



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:10 PM UTC

PDB ID : 7LDC / pdb_00007ldc
Title : Zoogloea ramigera biosynthetic thiolase Q183Y/Y218E mutant
Authors : Marshall, A.C.; Bruning, J.B.
Deposited on : 2021-01-13
Resolution : 2.50 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

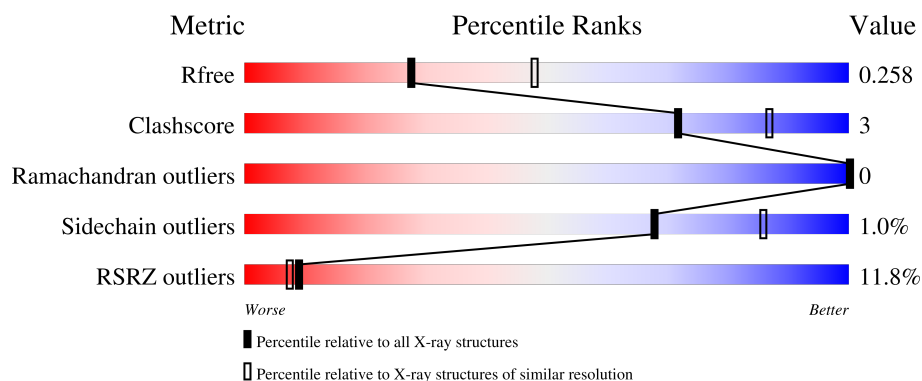
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	399	5% 93% 5% .
1	B	399	6% 90% 6% .
1	C	399	9% 90% 8% .
1	D	399	26% 86% 11% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11847 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	0	0
			2786	1732	499	534	21			
1	B	387	Total	C	N	O	S	0	0	0
			2781	1729	497	534	21			
1	C	389	Total	C	N	O	S	0	0	0
			2789	1735	501	532	21			
1	D	387	Total	C	N	O	S	0	0	0
			2714	1684	488	522	20			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	initiating methionine	UNP P07097
A	-5	HIS	-	expression tag	UNP P07097
A	-4	HIS	-	expression tag	UNP P07097
A	-3	HIS	-	expression tag	UNP P07097
A	-2	HIS	-	expression tag	UNP P07097
A	-1	HIS	-	expression tag	UNP P07097
A	0	HIS	-	expression tag	UNP P07097
A	11	ALA	-	insertion	UNP P07097
A	129	ARG	ALA	conflict	UNP P07097
A	183	TYR	GLN	engineered mutation	UNP P07097
A	218	GLU	TYR	engineered mutation	UNP P07097
B	-6	MET	-	initiating methionine	UNP P07097
B	-5	HIS	-	expression tag	UNP P07097
B	-4	HIS	-	expression tag	UNP P07097
B	-3	HIS	-	expression tag	UNP P07097
B	-2	HIS	-	expression tag	UNP P07097
B	-1	HIS	-	expression tag	UNP P07097
B	0	HIS	-	expression tag	UNP P07097
B	11	ALA	-	insertion	UNP P07097
B	129	ARG	ALA	conflict	UNP P07097
B	183	TYR	GLN	engineered mutation	UNP P07097

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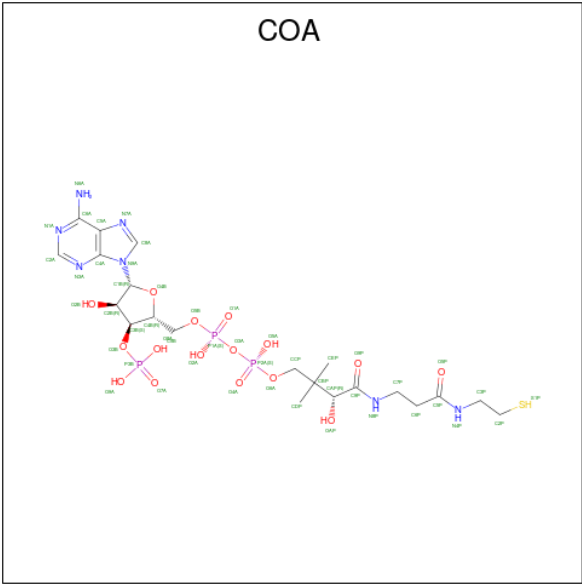
Chain	Residue	Modelled	Actual	Comment	Reference
B	218	GLU	TYR	engineered mutation	UNP P07097
C	-6	MET	-	initiating methionine	UNP P07097
C	-5	HIS	-	expression tag	UNP P07097
C	-4	HIS	-	expression tag	UNP P07097
C	-3	HIS	-	expression tag	UNP P07097
C	-2	HIS	-	expression tag	UNP P07097
C	-1	HIS	-	expression tag	UNP P07097
C	0	HIS	-	expression tag	UNP P07097
C	11	ALA	-	insertion	UNP P07097
C	129	ARG	ALA	conflict	UNP P07097
C	183	TYR	GLN	engineered mutation	UNP P07097
C	218	GLU	TYR	engineered mutation	UNP P07097
D	-6	MET	-	initiating methionine	UNP P07097
D	-5	HIS	-	expression tag	UNP P07097
D	-4	HIS	-	expression tag	UNP P07097
D	-3	HIS	-	expression tag	UNP P07097
D	-2	HIS	-	expression tag	UNP P07097
D	-1	HIS	-	expression tag	UNP P07097
D	0	HIS	-	expression tag	UNP P07097
D	11	ALA	-	insertion	UNP P07097
D	129	ARG	ALA	conflict	UNP P07097
D	183	TYR	GLN	engineered mutation	UNP P07097
D	218	GLU	TYR	engineered mutation	UNP P07097

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



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

- Molecule 3 is COENZYME A (CCD ID: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S) (labeled as "Ligand of Interest" by depositor).



