	ALA	3.0
2	B	288	LEU	3.0
2	B	345	PRO	3.0
2	D	380	ASP	3.0
2	B	315	ILE	3.0
2	D	279	LEU	3.0
1	A	255	GLY	2.9
2	D	347	VAL	2.9
2	D	297	GLU	2.9
2	D	309	ASP	2.9
2	D	308	ASP	2.9
2	D	310	GLU	2.8
2	B	323	ILE	2.8
2	B	42	PHE	2.8
2	B	84	PHE	2.7
2	D	249	HIS	2.7
2	D	316	LEU	2.7
2	D	33	GLN	2.7
2	B	373	ASP	2.6
2	D	321	GLY	2.6
2	B	55	GLY	2.5
2	D	378	ALA	2.5
1	C	183	ILE	2.4
2	B	377	ASP	2.4
2	B	255	ALA	2.4
2	B	316	LEU	2.4
2	B	326	CYS	2.4
2	D	122	VAL	2.4
1	C	103	LEU	2.4
1	C	236	GLY	2.4
2	B	56	LYS	2.4
2	B	278	GLN	2.4
1	C	224	HIS	2.3
2	D	282	GLY	2.3
2	D	349	ARG	2.3
2	D	260	ILE	2.3
2	D	69	THR	2.3
1	C	141	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
2	D	254	VAL	2.2
2	D	301	GLU	2.2
2	B	286	ASN	2.2
