



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 05:40 PM UTC

PDB ID : 2VJO / pdb_00002vjo
Title : Formyl-CoA transferase mutant variant Q17A with aspartyl-CoA thioester intermediates and oxalate
Authors : Berthold, C.L.; Toyota, C.G.; Richards, N.G.J.; Lindqvist, Y.
Deposited on : 2007-12-11
Resolution : 2.20 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 Phenix2.0
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

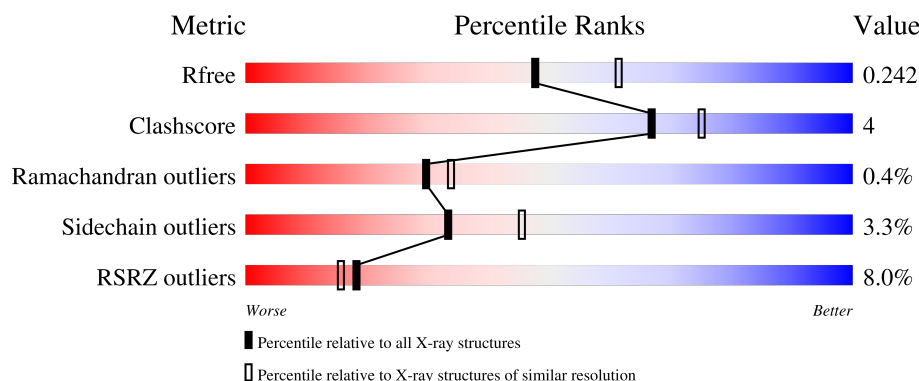
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	428	3% 89% 9%
1	B	428	13% 88% 11%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7210 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.

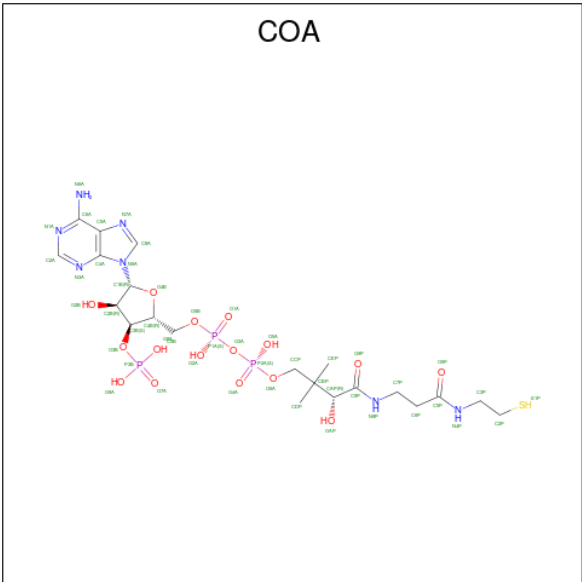
- Molecule 1 is a protein called FORMYL-COENZYME A TRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	427	Total	C	N	O	S	0	6	0
			3338	2113	572	630	23			
1	B	427	Total	C	N	O	S	0	1	0
			3313	2097	568	625	23			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	ALA	GLN	engineered mutation	UNP O06644
B	17	ALA	GLN	engineered mutation	UNP O06644
A	186	ILE	MET	conflict	UNP O06644
B	186	ILE	MET	conflict	UNP O06644

- Molecule 2 is COENZYME A (CCD ID: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S).

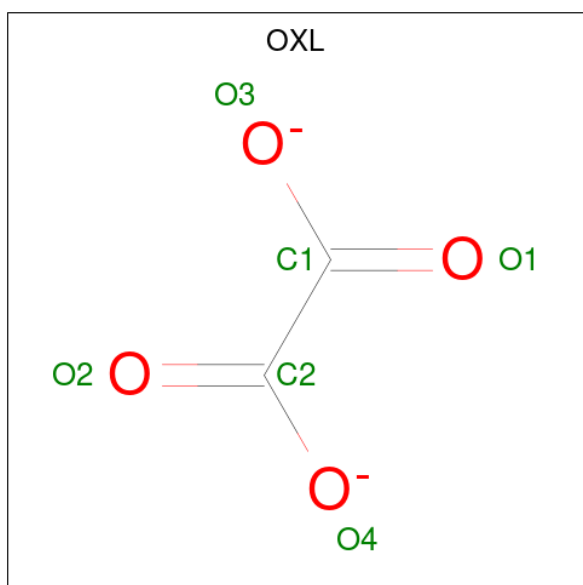


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	
			48	21	7	16	3	1	0
2	B	1	Total	C	N	O	P	S	
			48	21	7	16	3	1	0