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

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

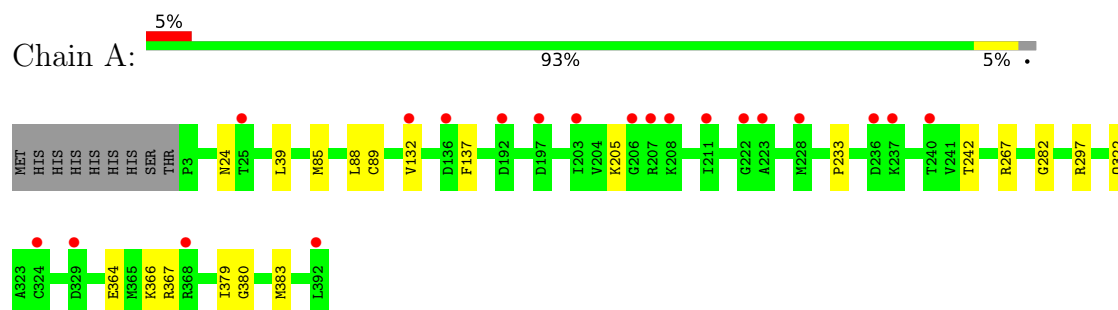
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	203	Total	O	0	0
			203	203		
4	B	179	Total	O	0	0
			179	179		
4	C	94	Total	O	0	0
			94	94		
4	D	59	Total	O	0	0
			59	59		

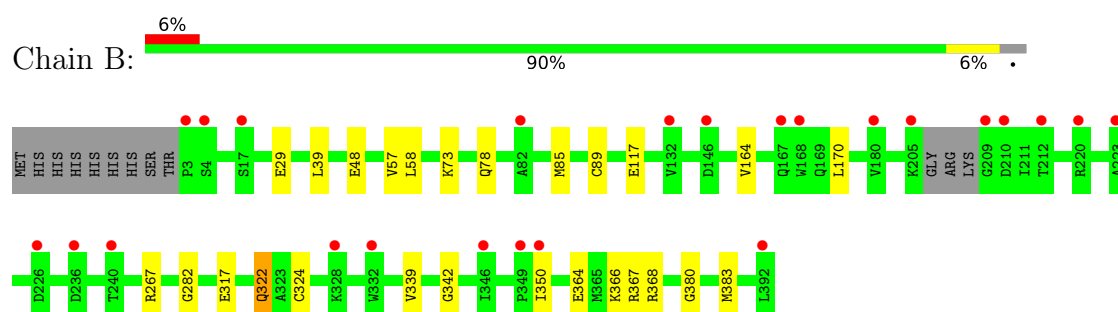
3 Residue-property plots [i](#)

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.

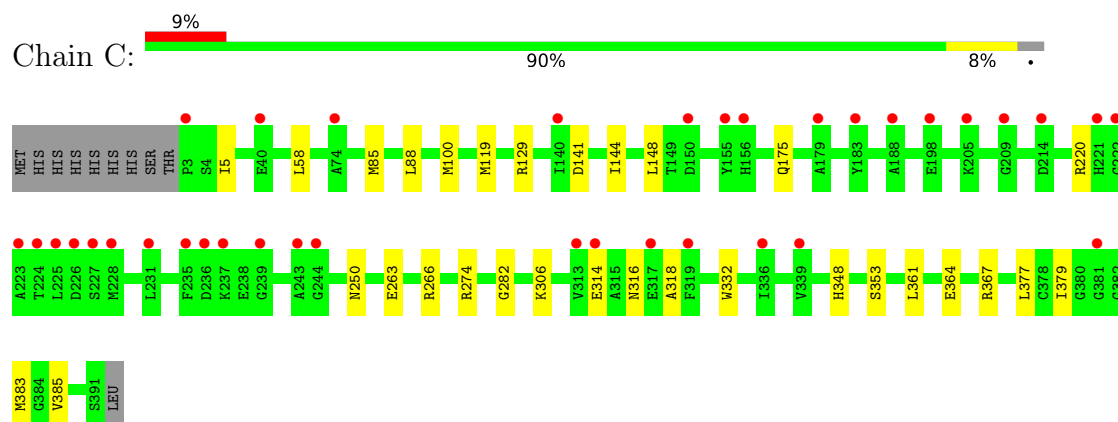
- Molecule 1: Acetyl-CoA acetyltransferase



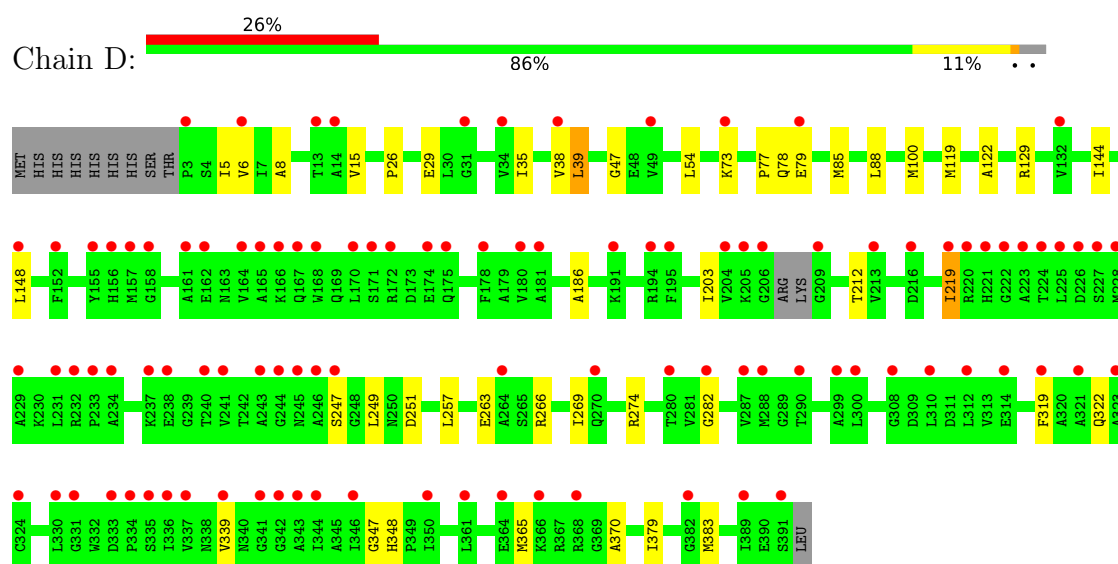
- Molecule 1: Acetyl-CoA acetyltransferase



