



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 9, 2025 – 02:17 PM JST

PDB ID : 8ZW1 / pdb_00008zw1
Title : citrate synthases complexed with oxaloacetate and acetyl-CoA
Authors : Yang, L.Y.; Fang, Y.J.
Deposited on : 2024-06-12
Resolution : 2.10 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 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 Phenix2.0rc1
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

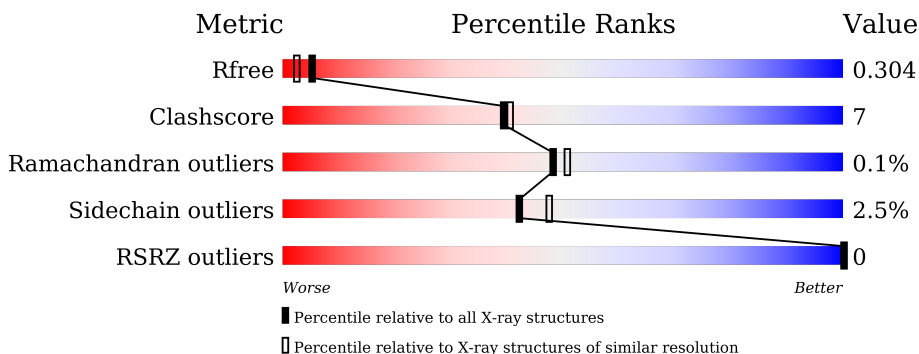
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	164625	6234 (2.10-2.10)
Clashscore	180529	6893 (2.10-2.10)
Ramachandran outliers	177936	6839 (2.10-2.10)
Sidechain outliers	177891	6840 (2.10-2.10)
RSRZ outliers	164620	6234 (2.10-2.10)

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	A	434	<div> <div style="width: 88%; background-color: green;"></div> <div style="width: 12%; background-color: yellow;"></div> </div> <div>88% 12%</div>
1	B	434	<div> <div style="width: 80%; background-color: green;"></div> <div style="width: 19%; background-color: yellow;"></div> </div> <div>80% 19%</div>

2 Entry composition [i](#)

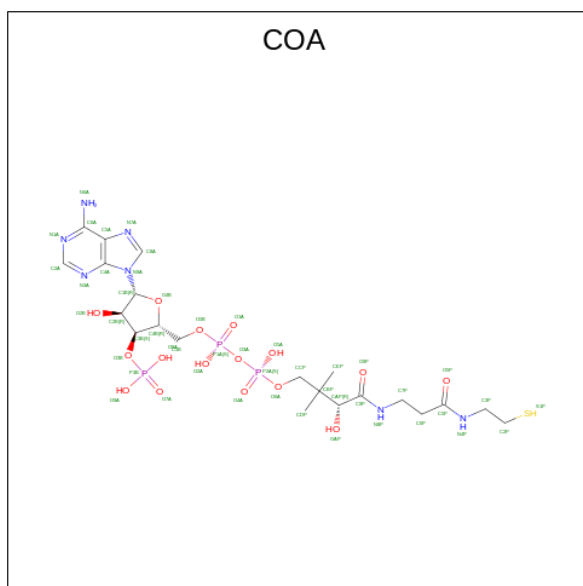
There are 6 unique types of molecules in this entry. The entry contains 7082 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Citrate synthase, mitochondrial.

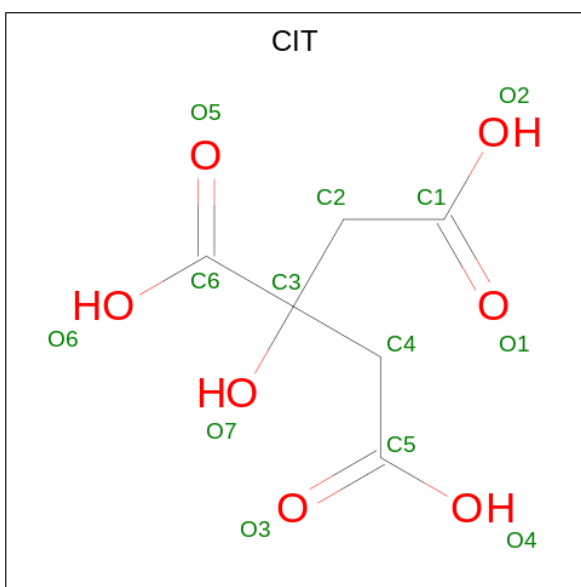
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	434	Total	C	N	O	S	0	1	0
			3417	2184	586	630	17			
1	B	434	Total	C	N	O	S	0	1	0
			3402	2175	580	630	17			

- Molecule 2 is COENZYME A (CCD ID: COA) (formula: $C_{21}H_{36}N_7O_{16}P_3S$).



