



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 05:24 AM UTC

PDB ID : 1M3Z / pdb_00001m3z
Title : Biosynthetic thiolase, C89A mutant, complexed with acetyl coenzyme A
Authors : Kursula, P.; Ojala, J.; Lambeir, A.-M.; Wierenga, R.K.
Deposited on : 2002-07-03
Resolution : 1.87 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

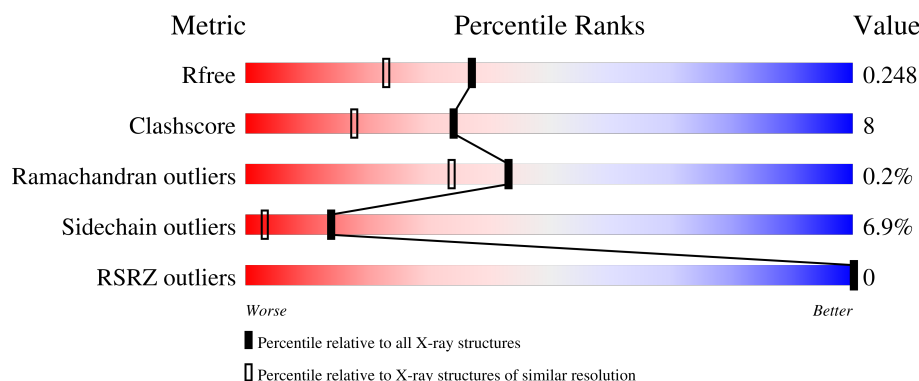
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.87 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	1220 (1.88-1.88)
Clashscore	190562	1234 (1.88-1.88)
Ramachandran outliers	187476	1222 (1.88-1.88)
Sidechain outliers	187428	1222 (1.88-1.88)
RSRZ outliers	180081	1220 (1.88-1.88)

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	392	 85% 13% ..
1	B	392	 82% 15% ..
1	C	392	 85% 12% ..
1	D	392	 79% 19% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12568 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.

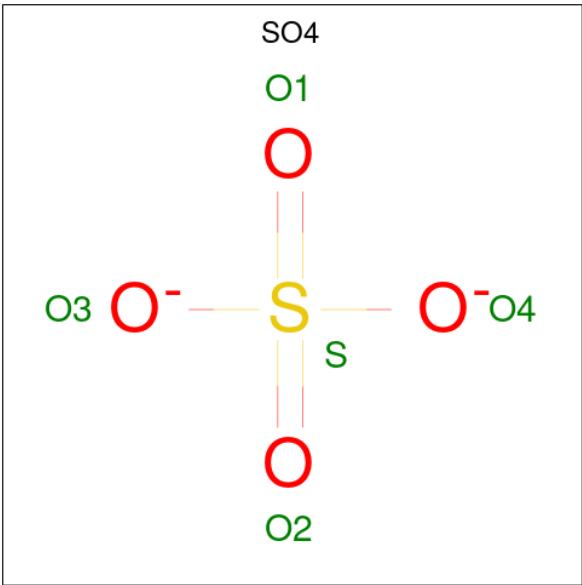
- Molecule 1 is a protein called Acetyl-CoA acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	2	0
			2823	1753	510	540	20			
1	B	390	Total	C	N	O	S	0	2	0
			2823	1753	510	540	20			
1	C	390	Total	C	N	O	S	0	2	0
			2823	1753	510	540	20			
1	D	390	Total	C	N	O	S	0	2	0
			2823	1753	510	540	20			

There are 12 discrepancies between the modelled and reference sequences:

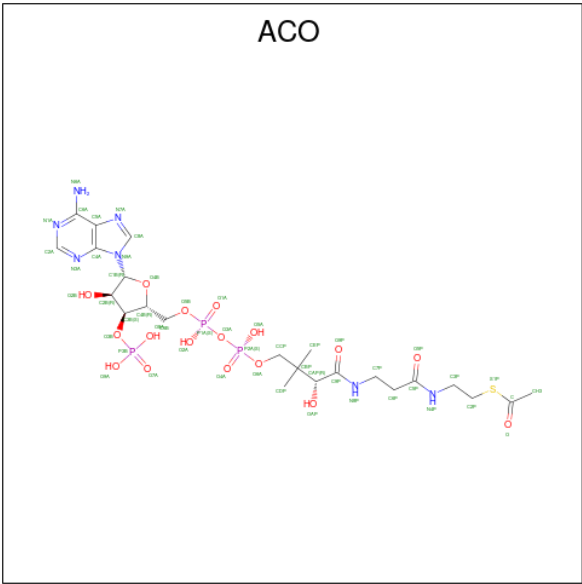
Chain	Residue	Modelled	Actual	Comment	Reference
A	10	ALA	-	insertion	UNP P07097
A	89	ALA	CYS	engineered mutation	UNP P07097
A	129	ARG	ALA	conflict	UNP P07097
B	10	ALA	-	insertion	UNP P07097
B	89	ALA	CYS	engineered mutation	UNP P07097
B	129	ARG	ALA	conflict	UNP P07097
C	10	ALA	-	insertion	UNP P07097
C	89	ALA	CYS	engineered mutation	UNP P07097
C	129	ARG	ALA	conflict	UNP P07097
D	10	ALA	-	insertion	UNP P07097
D	89	ALA	CYS	engineered mutation	UNP P07097
D	129	ARG	ALA	conflict	UNP P07097

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is ACETYL COENZYME *A (CCD ID: ACO) (formula: C₂₃H₃₈N₇O₁₇P₃S).



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

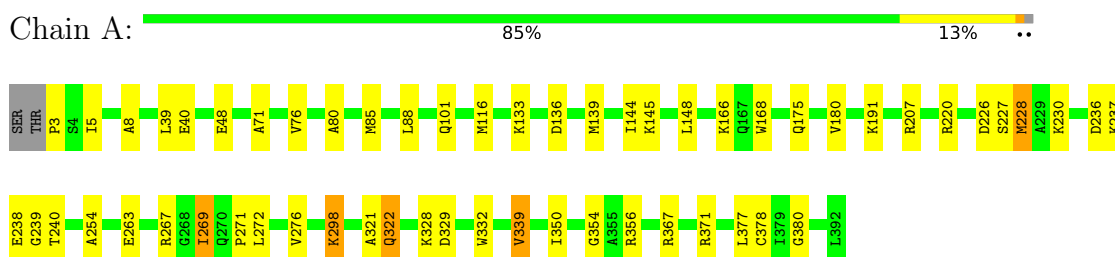
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	343	Total	O	0	0
			343	343		
4	B	346	Total	O	0	0
			346	346		
4	C	178	Total	O	0	0
			178	178		
4	D	185	Total	O	0	0
			185	185		

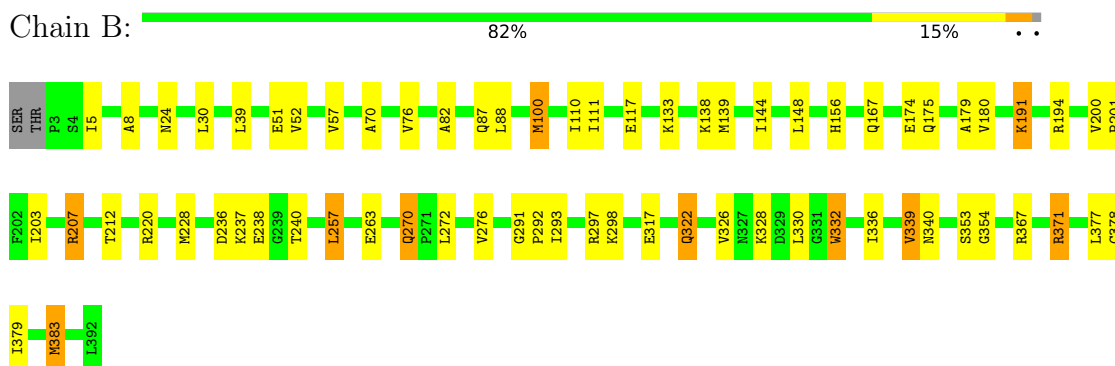
3 Residue-property plots [i](#)

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.