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

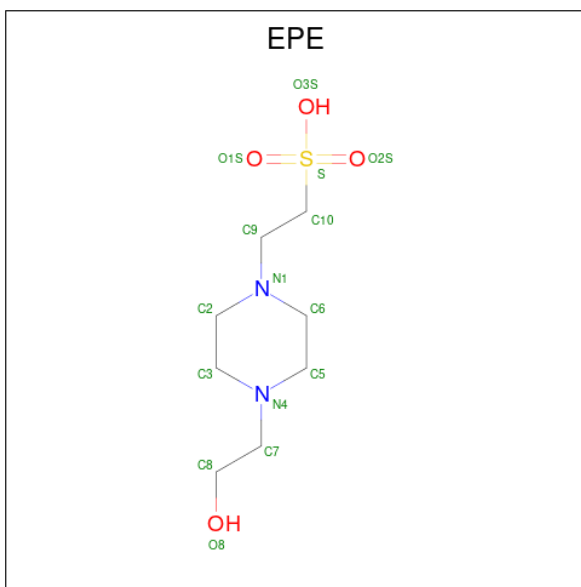
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		
3	B	1	Total	Cl	0	0
			1	1		

- Molecule 4 is OXALATE ION (CCD ID: OXL) (formula: C₂O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O		
			6	2	4	0	0

- Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

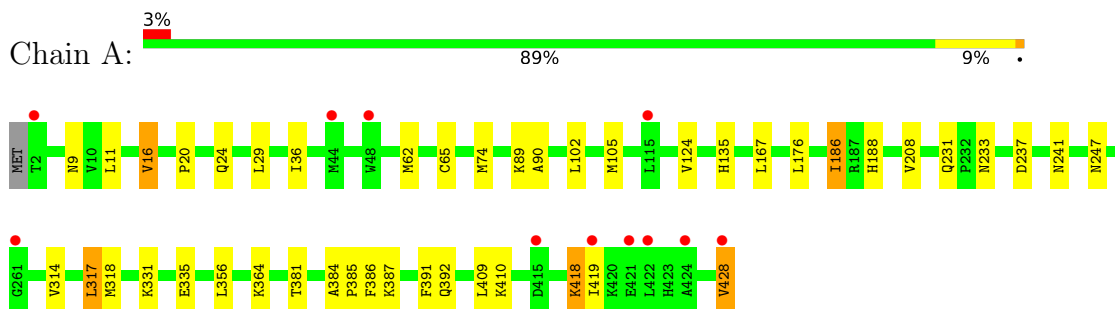
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	249	Total	O	0	0
			249	249		
6	B	191	Total	O	0	0
			191	191		