- 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	83.72Å 79.55Å 151.54Å 90.00° 93.95° 90.00°	Depositor
Resolution (Å)	34.71 – 2.50 34.71 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (34.71-2.50) 99.8 (34.71-2.50)	Depositor EDS
R_{merge}	0.38	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.35 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.15_3459	Depositor
R, R_{free}	0.219 , 0.260 0.218 , 0.258	Depositor DCC
R_{free} test set	3451 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	32.3	Xtriage
Anisotropy	0.382	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 63.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11847	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.93% 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: SO4, SCY, 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	0.11	0/2818	0.30	0/3810
1	B	0.12	0/2812	0.30	0/3800
1	C	0.10	0/2821	0.28	0/3812
1	D	0.12	0/2743	0.30	0/3715
All	All	0.11	0/11194	0.29	0/15137

There are no bond length outliers.

There are no bond angle outliers.

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	2786	0	2750	13	0
1	B	2781	0	2759	15	0
1	C	2789	0	2759	23	0
1	D	2714	0	2618	27	0
2	A	15	0	0	0	0
2	B	15	0	0	0	0
2	C	10	0	0	0	0
2	D	10	0	0	0	0
3	A	48	0	32	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	48	0	32	0	0
3	C	48	0	32	1	0
3	D	48	0	32	0	0
4	A	203	0	0	4	0
4	B	179	0	0	2	0
4	C	94	0	0	4	0
4	D	59	0	0	1	0
All	All	11847	0	11014	74	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 (74) 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:D:29:GLU:HA	1:D:73:LYS:HZ2	1.47	0.78
1:D:29:GLU:HA	1:D:73:LYS:NZ	2.01	0.74
1:B:57:VAL:HG23	1:B:58:LEU:HG	1.72	0.70
1:C:88:LEU:HB2	1:C:379:ILE:HG23	1.75	0.68
1:B:364:GLU:OE1	1:B:367:ARG:NH1	2.31	0.63
1:C:316:ASN:HD22	1:C:377:LEU:HD23	1.63	0.63
1:B:366:LYS:NZ	4:B:506:HOH:O	2.31	0.62
1:A:85:MET:HA	1:B:85:MET:HA	1.83	0.60
1:D:203:ILE:HG12	1:D:212:THR:HG22	1.84	0.59
1:C:220:ARG:NH1	4:C:508:HOH:O	2.37	0.58
1:A:366:LYS:NZ	4:A:516:HOH:O	2.36	0.57
1:D:144:ILE:HD13	1:D:148:LEU:HD12	1.86	0.57
1:A:89:SCY:OCD	1:A:380:GLY:N	2.34	0.56
1:C:85:MET:HA	1:D:85:MET:HA	1.87	0.55
1:D:282:GLY:HA2	1:D:383:MET:HA	1.88	0.55
1:A:24:ASN:ND2	4:A:511:HOH:O	2.33	0.55
1:D:77:PRO:HB2	1:D:79:GLU:OE1	2.07	0.55
1:D:5:ILE:HG13	1:D:100:MET:HG2	1.89	0.54
1:B:29:GLU:HG2	1:B:73:LYS:NZ	2.22	0.54
1:D:8:ALA:HB3	1:D:257:LEU:HD12	1.90	0.54
1:C:318:ALA:HB1	3:C:401:COA:H22	1.89	0.54
1:A:282:GLY:HA2	1:A:383:MET:HA	1.91	0.52
1:C:282:GLY:HA2	1:C:383:MET:HA	1.92	0.52
1:C:144:ILE:HD13	1:C:148:LEU:HD12	1.91	0.51
1:B:282:GLY:HA2	1:B:383:MET:HA	1.91	0.51
1:C:314:GLU:HG3	1:C:361:LEU:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:364:GLU:HA	1:A:367:ARG:HG2	1.93	0.50
1:C:175:GLN:NE2	4:C:514:HOH:O	2.44	0.50
1:D:38:VAL:HG23	1:D:39:LEU:HD13	1.94	0.50
1:D:186:ALA:HB1	1:D:219:ILE:HD11	1.94	0.49
1:C:364:GLU:OE1	1:C:367:ARG:NH1	2.46	0.48
1:B:339:VAL:HG11	1:B:368:ARG:NH2	2.28	0.48
1:C:58:LEU:HD12	1:C:119:MET:HG2	1.96	0.47
1:D:26:PRO:HD2	1:D:29:GLU:CD	2.40	0.47
1:C:316:ASN:ND2	1:C:377:LEU:HD23	2.28	0.47
1:C:379:ILE:HD11	1:C:385:VAL:HG12	1.96	0.47
1:B:317:GLU:CD	1:B:342:GLY:HA3	2.40	0.46
1:C:306:LYS:NZ	4:C:516:HOH:O	2.48	0.46
1:A:267:ARG:NH1	4:A:530:HOH:O	2.48	0.46
1:B:89:SCY:OCD	1:B:380:GLY:N	2.35	0.46
1:A:364:GLU:OE1	1:A:367:ARG:NH1	2.37	0.46
1:D:78:GLN:NE2	4:D:502:HOH:O	2.39	0.46
1:D:47:GLY:HA2	1:D:77:PRO:HG3	1.97	0.46
1:D:15:VAL:HG11	1:D:347:GLY:HA3	1.98	0.45
1:D:263:GLU:OE2	1:D:266:ARG:NH1	2.49	0.45
1:C:306:LYS:HA	1:C:306:LYS:HD2	1.80	0.45
1:A:233:PRO:HA	1:A:242:THR:HG22	1.97	0.45
1:C:141:ASP:OD1	1:D:129:ARG:NH2	2.38	0.45
1:C:348:HIS:ND1	1:C:353:SER:OG	2.51	0.44
1:D:88:LEU:HB2	1:D:379:ILE:HG23	2.00	0.44
1:A:297:ARG:NE	4:A:527:HOH:O	2.47	0.44
1:D:6:VAL:HA	1:D:274:ARG:HA	2.00	0.44
1:B:85:MET:HE2	1:B:85:MET:HB2	1.86	0.43
1:B:57:VAL:HG22	1:B:117:GLU:OE1	2.19	0.43
1:A:132:VAL:HG21	1:A:137:PHE:CD1	2.54	0.42
1:D:8:ALA:HB1	1:D:269:ILE:HG21	2.00	0.42
1:C:274:ARG:NE	4:C:518:HOH:O	2.52	0.42
1:A:88:LEU:HB2	1:A:379:ILE:HG23	2.01	0.42
1:D:247:SER:HB2	1:D:348:HIS:HB2	2.01	0.42
1:D:319:PHE:O	1:D:322:GLN:HG3	2.20	0.42
1:D:35:ILE:HD11	1:D:54:LEU:HD11	2.02	0.42
1:D:119:MET:HE2	1:D:249:LEU:HB3	2.02	0.42
1:D:365:MET:HG2	1:D:370:ALA:HB3	2.02	0.41
1:C:85:MET:HE2	1:C:85:MET:HB2	1.89	0.41
1:B:78:GLN:HG2	4:B:508:HOH:O	2.21	0.41
1:A:364:GLU:OE1	1:A:367:ARG:HD2	2.20	0.41
1:B:48:GLU:OE1	1:B:267:ARG:NH1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:5:ILE:HG13	1:C:100:MET:HG2	2.03	0.41
1:B:170:LEU:HD13	1:B:324:CYS:HB2	2.03	0.41
1:C:129:ARG:HH21	1:D:122:ALA:HB3	1.86	0.41
1:B:164:VAL:HG11	1:B:322:GLN:HA	2.01	0.41
1:C:119:MET:CE	1:C:250:ASN:H	2.33	0.41
1:C:263:GLU:OE1	1:C:266:ARG:NH2	2.37	0.40
1:D:119:MET:N	1:D:251:ASP:OD1	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	387/399 (97%)	379 (98%)	8 (2%)	0	100	100
1	B	382/399 (96%)	376 (98%)	6 (2%)	0	100	100
1	C	386/399 (97%)	379 (98%)	7 (2%)	0	100	100
1	D	382/399 (96%)	375 (98%)	7 (2%)	0	100	100
All	All	1537/1596 (96%)	1509 (98%)	28 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	266/285 (93%)	263 (99%)	3 (1%)	65	84
1	B	269/285 (94%)	266 (99%)	3 (1%)	65	84
1	C	265/285 (93%)	264 (100%)	1 (0%)	84	93
1	D	248/285 (87%)	245 (99%)	3 (1%)	63	83
All	All	1048/1140 (92%)	1038 (99%)	10 (1%)	68	86