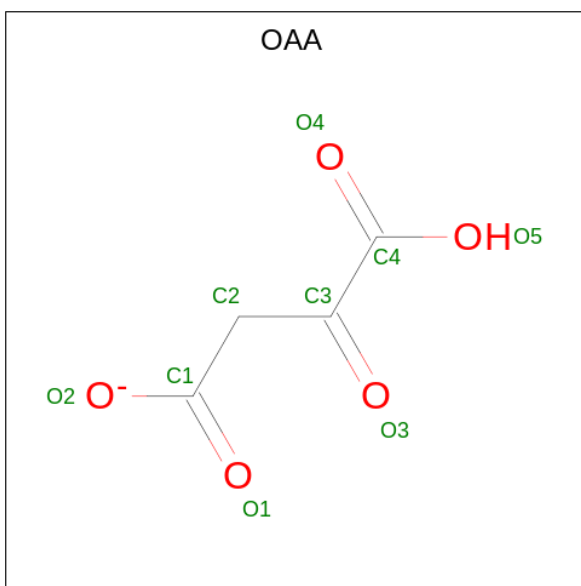
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P S	0	0
			48	21	7	16	3 1		

- Molecule 3 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



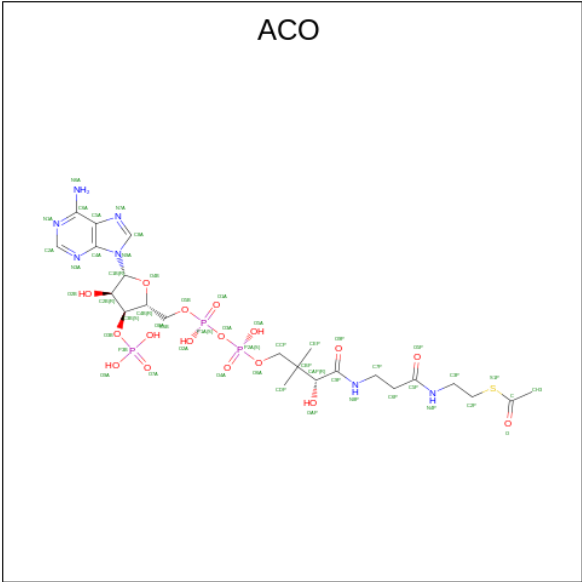
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is OXALOACETATE ION (CCD ID: OAA) (formula: $C_4H_3O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			9	4	5		

- Molecule 5 is ACETYL COENZYME *A (CCD ID: ACO) (formula: $C_{23}H_{38}N_7O_{17}P_3S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
5	B	1	Total	C	N	O	P	S	0	0
			51	23	7	17	3	1		


- Molecule 6 is water.

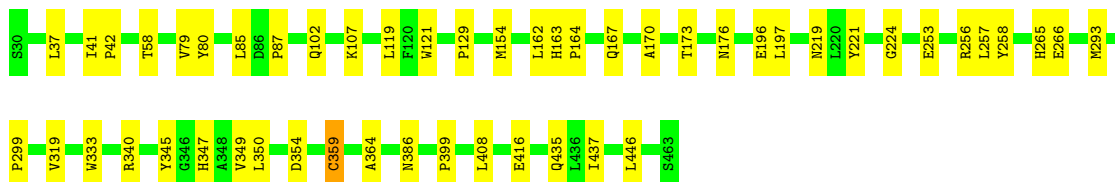
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	68	Total O 68 68	0	0
6	B	74	Total O 74 74	0	0

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.

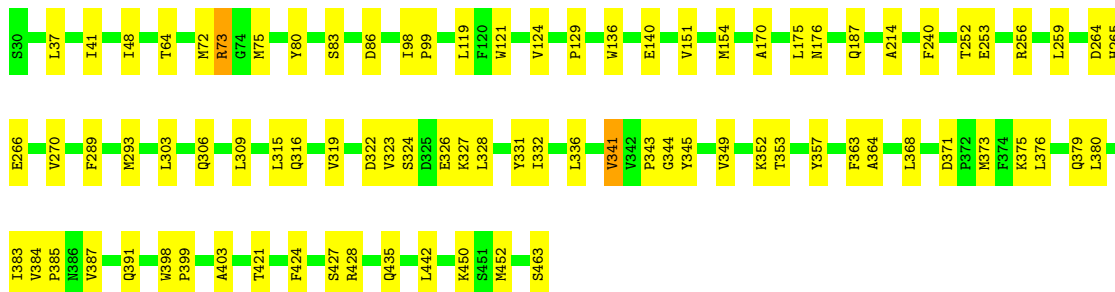
- Molecule 1: Citrate synthase, mitochondrial