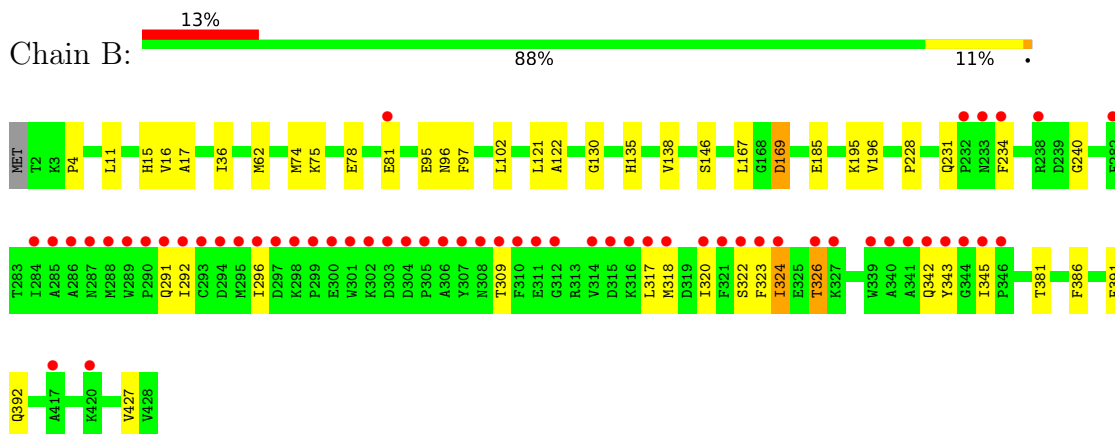
3 Residue-property plots

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: FORMYL-COENZYME A TRANSFERASE



• Molecule 1: FORMYL-COENZYME A TRANSFERASE



4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	153.59Å 153.59Å 98.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.20 30.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.4 (30.00-2.20) 99.3 (30.00-2.20)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.206 , 0.248 0.202 , 0.242	Depositor DCC
R_{free} test set	2895 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	30.5	Xtriage
Anisotropy	0.070	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 34.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.037 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7210	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% 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: CL, EPE, OXL, 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	0.57	0/3431	0.86	0/4640
1	B	0.56	0/3390	0.88	2/4584 (0.0%)
All	All	0.56	0/6821	0.87	2/9224 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	169	ASP	CA-CB-CG	-5.29	107.31	112.60
1	B	17	ALA	N-CA-C	5.05	119.18	112.72

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	3338	0	3283	23	0
1	B	3313	0	3255	32	0
2	A	48	0	31	0	0
2	B	48	0	31	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	15	0	17	0	0
6	A	249	0	0	2	0
6	B	191	0	0	3	0
All	All	7210	0	6617	50	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 4.