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	LEU
1	A	205	LYS
1	A	322	GLN
1	B	39	LEU
1	B	322	GLN
1	B	350	ILE
1	C	332	TRP
1	D	39	LEU
1	D	219	ILE
1	D	339	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	167	GLN
1	C	190	GLN
1	C	322	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	SCY	C	89	1	7,8,9	0.91	0	4,9,11	1.03	0
1	SCY	A	89	1	7,8,9	0.97	0	4,9,11	0.96	0
1	SCY	D	89	1	7,8,9	0.95	0	4,9,11	0.97	0
1	SCY	B	89	1	7,8,9	0.92	0	4,9,11	0.98	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SCY	C	89	1	-	2/5/7/9	-
1	SCY	A	89	1	-	2/5/7/9	-
1	SCY	D	89	1	-	2/5/7/9	-
1	SCY	B	89	1	-	2/5/7/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	89	SCY	OCD-CD-SG-CB
1	B	89	SCY	OCD-CD-SG-CB
1	C	89	SCY	OCD-CD-SG-CB
1	D	89	SCY	OCD-CD-SG-CB
1	A	89	SCY	CE-CD-SG-CB
1	B	89	SCY	CE-CD-SG-CB
1	C	89	SCY	CE-CD-SG-CB
1	D	89	SCY	CE-CD-SG-CB

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	89	SCY	1	0
1	B	89	SCY	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

14 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	B	402	-	4,4,4	0.24	0	6,6,6	0.09	0
2	SO4	C	403	-	4,4,4	0.24	0	6,6,6	0.07	0
2	SO4	A	401	-	4,4,4	0.24	0	6,6,6	0.11	0
2	SO4	A	402	-	4,4,4	0.23	0	6,6,6	0.09	0
3	COA	B	404	-	47,50,50	1.15	5 (10%)	69,75,75	1.86	13 (18%)
2	SO4	B	403	-	4,4,4	0.24	0	6,6,6	0.06	0
2	SO4	D	402	-	4,4,4	0.25	0	6,6,6	0.07	0
2	SO4	A	403	-	4,4,4	0.24	0	6,6,6	0.06	0
2	SO4	D	403	-	4,4,4	0.24	0	6,6,6	0.06	0
3	COA	D	401	-	47,50,50	1.11	5 (10%)	69,75,75	1.88	14 (20%)
2	SO4	C	402	-	4,4,4	0.23	0	6,6,6	0.08	0
3	COA	A	404	-	47,50,50	1.10	5 (10%)	69,75,75	1.86	14 (20%)
3	COA	C	401	-	47,50,50	1.12	6 (12%)	69,75,75	1.82	15 (21%)
2	SO4	B	401	-	4,4,4	0.24	0	6,6,6	0.08	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	COA	D	401	-	-	20/48/64/64	0/3/3/3
3	COA	B	404	-	-	8/48/64/64	0/3/3/3
3	COA	A	404	-	-	9/48/64/64	0/3/3/3
3	COA	C	401	-	-	11/48/64/64	0/3/3/3