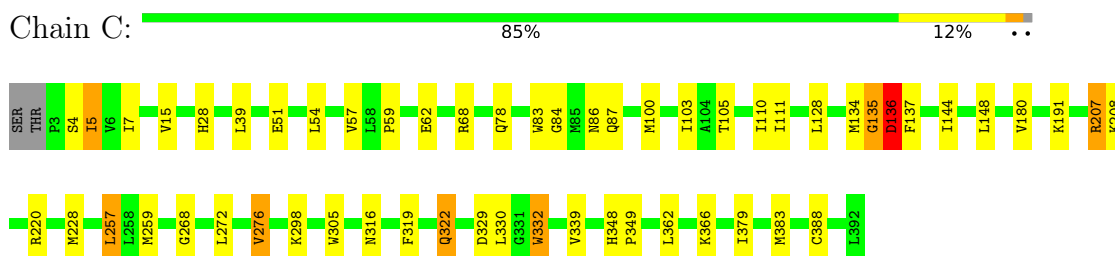
• Molecule 1: Acetyl-CoA acetyltransferase



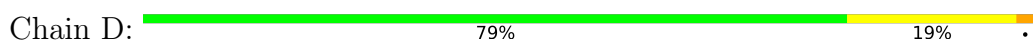
• Molecule 1: Acetyl-CoA acetyltransferase

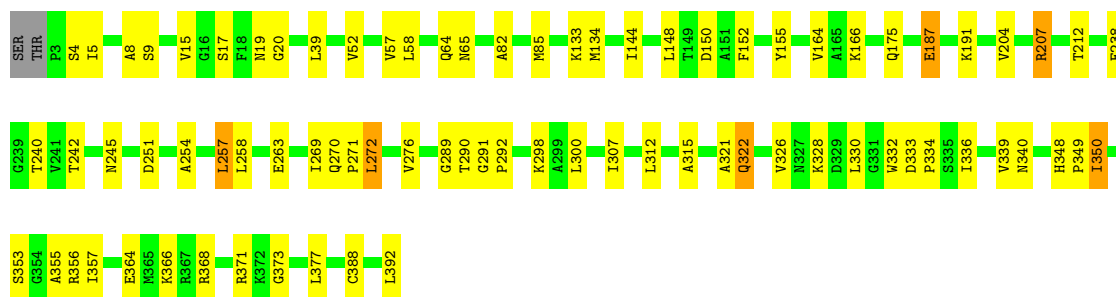


• Molecule 1: Acetyl-CoA acetyltransferase



• Molecule 1: Acetyl-CoA acetyltransferase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	84.60Å 79.68Å 149.32Å 90.00° 92.83° 90.00°	Depositor
Resolution (Å)	20.00 – 1.87 20.00 – 1.87	Depositor EDS
% Data completeness (in resolution range)	90.9 (20.00-1.87) 78.5 (20.00-1.87)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 1.87Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.192 , 0.242 0.203 , 0.248	Depositor DCC
R_{free} test set	6848 reflections (4.60%)	wwPDB-VP
Wilson B-factor (Å ²)	23.1	Xtriage
Anisotropy	0.272	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 46.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	0.149 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12568	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.24% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACO, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.16	5/2873 (0.2%)	1.11	4/3879 (0.1%)
1	B	1.17	7/2873 (0.2%)	1.10	3/3879 (0.1%)
1	C	0.90	6/2873 (0.2%)	0.99	0/3879
1	D	0.79	0/2873	0.96	0/3879
All	All	1.02	18/11492 (0.2%)	1.04	7/15516 (0.0%)

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	383	MET	SD-CE	-7.12	1.61	1.79
1	C	134	MET	C-O	6.88	1.32	1.23
1	C	136	ASP	C-O	6.53	1.32	1.24
1	A	116	MET	SD-CE	-6.34	1.63	1.79
1	B	117	GLU	CA-C	-6.17	1.45	1.52

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	353	SER	N-CA-C	7.26	119.19	111.28
1	A	76	VAL	N-CA-C	-6.89	102.20	108.95
1	A	339	VAL	N-CA-CB	-5.64	101.00	110.65
1	A	356	ARG	N-CA-C	-5.54	105.15	111.14
1	A	101	GLN	N-CA-C	5.52	117.30	111.28

There are no chirality outliers.

There are no planarity outliers.