All (50) 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:418:LYS:H	1:A:418:LYS:HD2	1.55	0.72
1:A:186:ILE:HG23	1:B:4:PRO:HA	1.77	0.66
1:B:11:LEU:HD11	1:B:36:ILE:HD11	1.79	0.65
1:A:167:LEU:HD21	1:B:167:LEU:HD21	1.78	0.64
1:A:9[B]:ASN:HD22	1:A:90:ALA:HA	1.63	0.64
1:A:135[B]:HIS:CD2	1:A:135[B]:HIS:H	2.15	0.64
1:B:11:LEU:CD1	1:B:36:ILE:HD11	2.27	0.64
1:A:74:MET:HE2	1:A:105:MET:SD	2.38	0.63
1:A:364:LYS:HE3	1:B:130:GLY:O	2.02	0.59
1:B:291:GLN:HB3	1:B:343:TYR:HB3	1.88	0.55
1:A:124:VAL:HG23	1:A:176:LEU:HD22	1.90	0.54
1:A:24:GLN:HE21	1:A:65:CYS:H	1.55	0.52
1:A:11:LEU:HD11	1:A:36:ILE:HD11	1.92	0.52
1:B:74:MET:HE1	1:B:97:PHE:CZ	2.45	0.51
1:B:228:PRO:HA	1:B:231:GLN:HG2	1.91	0.51
1:A:331:LYS:HB3	1:A:335:GLU:HG3	1.93	0.50
1:B:74:MET:HE1	1:B:97:PHE:HZ	1.76	0.50
1:B:228:PRO:HB3	1:B:234:PHE:HE2	1.77	0.50
1:A:29:LEU:HD22	1:A:391:PHE:HZ	1.76	0.49
1:A:237:ASP:OD2	1:A:241:ASN:HB2	2.13	0.49
1:B:323:PHE:O	1:B:326:THR:OG1	2.28	0.49
1:B:62:MET:HE3	1:B:381:THR:HA	1.94	0.49
1:B:78:GLU:HB2	1:B:427:VAL:HG21	1.93	0.48
1:B:96:ASN:ND2	6:B:2049:HOH:O	2.46	0.47
1:B:292:ILE:O	1:B:296:ILE:HG12	2.15	0.47
1:B:95:GLU:HG2	1:B:102:LEU:HD22	1.98	0.46
1:A:409:LEU:HD11	1:A:428:VAL:HG21	1.99	0.45
1:B:234:PHE:CG	1:B:318:MET:HG3	2.52	0.45
1:A:384:ALA:O	1:A:387:LYS:NZ	2.49	0.45
1:B:121:LEU:HD23	1:B:195:LYS:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:75:LYS:HG2	2:B:1169:COA:H2A	1.99	0.44
1:B:324:ILE:O	1:B:324:ILE:HG13	2.17	0.44
1:A:318:MET:HE3	6:A:2178:HOH:O	2.16	0.44
1:B:343:TYR:HB2	1:B:345:ILE:HG13	2.00	0.43
1:A:384:ALA:HA	1:A:385:PRO:HD3	1.83	0.43
1:B:195:LYS:HE2	6:B:2058:HOH:O	2.18	0.43
1:B:122:ALA:HA	1:B:196:VAL:O	2.19	0.43
1:B:4:PRO:HD3	1:B:391:PHE:CE2	2.54	0.42
1:B:320:ILE:O	1:B:324:ILE:HG23	2.20	0.42
1:A:188:HIS:HE1	1:B:185:GLU:OE1	2.03	0.42
1:B:342:GLN:H	1:B:342:GLN:HG2	1.72	0.42
1:A:356:LEU:HD21	1:B:146:SER:O	2.19	0.42
1:B:234:PHE:CZ	1:B:318:MET:HE2	2.54	0.41
1:B:234:PHE:CD2	1:B:318:MET:HG3	2.56	0.41
1:B:322:SER:HB2	6:B:2138:HOH:O	2.20	0.41
1:A:233[B]:ASN:ND2	6:A:2109:HOH:O	2.53	0.41
1:A:62:MET:HE3	1:A:381:THR:HA	2.02	0.41
1:A:16:VAL:O	1:A:20:PRO:HG2	2.21	0.40
1:A:231:GLN:OE1	1:A:317:LEU:HB2	2.20	0.40
1:B:135:HIS:CD2	1:B:135:HIS:H	2.38	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	431/428 (101%)	420 (97%)	10 (2%)	1 (0%)	43	51
1	B	426/428 (100%)	412 (97%)	12 (3%)	2 (0%)	24	27
All	All	857/856 (100%)	832 (97%)	22 (3%)	3 (0%)	30	34

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	16	VAL
1	B	16	VAL
1	B	240	GLY

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	355/350 (101%)	342 (96%)	13 (4%)	30	41
1	B	350/350 (100%)	340 (97%)	10 (3%)	37	51
All	All	705/700 (101%)	682 (97%)	23 (3%)	33	45

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	89	LYS
1	A	102	LEU
1	A	186	ILE
1	A	208	VAL
1	A	247	ASN
1	A	314	VAL
1	A	317	LEU
1	A	386	PHE
1	A	392	GLN
1	A	410	LYS
1	A	418	LYS
1	A	419	ILE
1	A	428	VAL
1	B	15	HIS
1	B	81	GLU
1	B	138	VAL
1	B	169	ASP
1	B	309	THR
1	B	317	LEU
1	B	324	ILE
1	B	326	THR

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Mol	Chain	Res	Type
1	B	386	PHE
1	B	392	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	HIS
1	A	24	GLN
1	A	85	GLN
1	A	113	GLN
1	A	188	HIS
1	A	342	GLN
1	A	363	GLN
1	B	135	HIS
1	B	233	ASN
1	B	262	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	EPE	A	1431	-	15,15,15	0.83	1 (6%)	19,20,20	1.76	4 (21%)
2	COA	A	1169	1	47,50,50	1.20	5 (10%)	69,75,75	1.52	9 (13%)
2	COA	B	1169	1	47,50,50	1.29	4 (8%)	69,75,75	1.51	9 (13%)
4	OXL	A	1430	-	5,5,5	1.32	0	6,6,6	1.95	3 (50%)