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	404	COA	P2A-O3A	3.31	1.63	1.59
3	C	401	COA	P1A-O3A	2.97	1.62	1.59
3	D	401	COA	P2A-O3A	2.83	1.62	1.59
3	B	404	COA	P1A-O3A	2.70	1.62	1.59
3	A	404	COA	P1A-O3A	2.58	1.62	1.59
3	A	404	COA	P2A-O3A	2.39	1.62	1.59
3	D	401	COA	P1A-O3A	2.36	1.62	1.59
3	C	401	COA	P3B-O8A	2.32	1.63	1.54
3	C	401	COA	P2A-O3A	2.31	1.62	1.59
3	A	404	COA	C5A-N7A	-2.27	1.34	1.39
3	B	404	COA	C5A-N7A	-2.25	1.35	1.39
3	D	401	COA	P3B-O9A	2.24	1.63	1.54
3	B	404	COA	P3B-O8A	2.23	1.63	1.54
3	C	401	COA	C5A-N7A	-2.22	1.35	1.39
3	D	401	COA	P3B-O8A	2.22	1.63	1.54
3	C	401	COA	P3B-O9A	2.21	1.63	1.54
3	B	404	COA	P3B-O9A	2.21	1.63	1.54
3	A	404	COA	P3B-O8A	2.20	1.63	1.54
3	A	404	COA	P3B-O9A	2.17	1.62	1.54
3	D	401	COA	C5A-N7A	-2.16	1.35	1.39
3	C	401	COA	O4B-C1B	2.01	1.46	1.42

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	401	COA	C5A-C4A-N3A	-6.63	117.59	126.72
3	B	404	COA	C5A-C4A-N3A	-6.63	117.59	126.72
3	A	404	COA	C5A-C4A-N3A	-6.47	117.81	126.72
3	C	401	COA	C5A-C4A-N3A	-6.39	117.92	126.72
3	D	401	COA	N3A-C4A-N9A	6.22	137.75	127.17
3	B	404	COA	N3A-C4A-N9A	6.19	137.70	127.17
3	C	401	COA	N3A-C4A-N9A	6.14	137.62	127.17
3	A	404	COA	N3A-C4A-N9A	6.06	137.48	127.17
3	B	404	COA	P3B-O3B-C3B	-5.37	109.10	123.43
3	A	404	COA	P3B-O3B-C3B	-5.11	109.78	123.43
3	D	401	COA	P3B-O3B-C3B	-4.50	111.42	123.43
3	C	401	COA	P3B-O3B-C3B	-4.22	112.16	123.43
3	C	401	COA	N3A-C2A-N1A	-3.68	123.01	128.58
3	D	401	COA	N3A-C2A-N1A	-3.67	123.03	128.58
3	B	404	COA	N3A-C2A-N1A	-3.62	123.10	128.58
3	A	404	COA	N3A-C2A-N1A	-3.61	123.12	128.58
3	D	401	COA	C2A-N3A-C4A	3.41	120.16	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	404	COA	C2A-N3A-C4A	3.40	120.13	111.83
3	A	404	COA	C5A-N7A-C8A	3.35	108.71	103.45
3	C	401	COA	C2A-N3A-C4A	3.34	120.00	111.83
3	A	404	COA	C2A-N3A-C4A	3.33	119.97	111.83
3	D	401	COA	C5A-N7A-C8A	3.31	108.65	103.45
3	B	404	COA	C5A-N7A-C8A	3.24	108.53	103.45
3	C	401	COA	C5A-N7A-C8A	3.23	108.52	103.45
3	C	401	COA	N6A-C6A-N1A	2.82	124.65	118.38
3	D	401	COA	N6A-C6A-N1A	2.76	124.52	118.38
3	C	401	COA	C5A-C6A-N6A	-2.64	116.75	123.29
3	B	404	COA	N6A-C6A-N1A	2.63	124.24	118.38
3	B	404	COA	CAP-C9P-N8P	2.55	121.32	116.48
3	A	404	COA	N6A-C6A-N1A	2.55	124.05	118.38
3	B	404	COA	C6A-C5A-C4A	2.53	120.64	117.18
3	D	401	COA	C5A-C6A-N6A	-2.53	117.03	123.29
3	D	401	COA	C6A-C5A-C4A	2.53	120.63	117.18
3	C	401	COA	N9A-C8A-N7A	-2.52	110.36	113.94
3	A	404	COA	C6A-C5A-C4A	2.45	120.53	117.18
3	A	404	COA	CAP-C9P-N8P	2.44	121.11	116.48
3	A	404	COA	N9A-C8A-N7A	-2.43	110.48	113.94
3	B	404	COA	C5A-C6A-N6A	-2.39	117.38	123.29
3	D	401	COA	N9A-C8A-N7A	-2.38	110.56	113.94
3	B	404	COA	P2A-O6A-CCP	-2.37	108.22	121.12
3	C	401	COA	C6A-C5A-C4A	2.36	120.41	117.18
3	C	401	COA	P1A-O5B-C5B	-2.31	108.10	121.35
3	B	404	COA	N9A-C8A-N7A	-2.30	110.67	113.94
3	A	404	COA	C5A-C6A-N6A	-2.30	117.60	123.29
3	C	401	COA	C2B-C3B-C4B	-2.26	99.29	103.24
3	D	401	COA	CAP-C9P-N8P	2.25	120.75	116.48
3	A	404	COA	P1A-O5B-C5B	-2.15	109.03	121.35
3	A	404	COA	P2A-O6A-CCP	-2.14	109.48	121.12
3	A	404	COA	C6P-C5P-N4P	2.10	120.17	116.34
3	D	401	COA	P2A-O6A-CCP	-2.10	109.67	121.12
3	D	401	COA	P1A-O5B-C5B	-2.04	109.66	121.35
3	C	401	COA	C6P-C5P-N4P	2.02	120.03	116.34
3	B	404	COA	P1A-O5B-C5B	-2.02	109.79	121.35
3	D	401	COA	C6P-C5P-N4P	2.01	120.00	116.34
3	C	401	COA	P2A-O6A-CCP	-2.01	110.19	121.12
3	C	401	COA	CAP-C9P-N8P	2.00	120.28	116.48

There are no chirality outliers.