Chain A:  88% 12%



- Molecule 1: Citrate synthase, mitochondrial

Chain B:  80% 19%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	57.52Å 59.79Å 72.58Å 102.52° 98.23° 118.76°	Depositor
Resolution (Å)	41.12 – 2.10 41.12 – 2.10	Depositor EDS
% Data completeness (in resolution range)	93.9 (41.12-2.10) 93.9 (41.12-2.10)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.35 (at 2.03Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, R_{free}	0.233 , 0.299 0.236 , 0.304	Depositor DCC
R_{free} test set	2024 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å ²)	33.7	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7082	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.10% 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: OAA, ACO, CIT, 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	0.48	0/3505	0.97	2/4760 (0.0%)
1	B	0.47	0/3490	0.97	1/4744 (0.0%)
All	All	0.48	0/6995	0.97	3/9504 (0.0%)

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	B	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	252	THR	CA-CB-OG1	-5.43	101.46	109.60
1	A	173	THR	CA-CB-OG1	-5.36	101.56	109.60
1	A	354	ASP	CA-CB-CG	5.28	117.88	112.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	428	ARG	Sidechain
1	B	73	ARG	Sidechain

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	3417	0	3387	35	0
1	B	3402	0	3349	59	0
2	A	48	0	32	1	0
3	A	13	0	5	3	0
4	B	9	0	2	0	0
5	B	51	0	34	4	0
6	A	68	0	0	2	0
6	B	74	0	0	18	0
All	All	7082	0	6809	91	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 7.