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	EPE	A	1431	-	-	1/9/19/19	0/1/1/1
2	COA	A	1169	1	-	8/48/64/64	0/3/3/3
2	COA	B	1169	1	-	7/48/64/64	0/3/3/3
4	OXL	A	1430	-	-	0/4/4/4	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1169	COA	O9P-C9P	5.27	1.33	1.23
2	A	1169	COA	O9P-C9P	5.00	1.33	1.23
2	B	1169	COA	P2A-O3A	3.33	1.63	1.59
2	B	1169	COA	P1A-O3A	3.12	1.62	1.59
5	A	1431	EPE	C10-S	2.81	1.81	1.77
2	A	1169	COA	P1A-O3A	2.76	1.62	1.59
2	A	1169	COA	P2A-O3A	2.54	1.62	1.59
2	A	1169	COA	C5A-N7A	-2.15	1.35	1.39
2	B	1169	COA	C5A-N7A	-2.14	1.35	1.39
2	A	1169	COA	C8A-N7A	2.07	1.35	1.31

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1169	COA	C5A-C4A-N3A	-5.45	119.21	126.72
2	A	1169	COA	C5A-C4A-N3A	-5.16	119.62	126.72
2	B	1169	COA	N3A-C2A-N1A	-4.90	121.17	128.58
2	A	1169	COA	N3A-C2A-N1A	-4.87	121.20	128.58
5	A	1431	EPE	C5-N4-C3	4.79	119.17	108.84
2	B	1169	COA	C2A-N3A-C4A	3.56	120.52	111.83
2	B	1169	COA	N3A-C4A-N9A	3.46	133.05	127.17
2	A	1169	COA	C2A-N3A-C4A	3.39	120.10	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1169	COA	N9A-C8A-N7A	-3.37	109.16	113.94
2	A	1169	COA	N3A-C4A-N9A	3.34	132.84	127.17
2	B	1169	COA	N9A-C8A-N7A	-3.25	109.33	113.94
4	A	1430	OXL	O3-C1-C2	3.20	119.04	112.83
5	A	1431	EPE	C7-N4-C3	3.02	119.30	111.24
2	B	1169	COA	C4A-C5A-N7A	-2.99	107.16	110.58
2	A	1169	COA	C4A-C5A-N7A	-2.90	107.26	110.58
2	A	1169	COA	O4B-C1B-N9A	2.76	113.38	108.09
2	A	1169	COA	C5A-N7A-C8A	2.69	107.68	103.45
2	B	1169	COA	C5A-N7A-C8A	2.67	107.65	103.45
5	A	1431	EPE	C7-N4-C5	2.59	118.13	111.24
5	A	1431	EPE	O2S-S-C10	2.57	110.61	106.73
4	A	1430	OXL	O4-C2-C1	2.51	117.69	112.83
2	A	1169	COA	C4A-N9A-C8A	2.49	108.35	105.74
2	B	1169	COA	C4A-N9A-C8A	2.26	108.12	105.74
4	A	1430	OXL	O1-C1-C2	-2.19	116.08	120.63
2	B	1169	COA	O4B-C1B-N9A	2.08	112.08	108.09

There are no chirality outliers.

All (16) torsion outliers are listed below:

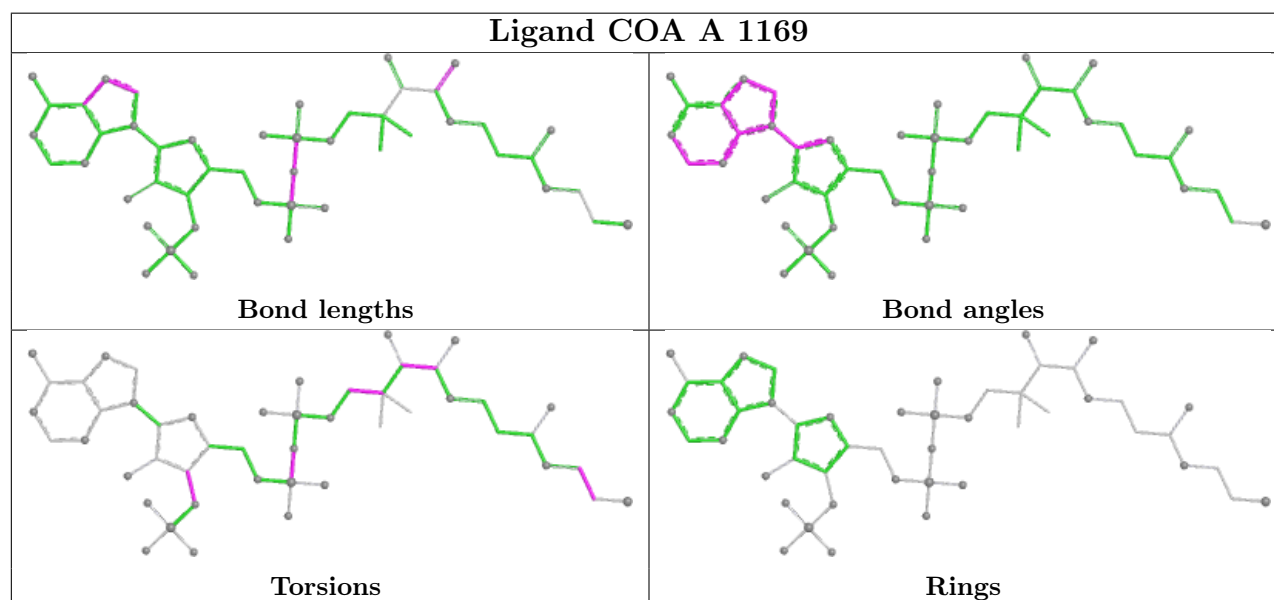
Mol	Chain	Res	Type	Atoms
2	A	1169	COA	S1P-C2P-C3P-N4P
2	B	1169	COA	CCP-O6A-P2A-O3A
2	B	1169	COA	CCP-O6A-P2A-O5A
2	B	1169	COA	C2P-C3P-N4P-C5P
2	A	1169	COA	C2B-C3B-O3B-P3B
2	A	1169	COA	C4B-C3B-O3B-P3B
2	B	1169	COA	C2B-C3B-O3B-P3B
2	B	1169	COA	C4B-C3B-O3B-P3B
2	A	1169	COA	P2A-O3A-P1A-O2A
2	A	1169	COA	CEP-CBP-CCP-O6A
2	B	1169	COA	CCP-O6A-P2A-O4A
5	A	1431	EPE	C8-C7-N4-C5
2	A	1169	COA	P2A-O3A-P1A-O1A
2	A	1169	COA	CDP-CBP-CCP-O6A
2	A	1169	COA	N8P-C9P-CAP-OAP
2	B	1169	COA	P1A-O3A-P2A-O5A