All (48) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	404	COA	CCP-O6A-P2A-O5A
3	A	404	COA	S1P-C2P-C3P-N4P
3	B	404	COA	C5B-O5B-P1A-O2A
3	B	404	COA	C5B-O5B-P1A-O3A
3	B	404	COA	CCP-O6A-P2A-O3A
3	B	404	COA	CCP-O6A-P2A-O4A
3	B	404	COA	CCP-O6A-P2A-O5A
3	B	404	COA	CDP-CBP-CCP-O6A
3	B	404	COA	CEP-CBP-CCP-O6A
3	B	404	COA	CAP-CBP-CCP-O6A
3	C	401	COA	C4B-C3B-O3B-P3B
3	C	401	COA	CCP-O6A-P2A-O3A
3	C	401	COA	CCP-O6A-P2A-O4A
3	C	401	COA	CCP-O6A-P2A-O5A
3	C	401	COA	CDP-CBP-CCP-O6A
3	C	401	COA	CEP-CBP-CCP-O6A
3	C	401	COA	CAP-CBP-CCP-O6A
3	C	401	COA	S1P-C2P-C3P-N4P
3	D	401	COA	CCP-O6A-P2A-O3A
3	D	401	COA	CCP-O6A-P2A-O4A
3	D	401	COA	CCP-O6A-P2A-O5A
3	D	401	COA	CDP-CBP-CCP-O6A
3	D	401	COA	CEP-CBP-CCP-O6A
3	D	401	COA	CAP-CBP-CCP-O6A
3	D	401	COA	OAP-CAP-CBP-CCP
3	D	401	COA	C9P-CAP-CBP-CCP
3	D	401	COA	OAP-CAP-CBP-CDP
3	D	401	COA	C9P-CAP-CBP-CDP
3	D	401	COA	OAP-CAP-CBP-CEP
3	D	401	COA	C9P-CAP-CBP-CEP
3	D	401	COA	S1P-C2P-C3P-N4P
3	A	404	COA	O4B-C4B-C5B-O5B
3	D	401	COA	C4B-C3B-O3B-P3B
3	D	401	COA	C2B-C3B-O3B-P3B
3	D	401	COA	P2A-O3A-P1A-O1A
3	A	404	COA	C3B-C4B-C5B-O5B
3	C	401	COA	O4B-C4B-C5B-O5B
3	A	404	COA	C5B-O5B-P1A-O1A
3	A	404	COA	CCP-O6A-P2A-O3A
3	A	404	COA	CCP-O6A-P2A-O4A
3	D	401	COA	C5B-O5B-P1A-O1A
3	A	404	COA	P2A-O3A-P1A-O2A
3	D	401	COA	O4B-C4B-C5B-O5B

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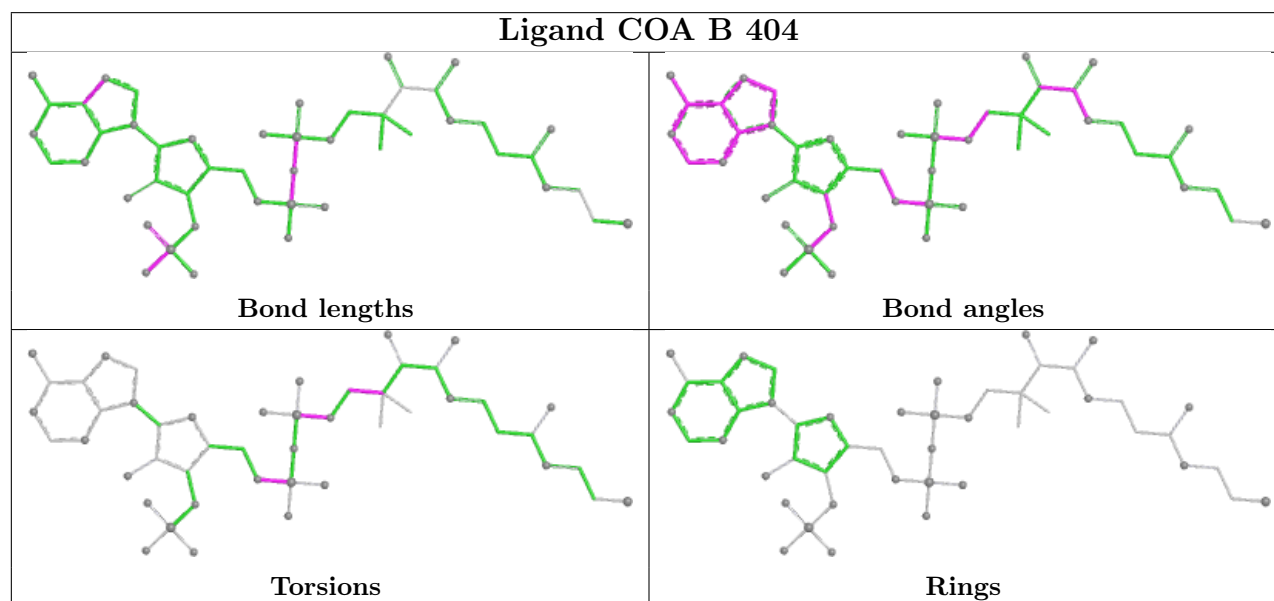
Mol	Chain	Res	Type	Atoms
3	C	401	COA	C2B-C3B-O3B-P3B
3	C	401	COA	C3B-O3B-P3B-O7A
3	A	404	COA	P2A-O3A-P1A-O1A
3	D	401	COA	C3B-O3B-P3B-O9A
3	D	401	COA	CBP-CCP-O6A-P2A