All (91) 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:347:HIS:HE1	3:A:502:CIT:H42	1.48	0.76
1:A:170:ALA:HB1	6:B:636:HOH:O	1.86	0.73
1:A:80:TYR:CE2	1:A:435:GLN:HG2	2.25	0.72
1:A:154:MET:HE3	1:B:154:MET:HE3	1.75	0.68
1:B:240:PHE:CE1	6:B:602:HOH:O	2.48	0.66
1:A:170:ALA:CB	6:B:636:HOH:O	2.43	0.64
2:A:501:COA:O2A	2:A:501:COA:H8A	1.97	0.64
1:B:363:PHE:CD2	6:B:617:HOH:O	2.50	0.64
1:B:170:ALA:HB1	6:B:636:HOH:O	2.00	0.60
1:A:265:HIS:O	1:A:266:GLU:HB2	2.01	0.59
1:B:259:LEU:O	1:B:427:SER:OG	2.21	0.59
1:A:170:ALA:CA	6:B:636:HOH:O	2.50	0.59
1:B:119:LEU:C	1:B:119:LEU:HD13	2.27	0.59
1:A:347:HIS:CE1	3:A:502:CIT:H42	2.35	0.58
1:A:257:LEU:HD11	1:A:359:CYS:SG	2.43	0.58
1:B:364:ALA:HA	6:B:617:HOH:O	2.04	0.57
1:A:170:ALA:HA	6:B:636:HOH:O	2.03	0.57
1:A:102:GLN:O	1:A:107:LYS:NZ	2.38	0.57
1:A:293:MET:HE2	1:A:293:MET:HA	1.88	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240:PHE:HE1	6:B:602:HOH:O	1.85	0.56
1:B:214:ALA:N	6:B:602:HOH:O	2.40	0.55
1:B:80:TYR:CE2	1:B:435:GLN:HG2	2.41	0.54
1:A:121:TRP:CG	1:A:129:PRO:HB3	2.42	0.54
1:B:306:GLN:NE2	6:B:603:HOH:O	2.41	0.54
1:B:323:VAL:HG23	1:B:327:LYS:HB2	1.90	0.54
1:A:197:LEU:HD22	6:A:655:HOH:O	2.09	0.53
1:B:170:ALA:CA	6:B:636:HOH:O	2.57	0.52
1:B:345:TYR:O	5:B:502:ACO:H71	2.10	0.52
3:A:502:CIT:O4	3:A:502:CIT:O7	2.28	0.52
1:B:170:ALA:HA	6:B:636:HOH:O	2.10	0.51
1:A:80:TYR:CD2	1:A:435:GLN:HG2	2.45	0.51
1:B:253:GLU:OE1	1:B:256:ARG:NH1	2.38	0.50
1:B:170:ALA:CB	6:B:636:HOH:O	2.59	0.50
1:B:316:GLN:NE2	1:B:373:MET:SD	2.85	0.50
1:B:214:ALA:HB2	6:B:602:HOH:O	2.12	0.50
1:A:87:PRO:HB3	1:A:349:VAL:O	2.12	0.49
1:B:332:ILE:HD11	1:B:380:LEU:HD22	1.94	0.49
1:A:119:LEU:C	1:A:119:LEU:HD13	2.38	0.49
1:A:347:HIS:HD2	1:A:349:VAL:H	1.59	0.48
1:B:341:VAL:HG21	5:B:502:ACO:H72	1.95	0.48
1:B:121:TRP:CG	1:B:129:PRO:HB3	2.48	0.48
1:A:219:ASN:HA	1:A:224:GLY:HA2	1.96	0.47
1:A:121:TRP:CD1	1:A:129:PRO:HB3	2.50	0.47
1:B:341:VAL:CG2	5:B:502:ACO:H72	2.43	0.47
1:A:37:LEU:HD21	1:A:437:ILE:HG21	1.97	0.47
1:B:72:MET:HA	1:B:75:MET:HE3	1.96	0.47
1:B:336:LEU:HD13	1:B:391:GLN:OE1	2.15	0.46
1:A:364:ALA:HB2	1:A:408:LEU:HD21	1.98	0.46
1:B:384:VAL:N	1:B:385:PRO:HD2	2.30	0.46
1:A:196:GLU:HB2	6:A:655:HOH:O	2.15	0.46
1:B:41:ILE:HD11	6:B:664:HOH:O	2.15	0.46
1:B:344:GLY:O	1:B:403:ALA:HB2	2.15	0.46
1:B:306:GLN:OE1	1:B:306:GLN:N	2.50	0.45
1:B:376:LEU:O	1:B:380:LEU:HG	2.16	0.45
1:B:37:LEU:HB3	6:B:664:HOH:O	2.15	0.45
1:B:151:VAL:HG21	1:B:175:LEU:HD23	1.98	0.45
1:B:343:PRO:HA	5:B:502:ACO:H62	1.98	0.45
1:B:371:ASP:O	1:B:375:LYS:HG3	2.17	0.45
1:B:121:TRP:CD1	1:B:129:PRO:HB3	2.52	0.45
1:B:345:TYR:HA	1:B:399:PRO:HA	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:58:THR:O	1:B:64:THR:HA	2.17	0.44
1:B:265:HIS:O	1:B:266:GLU:HB2	2.17	0.44
1:A:221:TYR:CD1	1:A:416:GLU:HG2	2.53	0.44
1:B:315:LEU:HD13	1:B:331:TYR:CG	2.53	0.44
1:B:332:ILE:HG21	1:B:387:VAL:HG21	1.99	0.44
1:A:162:LEU:HD23	1:A:167:GLN:HG2	1.98	0.43
1:B:384:VAL:N	1:B:385:PRO:CD	2.81	0.43
1:B:332:ILE:CG2	1:B:387:VAL:HG21	2.48	0.43
1:B:98:ILE:HB	1:B:99:PRO:HD3	2.00	0.43
1:B:37:LEU:HD13	1:B:124:VAL:HG12	2.01	0.42
1:A:258:TYR:C	1:A:258:TYR:CD1	2.98	0.42
1:B:136:TRP:CH2	1:B:140:GLU:HG3	2.55	0.42
1:B:289:PHE:CE1	1:B:293:MET:HE3	2.55	0.42
1:A:85:LEU:O	1:B:450:LYS:NZ	2.51	0.42
1:A:347:HIS:HB3	1:A:350:LEU:HB2	2.02	0.42
1:B:48:ILE:HD12	1:B:442:LEU:HD22	2.02	0.41
1:B:421:THR:O	1:B:424:PHE:HB3	2.20	0.41
1:B:187:GLN:NE2	6:B:613:HOH:O	2.53	0.41
1:B:352:LYS:HG2	1:B:353:THR:N	2.35	0.41
1:A:41:ILE:HB	1:A:42:PRO:HD3	2.03	0.41
1:A:446:LEU:HD11	1:B:270:VAL:HG21	2.01	0.41
1:A:79:VAL:HA	1:B:452:MET:O	2.20	0.41
1:B:83:SER:OG	1:B:264:ASP:OD2	2.24	0.41
1:B:315:LEU:O	1:B:319:VAL:HG22	2.20	0.41
1:B:306:GLN:O	1:B:309:LEU:N	2.53	0.41
1:B:357:TYR:CD2	1:B:399:PRO:HB2	2.56	0.41
1:B:398:TRP:HB3	1:B:399:PRO:HD2	2.02	0.41
1:A:253:GLU:OE1	1:A:256:ARG:NH1	2.53	0.41
1:B:328:LEU:CD2	1:B:379:GLN:HB3	2.51	0.40
1:A:163:HIS:CG	1:A:164:PRO:HD2	2.55	0.40
1:A:345:TYR:HA	1:A:399:PRO:HA	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	433/434 (100%)	414 (96%)	19 (4%)	0	100	100
1	B	433/434 (100%)	412 (95%)	20 (5%)	1 (0%)	44	45
All	All	866/868 (100%)	826 (95%)	39 (4%)	1 (0%)	48	51