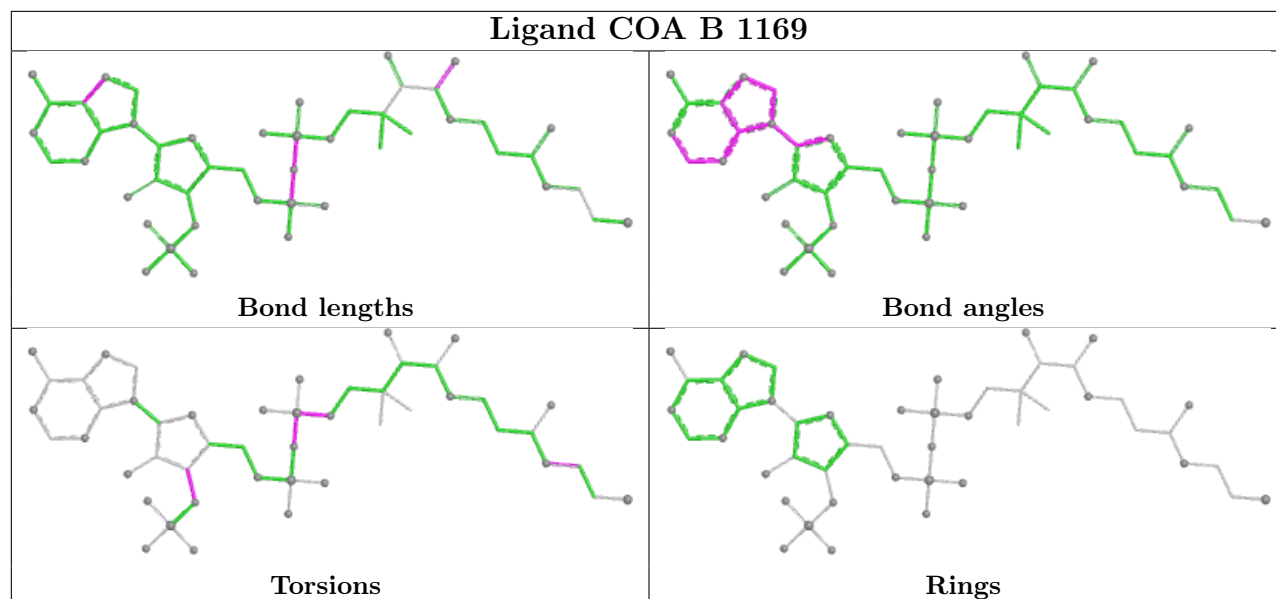
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1169	COA	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	427/428 (99%)	-0.03	11 (2%) 57 54	12, 26, 51, 67	6 (1%)
1	B	427/428 (99%)	0.40	57 (13%) 7 5	15, 29, 81, 94	1 (0%)
All	All	854/856 (99%)	0.19	68 (7%) 18 16	12, 28, 65, 94	7 (0%)

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	296	ILE	5.8
1	B	310	PHE	5.7
1	B	234	PHE	5.4
1	B	299	PRO	5.1
1	B	305	PRO	5.0
1	B	323	PHE	4.9
1	B	317	LEU	4.9
1	B	285	ALA	4.7
1	B	320	ILE	4.4
1	B	341	ALA	4.3
1	B	289	TRP	4.1
1	B	314	VAL	4.0
1	B	290	PRO	4.0
1	B	306	ALA	4.0
1	B	297	ASP	3.9
1	B	346	PRO	3.9
1	B	284	ILE	3.9
1	B	324	ILE	3.9
1	B	309	THR	3.8
1	A	419	ILE	3.8
1	B	298	LYS	3.7
1	B	288	MET	3.6
1	B	344	GLY	3.5
1	A	422	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	294	ASP	3.5
1	B	295	MET	3.5
1	B	340	ALA	3.5
1	B	292	ILE	3.4
1	B	321	PHE	3.4
1	B	293	CYS	3.3
1	B	316	LYS	3.3
1	B	301	TRP	3.2
1	B	286	ALA	3.2
1	B	307	TYR	3.1
1	A	44	MET	3.0
1	B	339	TRP	3.0
1	B	311	GLU	2.9
1	B	303	ASP	2.8
1	B	300	GLU	2.8
1	B	232	PRO	2.8
1	B	318	MET	2.7
1	A	2	THR	2.7
1	B	345	ILE	2.6
1	A	415	ASP	2.6
1	B	282	PHE	2.6
1	A	421	GLU	2.5
1	B	327	LYS	2.5
1	B	312	GLY	2.5
1	B	342	GLN	2.5
1	B	326	THR	2.4
1	A	428	VAL	2.4
1	B	304	ASP	2.4
1	B	417	ALA	2.4
1	B	315	ASP	2.3
1	B	302	LYS	2.3
1	B	238	ARG	2.3
1	B	343	TYR	2.3
1	A	261	GLY	2.3
1	A	424	ALA	2.3
1	B	81	GLU	2.2
1	B	291	GLN	2.2
1	B	420	LYS	2.2
1	B	287	ASN	2.2
1	A	115	LEU	2.2
1	B	233	ASN	2.1
1	A	48	TRP	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	322	SER	2.0
1	B	308	ASN	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