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	2823	0	2829	28	0
1	B	2823	0	2829	46	0
1	C	2823	0	2829	36	0
1	D	2823	0	2829	63	0
2	A	10	0	0	1	0
2	B	10	0	0	0	0
3	A	51	0	34	6	0
3	B	51	0	34	3	0
3	C	51	0	34	1	0
3	D	51	0	34	2	0
4	A	343	0	0	13	0
4	B	346	0	0	22	0
4	C	178	0	0	14	0
4	D	185	0	0	37	0
All	All	12568	0	11452	175	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 8.

The worst 5 of 175 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:B:332:TRP:HB2	4:B:445:HOH:O	1.59	1.02
1:D:326:VAL:HG22	4:D:4413:HOH:O	1.64	0.97
1:D:82:ALA:HB2	4:D:4563:HOH:O	1.73	0.89
1:B:340:ASN:ND2	4:B:455:HOH:O	2.05	0.89
1:D:290:THR:HA	4:D:4413:HOH:O	1.76	0.85

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	390/392 (100%)	379 (97%)	10 (3%)	1 (0%)	36	26
1	B	390/392 (100%)	379 (97%)	11 (3%)	0	100	100
1	C	390/392 (100%)	376 (96%)	13 (3%)	1 (0%)	36	26
1	D	390/392 (100%)	374 (96%)	15 (4%)	1 (0%)	36	26
All	All	1560/1568 (100%)	1508 (97%)	49 (3%)	3 (0%)	43	34

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	350	ILE
1	C	136	ASP
1	A	350	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	A	278/278 (100%)	258 (93%)	20 (7%)	13	3
1	B	278/278 (100%)	257 (92%)	21 (8%)	12	2
1	C	278/278 (100%)	264 (95%)	14 (5%)	22	7
1	D	278/278 (100%)	257 (92%)	21 (8%)	12	2
All	All	1112/1112 (100%)	1036 (93%)	76 (7%)	14	3

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	133	LYS
1	D	328	LYS
1	D	187	GLU
1	D	263	GLU
1	D	371	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	327	ASN
1	D	175	GLN
1	D	184	ASN
1	D	127	HIS
1	B	316	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](#)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	A	9722	-	4,4,4	0.24	0	6,6,6	0.27	0
2	SO4	B	9719	-	4,4,4	0.27	0	6,6,6	0.36	0
3	ACO	D	4393	-	51,53,53	1.74	10 (19%)	73,79,79	1.47	6 (8%)
3	ACO	C	3393	-	51,53,53	1.55	10 (19%)	73,79,79	1.57	8 (10%)
2	SO4	A	9720	-	4,4,4	0.16	0	6,6,6	0.34	0
3	ACO	A	1393	-	51,53,53	1.58	10 (19%)	73,79,79	1.48	7 (9%)
2	SO4	B	9721	-	4,4,4	0.22	0	6,6,6	0.38	0
3	ACO	B	2393	-	51,53,53	1.63	11 (21%)	73,79,79	1.48	12 (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
3	ACO	A	1393	-	-	6/51/67/67	0/3/3/3
3	ACO	D	4393	-	-	9/51/67/67	0/3/3/3
3	ACO	B	2393	-	-	9/51/67/67	0/3/3/3
3	ACO	C	3393	-	-	9/51/67/67	0/3/3/3

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2393	ACO	P3B-O9A	4.51	1.71	1.54
3	A	1393	ACO	P3B-O8A	4.42	1.71	1.54
3	D	4393	ACO	P3B-O8A	4.41	1.71	1.54
3	D	4393	ACO	P3B-O9A	4.39	1.71	1.54
3	C	3393	ACO	P3B-O8A	4.34	1.70	1.54

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	3393	ACO	C5A-C4A-N3A	-6.82	117.33	126.72
3	C	3393	ACO	N3A-C4A-N9A	5.88	137.16	127.17
3	B	2393	ACO	C5A-C4A-N3A	-5.66	118.92	126.72
3	D	4393	ACO	C5A-C4A-N3A	-5.61	119.00	126.72
3	A	1393	ACO	C5A-C4A-N3A	-5.59	119.02	126.72