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	324	SER

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	368/369 (100%)	361 (98%)	7 (2%)	52	59
1	B	364/369 (99%)	353 (97%)	11 (3%)	36	40
All	All	732/738 (99%)	714 (98%)	18 (2%)	42	47

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	176	ASN
1	A	299	PRO
1	A	319	VAL
1	A	333	TRP
1	A	340	ARG
1	A	359	CYS
1	A	386	ASN
1	B	73	ARG
1	B	86	ASP
1	B	176	ASN
1	B	303	LEU
1	B	322	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	326	GLU
1	B	341	VAL
1	B	349	VAL
1	B	368	LEU
1	B	383	ILE
1	B	463	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	GLN
1	A	127	HIS
1	A	150	HIS
1	A	180	ASN
1	A	262	HIS
1	A	314	GLN
1	A	347	HIS
1	A	410	GLN
1	B	54	GLN
1	B	55	HIS
1	B	150	HIS
1	B	242	ASN
1	B	250	GLN
1	B	314	GLN
1	B	316	GLN
1	B	347	HIS
1	B	367	HIS
1	B	386	ASN
1	B	404	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

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	CIT	A	502	-	12,12,12	1.10	1 (8%)	17,17,17	1.53	4 (23%)
4	OAA	B	501	-	8,8,8	5.93	2 (25%)	9,10,10	1.71	3 (33%)
2	COA	A	501	-	41,50,50	0.60	0	52,75,75	0.75	1 (1%)
5	ACO	B	502	-	45,53,53	0.57	0	56,79,79	0.74	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
3	CIT	A	502	-	-	12/16/16/16	-
4	OAA	B	501	-	-	0/8/8/8	-
2	COA	A	501	-	-	8/44/64/64	0/3/3/3
5	ACO	B	502	-	-	14/47/67/67	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	501	OAA	C3-C4	-16.43	1.31	1.53
4	B	501	OAA	O5-C4	-2.45	1.23	1.30
3	A	502	CIT	C3-C6	2.13	1.55	1.53

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502	CIT	O5-C6-C3	-3.62	117.13	122.25
5	B	502	ACO	C2P-S1P-C	3.06	117.75	101.68
4	B	501	OAA	C2-C3-C4	2.95	122.84	117.85
3	A	502	CIT	O6-C6-C3	2.70	117.74	113.05
4	B	501	OAA	O4-C4-C3	-2.55	118.32	121.72
2	A	501	COA	C5A-C6A-N6A	2.36	123.94	120.35
5	B	502	ACO	C5A-C6A-N6A	2.23	123.74	120.35
3	A	502	CIT	O3-C5-C4	-2.17	116.59	122.94
4	B	501	OAA	O5-C4-C3	2.13	119.78	113.97
3	A	502	CIT	O1-C1-C2	-2.00	117.09	122.94

There are no chirality outliers.