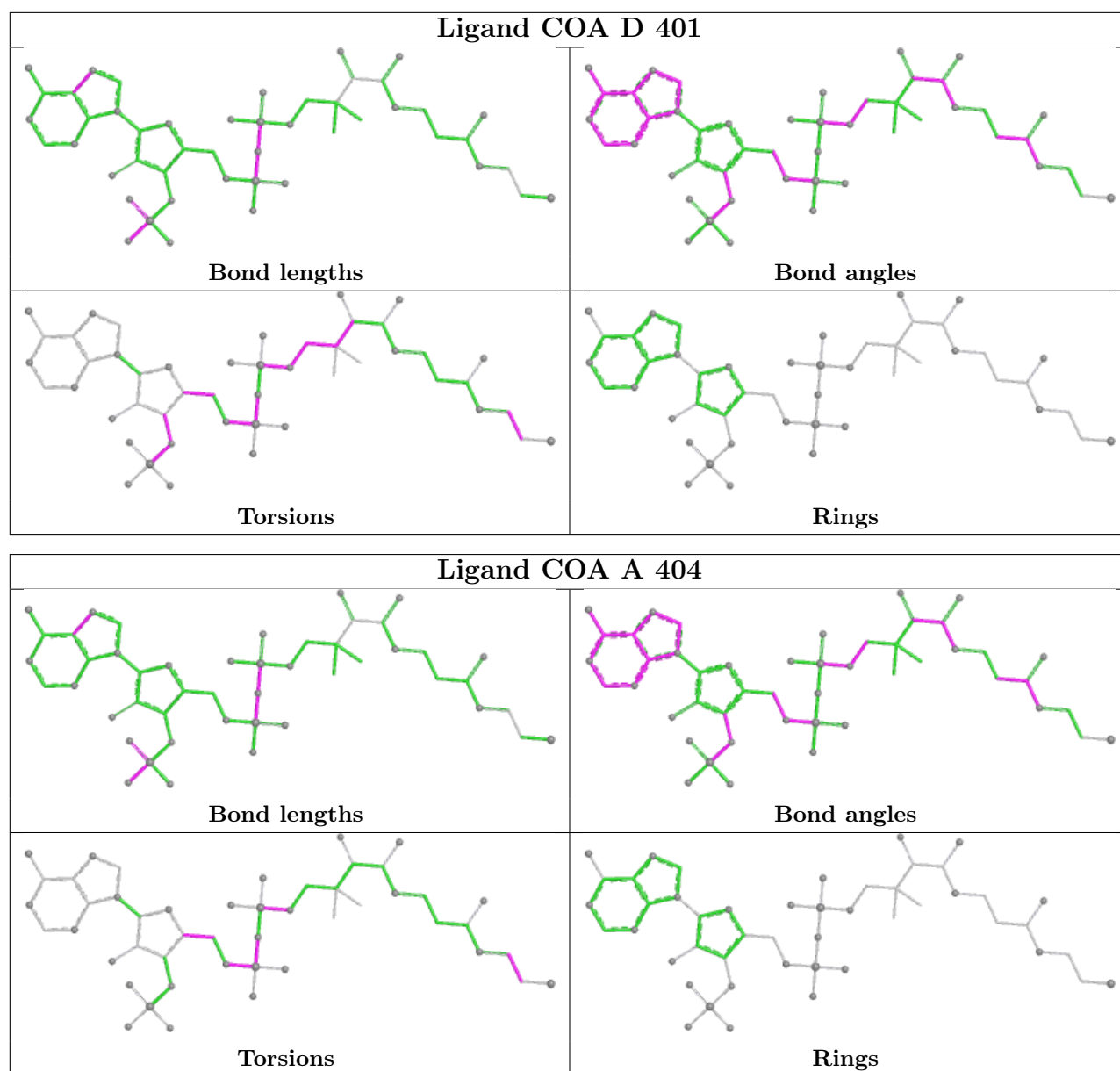
There are no ring outliers.

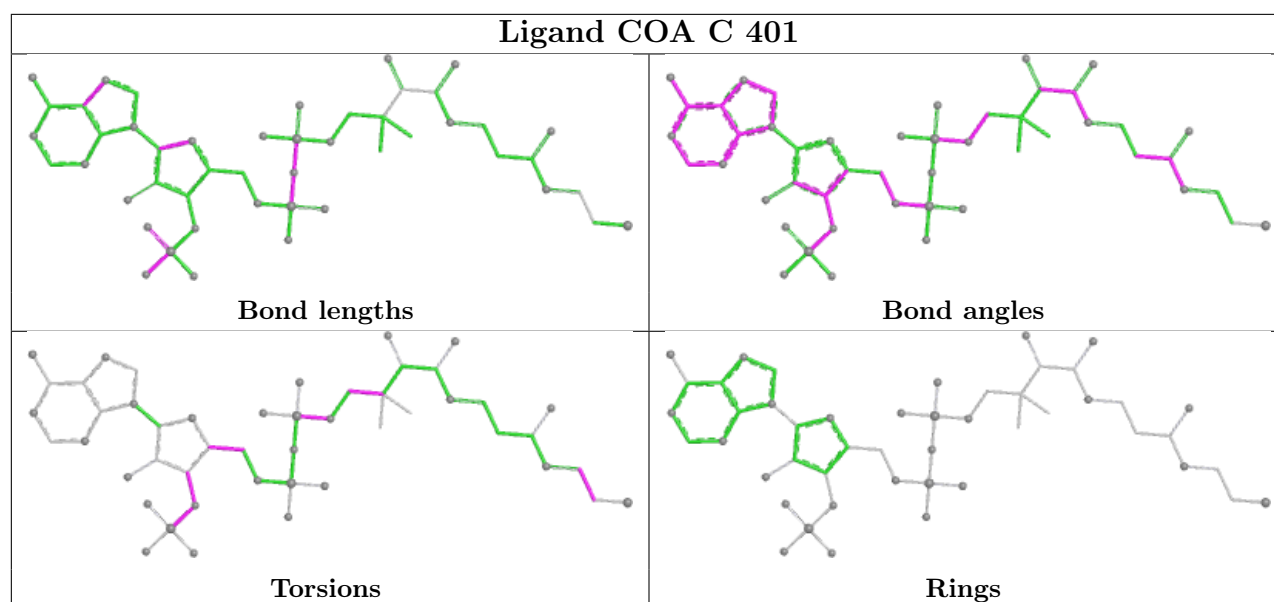
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	401	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	389/399 (97%)	0.62	20 (5%) 33 29	18, 32, 56, 89	0
1	B	386/399 (96%)	0.69	24 (6%) 26 23	15, 33, 58, 78	0
1	C	388/399 (97%)	0.96	36 (9%) 14 12	29, 50, 80, 100	0
1	D	386/399 (96%)	1.47	103 (26%) 1 1	29, 57, 97, 127	0
All	All	1549/1596 (97%)	0.94	183 (11%) 9 7	15, 43, 80, 127	0