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

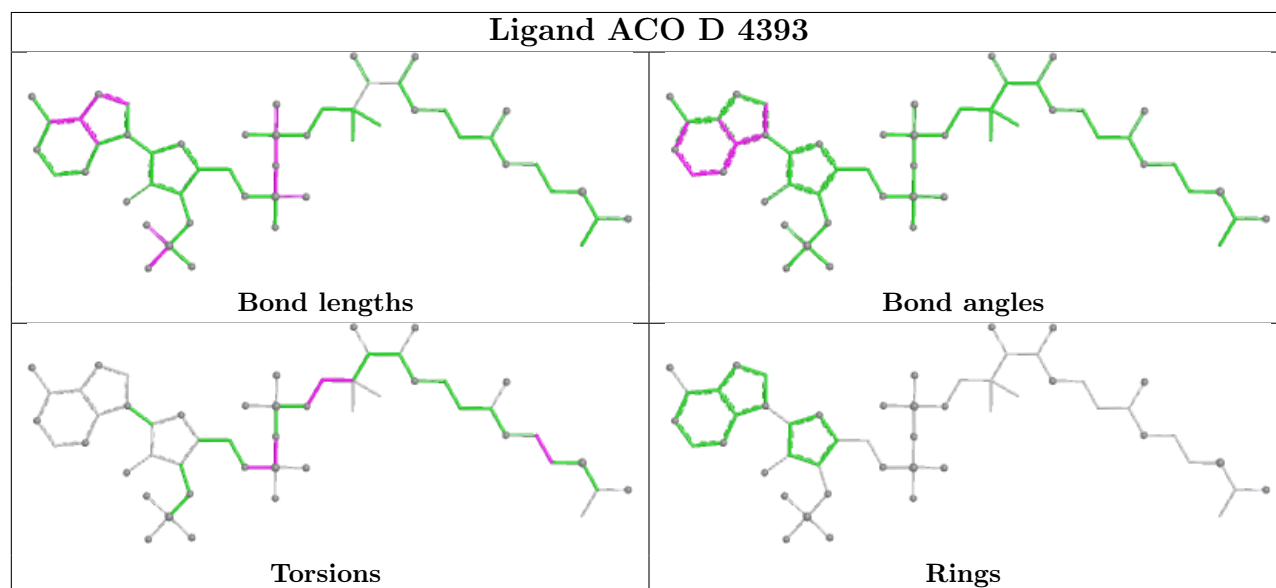
Mol	Chain	Res	Type	Atoms
3	A	1393	ACO	CCP-O6A-P2A-O3A
3	A	1393	ACO	CCP-O6A-P2A-O4A
3	A	1393	ACO	S1P-C2P-C3P-N4P
3	C	3393	ACO	CCP-O6A-P2A-O4A
3	C	3393	ACO	N8P-C9P-CAP-OAP