All (34) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	COA	C5B-O5B-P1A-O2A
2	A	501	COA	C5B-O5B-P1A-O3A
2	A	501	COA	CCP-O6A-P2A-O4A
2	A	501	COA	CCP-O6A-P2A-O5A
3	A	502	CIT	C2-C3-C4-C5
3	A	502	CIT	O7-C3-C4-C5
3	A	502	CIT	C6-C3-C4-C5
3	A	502	CIT	O7-C3-C6-O5
3	A	502	CIT	O7-C3-C6-O6
3	A	502	CIT	C4-C3-C6-O5
3	A	502	CIT	C4-C3-C6-O6
5	B	502	ACO	C5B-O5B-P1A-O1A
5	B	502	ACO	CCP-O6A-P2A-O3A
5	B	502	ACO	CCP-O6A-P2A-O4A
5	B	502	ACO	C5P-C6P-C7P-N8P
5	B	502	ACO	O-C-S1P-C2P
5	B	502	ACO	CH3-C-S1P-C2P
5	B	502	ACO	O4B-C4B-C5B-O5B
5	B	502	ACO	C3B-C4B-C5B-O5B
2	A	501	COA	P1A-O3A-P2A-O6A
5	B	502	ACO	P2A-O3A-P1A-O5B
5	B	502	ACO	P1A-O3A-P2A-O6A
5	B	502	ACO	C5B-O5B-P1A-O3A
2	A	501	COA	P1A-O3A-P2A-O4A
5	B	502	ACO	C5B-O5B-P1A-O2A
5	B	502	ACO	O9P-C9P-CAP-OAP
3	A	502	CIT	C1-C2-C3-O7
3	A	502	CIT	C3-C4-C5-O4

Continued on next page...

Continued from previous page...

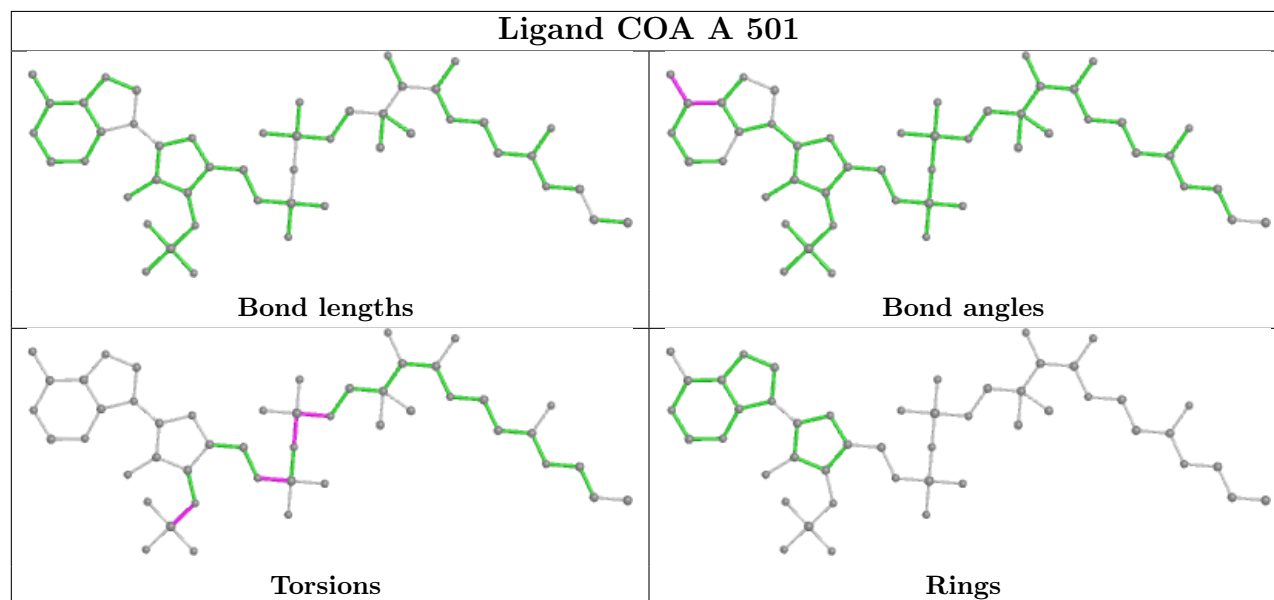
Mol	Chain	Res	Type	Atoms
3	A	502	CIT	O1-C1-C2-C3
3	A	502	CIT	O2-C1-C2-C3
5	B	502	ACO	C3P-C2P-S1P-C
3	A	502	CIT	C3-C4-C5-O3
2	A	501	COA	C3B-O3B-P3B-O8A
2	A	501	COA	CCP-O6A-P2A-O3A