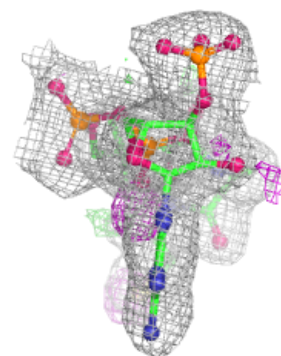
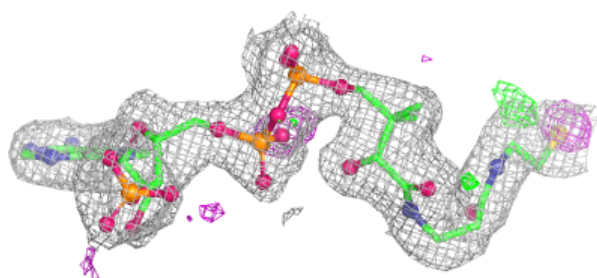
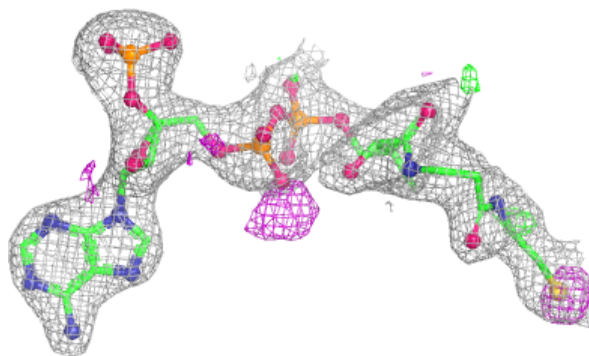
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	OXL	A	1430	6/6	0.81	0.25	55,57,57,57	0
5	EPE	A	1431	15/15	0.91	0.12	32,33,34,34	15
2	COA	B	1169	48/48	0.92	0.10	30,45,48,48	0
2	COA	A	1169	48/48	0.94	0.09	25,42,46,46	0
3	CL	B	1429	1/1	0.98	0.04	21,21,21,21	0
3	CL	A	1429	1/1	0.99	0.05	23,23,23,23	0

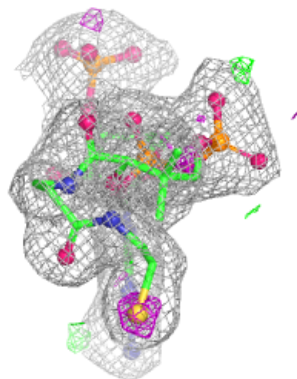
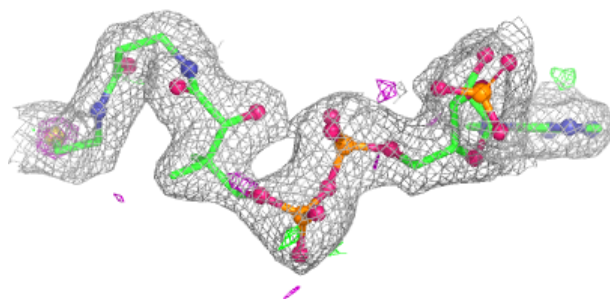
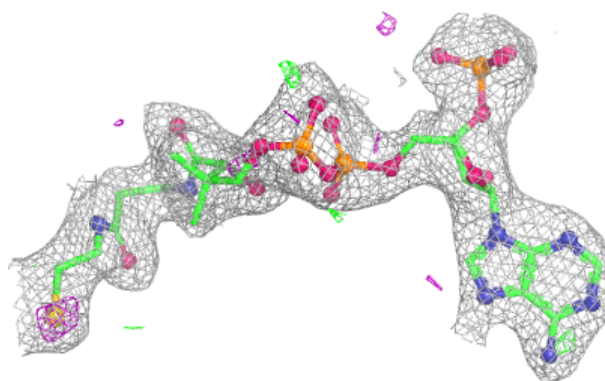
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around COA B 1169:

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

**Electron density around COA A 1169:**

$2mF_o-DF_c$ (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.