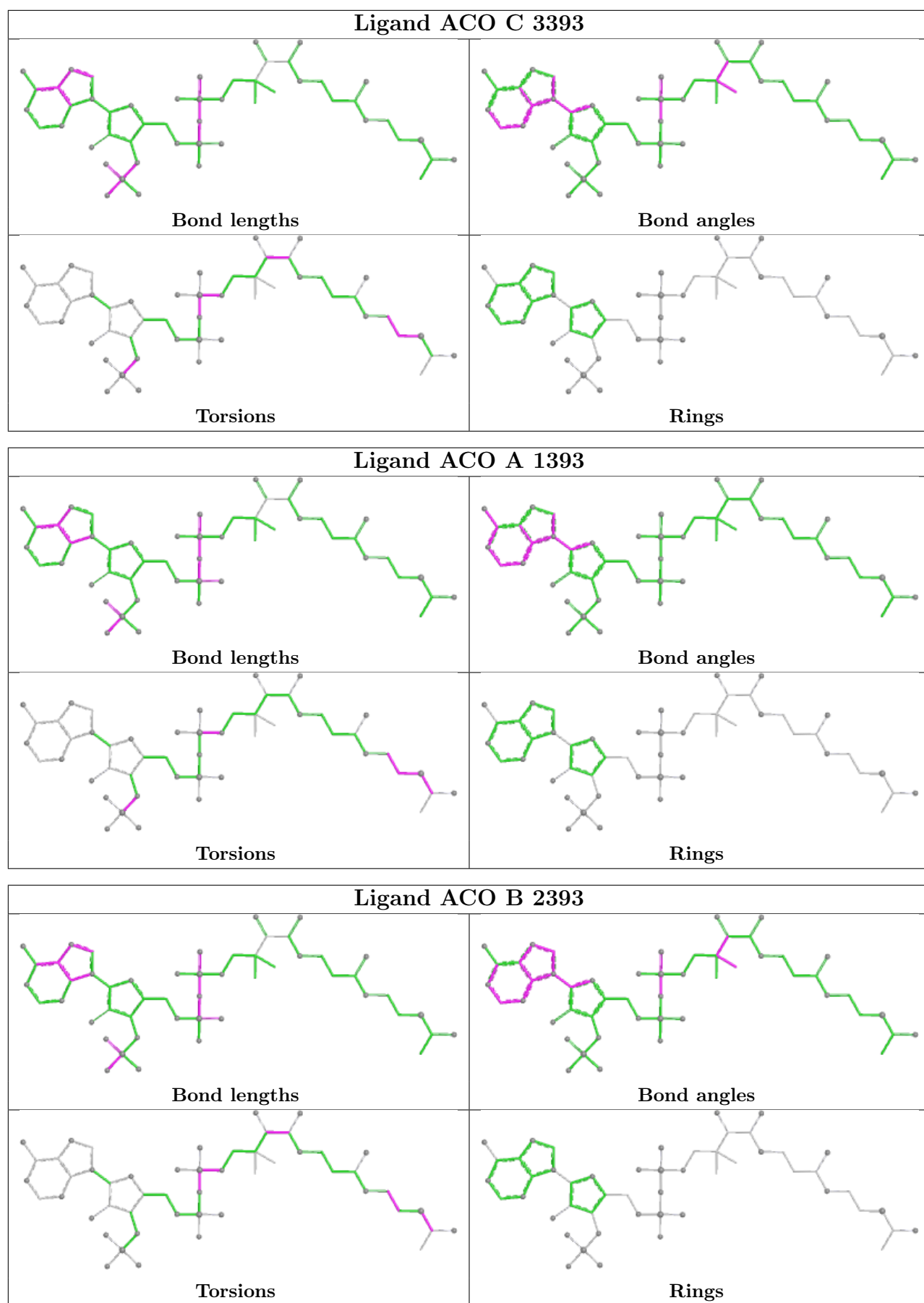
There are no ring outliers.

5 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	9722	SO4	1	0
3	D	4393	ACO	2	0
3	C	3393	ACO	1	0
3	A	1393	ACO	6	0
3	B	2393	ACO	3	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	390/392 (99%)	-1.23	0 100 100	10, 18, 32, 54	2 (0%)
1	B	390/392 (99%)	-1.20	0 100 100	9, 18, 32, 58	2 (0%)
1	C	390/392 (99%)	-1.05	0 100 100	9, 21, 33, 53	2 (0%)
1	D	390/392 (99%)	-0.99	0 100 100	7, 21, 36, 52	2 (0%)
All	All	1560/1568 (99%)	-1.12	0 100 100	7, 20, 34, 58	8 (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 oligosaccharides 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	ACO	A	1393	51/51	0.96	0.07	42,66,69,69	0
3	ACO	D	4393	51/51	0.96	0.08	73,94,96,97	0
3	ACO	B	2393	51/51	0.97	0.07	54,65,71,72	0
3	ACO	C	3393	51/51	0.97	0.07	76,84,90,92	0

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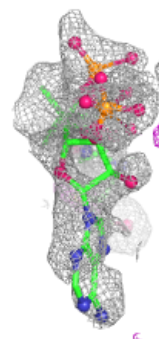
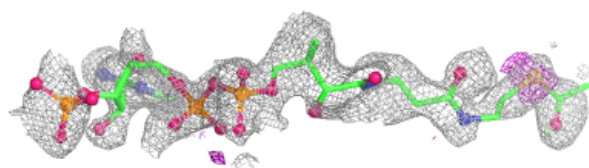
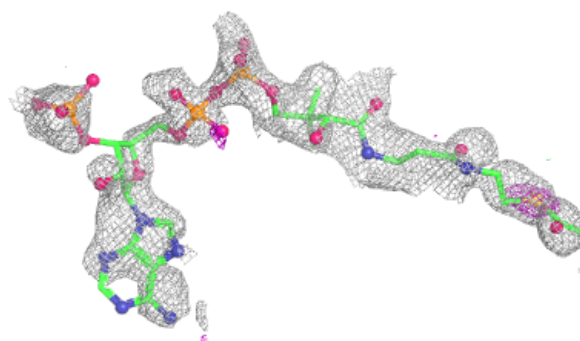
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SO4	A	9722	5/5	0.97	0.05	73,73,75,76	0
2	SO4	B	9719	5/5	0.98	0.04	62,62,63,63	0
2	SO4	A	9720	5/5	0.99	0.03	52,52,53,54	0
2	SO4	B	9721	5/5	0.99	0.04	50,50,53,57	0

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.