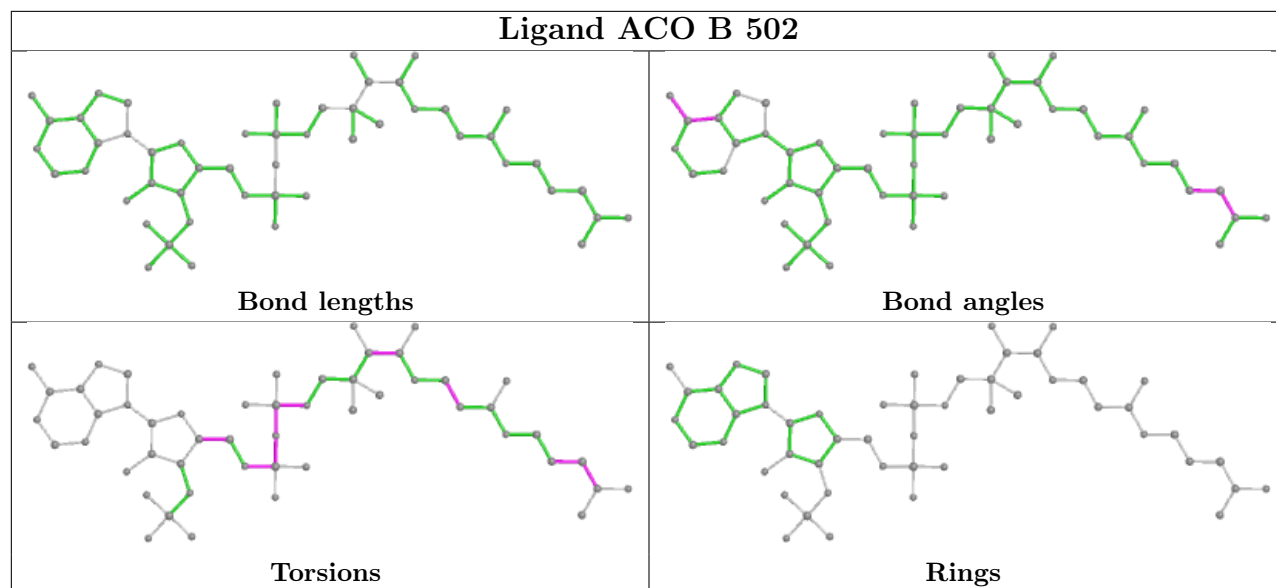
There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	502	CIT	3	0
2	A	501	COA	1	0
5	B	502	ACO	4	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, 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	434/434 (100%)	-1.76	0 100 100	22, 44, 78, 102	1 (0%)
1	B	434/434 (100%)	-1.71	0 100 100	24, 47, 101, 121	1 (0%)
All	All	868/868 (100%)	-1.73	0 100 100	22, 46, 90, 121	2 (0%)

There are no RSRZ outliers to report.

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, 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.

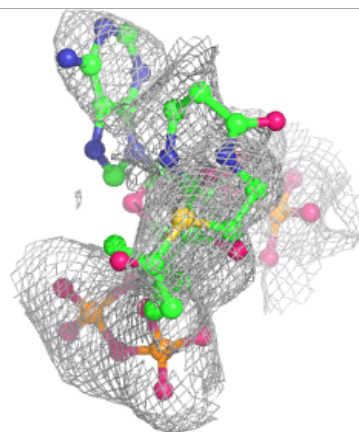
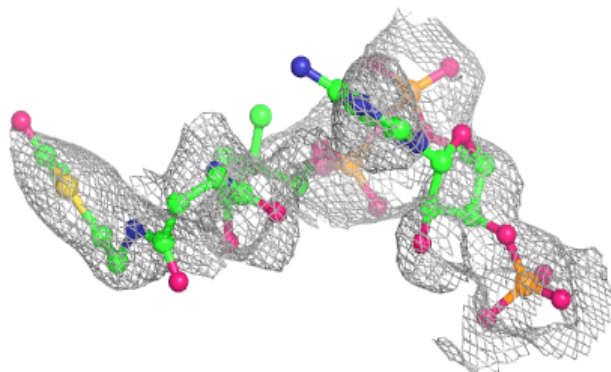
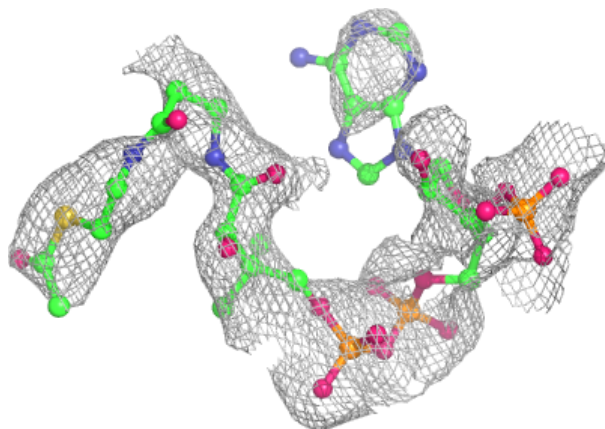
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	CIT	A	502	13/13	0.99	0.02	36,42,54,56	0
5	ACO	B	502	51/51	0.99	0.03	70,94,134,137	0
4	OAA	B	501	9/9	1.00	0.03	54,61,68,72	0
2	COA	A	501	48/48	1.00	0.02	42,68,76,79	0