2	B	204	VAL	2.2
2	D	190	ILE	2.2
2	D	317	ILE	2.2
2	D	67	GLN	2.2
2	B	261	GLY	2.2
2	D	37	GLN	2.2
2	D	38	LEU	2.2
2	D	39	GLY	2.2
2	D	255	ALA	2.2
1	C	291	GLU	2.1
1	A	240	PRO	2.1
1	C	257	GLY	2.1
2	B	61	LYS	2.1
2	D	74	GLU	2.1
2	B	287	PHE	2.1
2	B	324	VAL	2.0
2	D	304	LYS	2.0
2	D	115	VAL	2.0
2	D	312	VAL	2.0
2	B	106	THR	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.

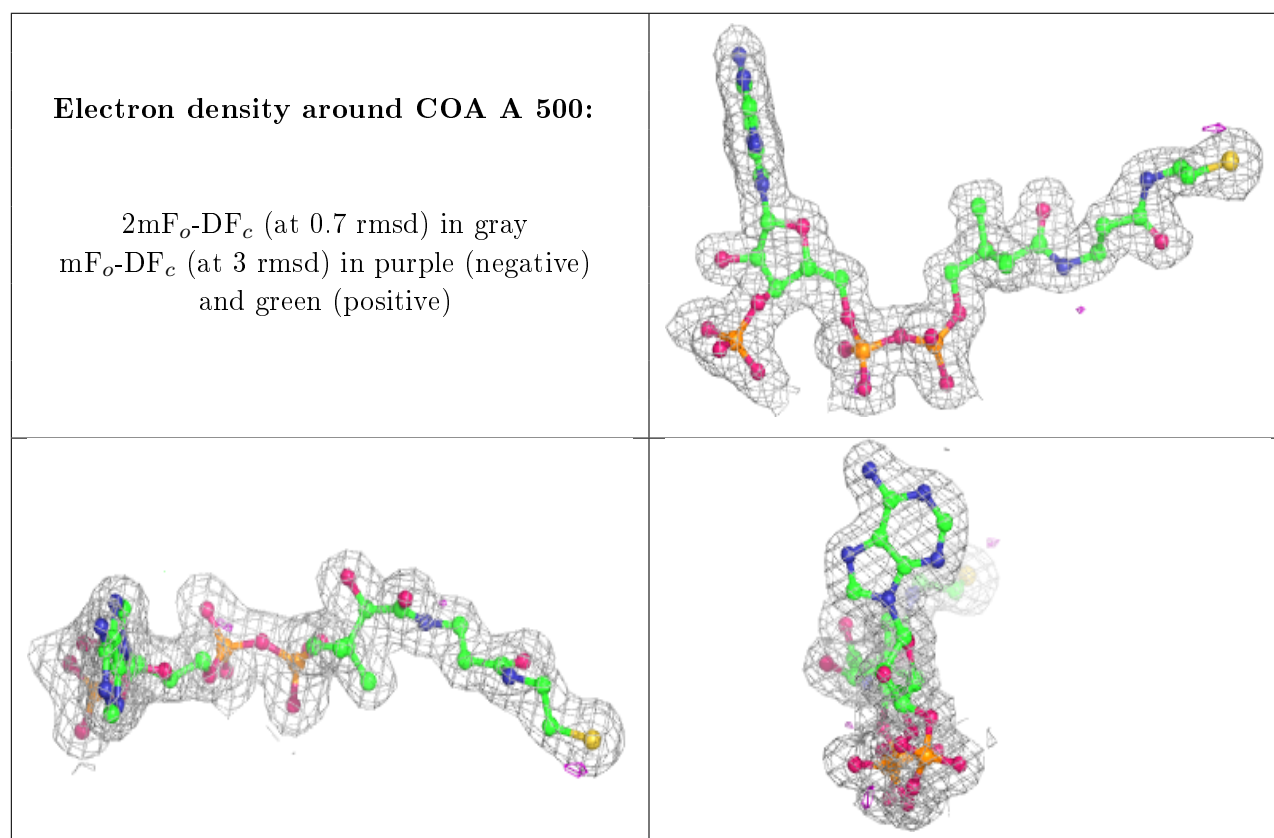
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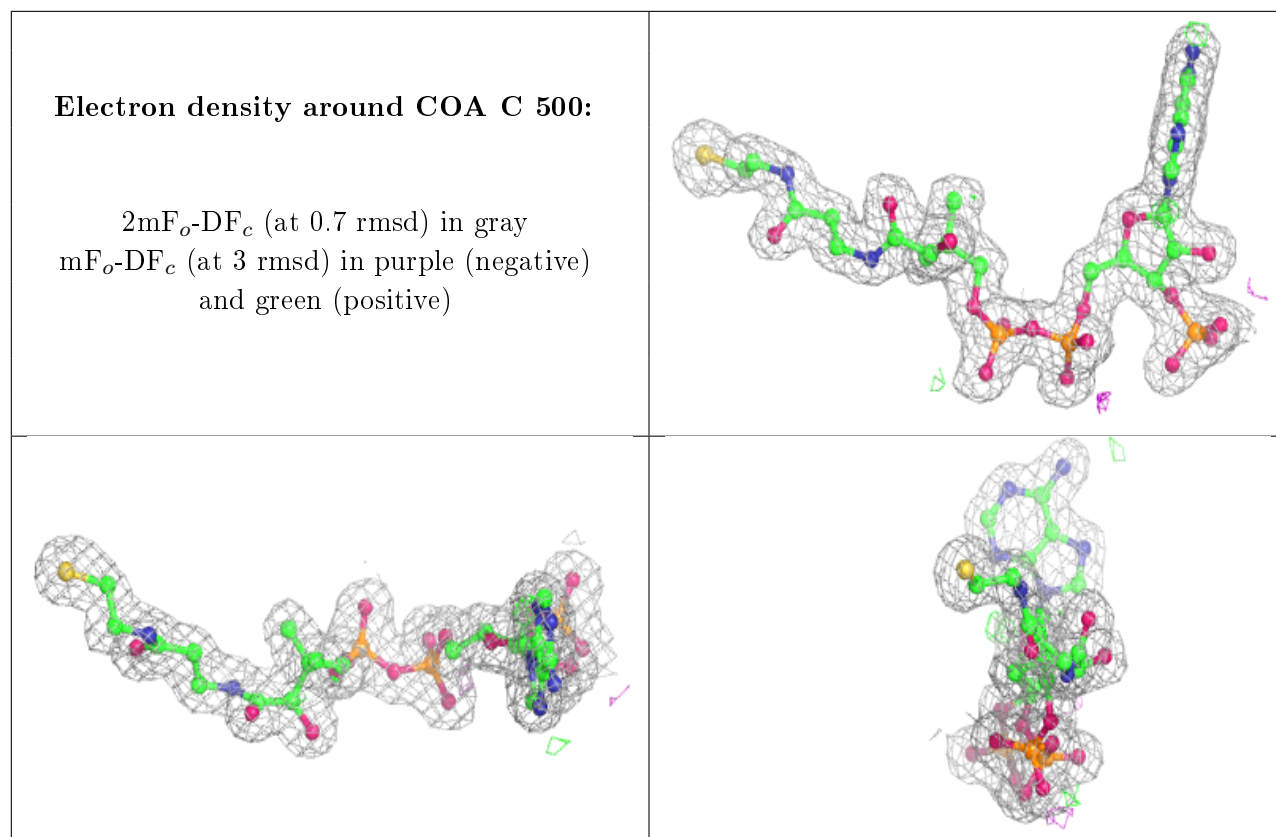
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	EDO	D	502	4/4	0.89	0.15	35,38,41,45	0
4	ACT	D	501	4/4	0.91	0.14	32,38,39,40	0
3	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.