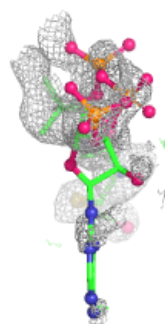
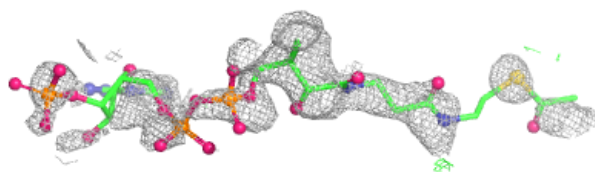
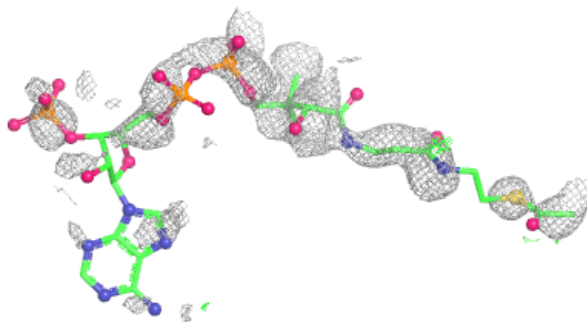
Electron density around ACO A 1393:

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

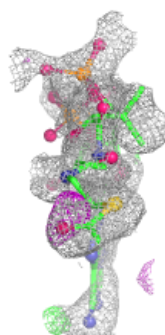
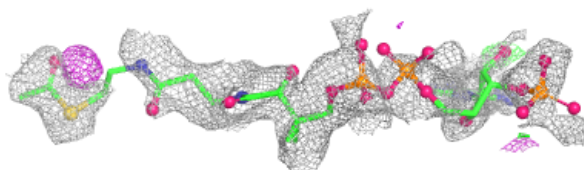
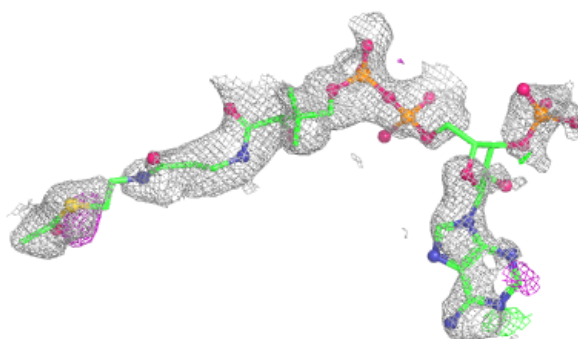


Electron density around ACO D 4393:

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

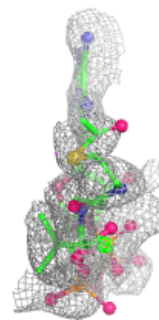
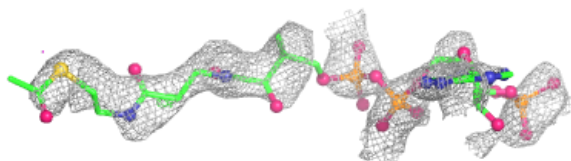
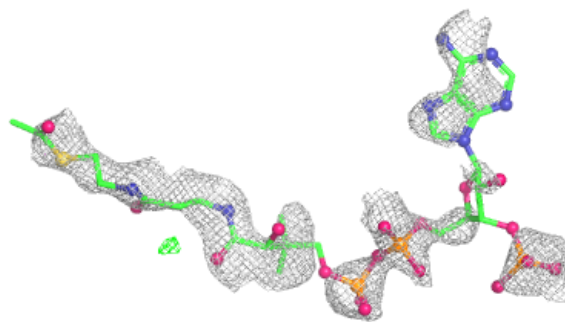
**Electron density around ACO B 2393:**

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



Electron density around ACO C 3393:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.