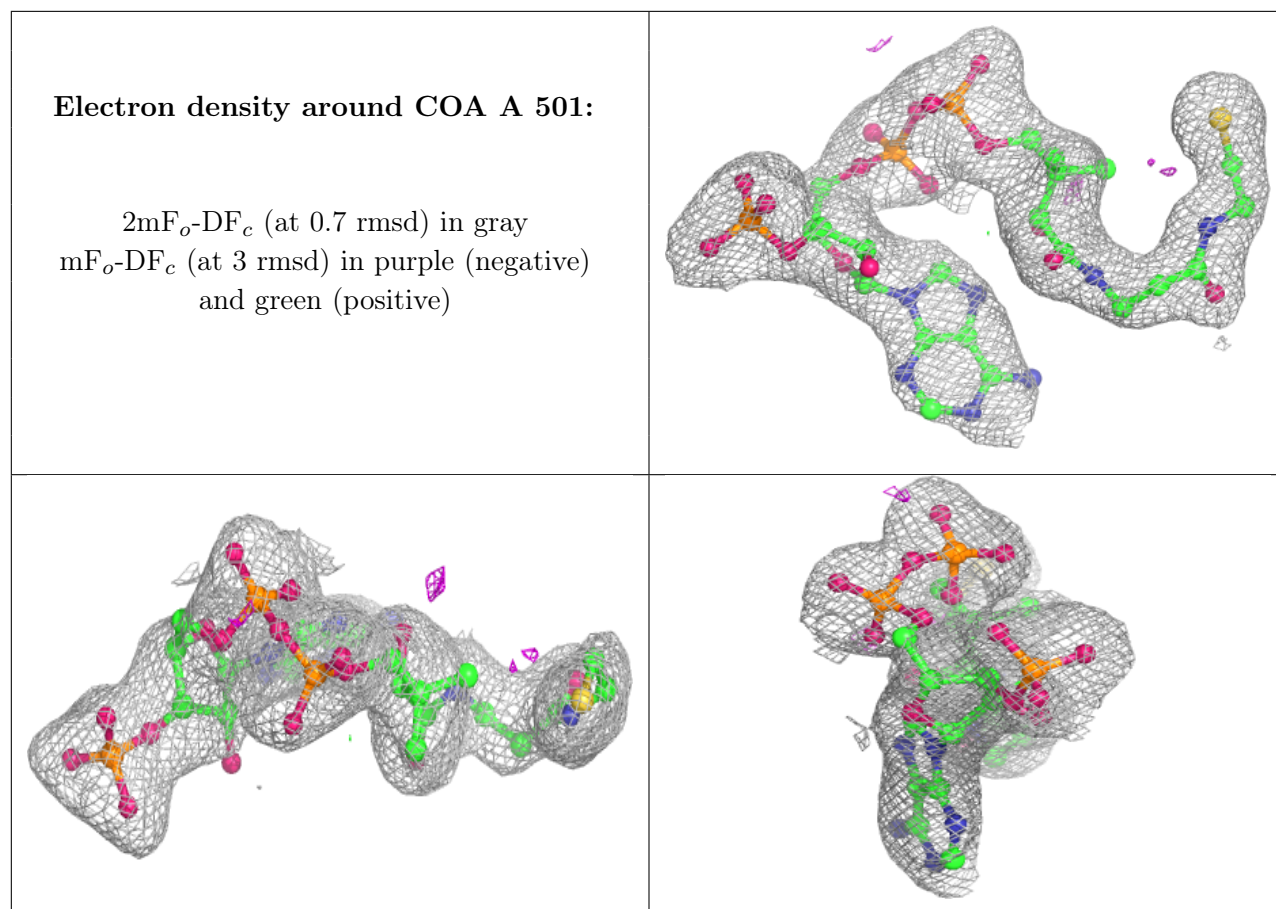
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around ACO B 502:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers ⓘ

There are no such residues in this entry.