All (183) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	225	LEU	6.1
1	D	227	SER	5.8
1	D	228	MET	5.1
1	D	206	GLY	4.9
1	D	224	THR	4.9
1	D	319	PHE	4.8
1	C	223	ALA	4.5
1	D	31	GLY	4.5
1	D	244	GLY	4.4
1	D	226	ASP	4.4
1	D	170	LEU	4.3
1	D	241	VAL	4.3
1	C	227	SER	4.2
1	D	171	SER	4.1
1	C	226	ASP	3.9
1	D	314	GLU	3.9
1	D	175	GLN	3.8
1	B	205	LYS	3.7
1	D	156	HIS	3.6
1	C	222	GLY	3.6
1	D	331	GLY	3.6

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Mol	Chain	Res	Type	RSRZ
1	D	243	ALA	3.5
1	C	244	GLY	3.5
1	C	228	MET	3.5
1	C	3	PRO	3.5
1	D	366	LYS	3.4
1	C	225	LEU	3.4
1	D	168	TRP	3.3
1	D	213	VAL	3.3
1	B	220	ARG	3.3
1	D	164	VAL	3.3
1	D	342	GLY	3.3
1	A	132	VAL	3.3
1	D	79	GLU	3.3
1	D	165	ALA	3.3
1	C	313	VAL	3.2
1	D	221	HIS	3.2
1	A	222	GLY	3.2
1	D	247	SER	3.2
1	D	3	PRO	3.2
1	B	209	GLY	3.2
1	D	231	LEU	3.2
1	D	219	ILE	3.2
1	D	391	SER	3.1
1	D	223	ALA	3.0
1	D	312	LEU	3.0
1	B	210	ASP	3.0
1	D	209	GLY	3.0
1	D	222	GLY	3.0
1	A	207	ARG	2.9
1	D	310	LEU	2.9
1	B	82	ALA	2.9
1	B	392	LEU	2.9
1	B	236	ASP	2.9
1	D	341	GLY	2.9
1	A	211	ILE	2.8
1	D	287	VAL	2.8
1	D	181	ALA	2.8
1	D	238	GLU	2.8
1	B	132	VAL	2.8
1	D	282	GLY	2.8
1	D	389	ILE	2.8
1	D	245	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	25	THR	2.8
1	B	223	ALA	2.7
1	D	240	THR	2.7
1	A	136	ASP	2.7
1	C	224	THR	2.7
1	C	235	PHE	2.7
1	D	382	GLY	2.7
1	D	324	CYS	2.7
1	D	132	VAL	2.7
1	D	343	ALA	2.7
1	B	226	ASP	2.6
1	D	288	MET	2.6
1	D	34	VAL	2.6
1	D	204	VAL	2.6
1	D	339	VAL	2.6
1	D	73	LYS	2.6
1	C	179	ALA	2.6
1	C	183	TYR	2.6
1	C	231	LEU	2.6
1	D	180	VAL	2.6
1	A	223	ALA	2.6
1	D	234	ALA	2.6
1	C	221	HIS	2.6
1	B	168	TRP	2.6
1	C	239	GLY	2.6
1	D	330	LEU	2.5
1	A	392	LEU	2.5
1	D	361	LEU	2.5
1	B	3	PRO	2.5
1	B	349	PRO	2.5
1	D	334	PRO	2.5
1	D	38	VAL	2.5
1	C	339	VAL	2.5
1	A	368	ARG	2.5
1	D	232	ARG	2.5
1	D	14	ALA	2.5
1	D	167	GLN	2.4
1	D	299	ALA	2.4
1	C	198	GLU	2.4
1	A	237	LYS	2.4
1	A	329	ASP	2.4
1	D	333	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	336	ILE	2.4
1	D	344	ILE	2.4
1	A	208	LYS	2.4
1	D	178	PHE	2.4
1	C	205	LYS	2.4
1	C	140	ILE	2.4
1	C	156	HIS	2.4
1	B	212	THR	2.3
1	D	13	THR	2.3
1	B	146	ASP	2.3
1	D	368	ARG	2.3
1	D	350	ILE	2.3
1	D	155	TYR	2.3
1	D	290	THR	2.3
1	D	172	ARG	2.3
1	D	346	ILE	2.3
1	C	236	ASP	2.3
1	D	216	ASP	2.3
1	D	195	PHE	2.3
1	D	246	ALA	2.2
1	C	381	GLY	2.2
1	B	4	SER	2.2
1	B	328	LYS	2.2
1	D	148	LEU	2.2
1	D	335	SER	2.2
1	D	337	VAL	2.2
1	C	243	ALA	2.2
1	A	240	THR	2.2
1	B	17	SER	2.2
1	D	174	GLU	2.2
1	D	194	ARG	2.2
1	D	233	PRO	2.2
1	C	155	TYR	2.2
1	A	206	GLY	2.2
1	D	158	GLY	2.2
1	A	236	ASP	2.2
1	C	74	ALA	2.2
1	A	228	MET	2.2
1	D	300	LEU	2.2
1	C	317	GLU	2.2
1	D	364	GLU	2.2
1	C	319	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	166	LYS	2.2
1	D	237	LYS	2.2
1	C	188	ALA	2.1
1	D	229	ALA	2.1
1	C	209	GLY	2.1
1	B	350	ILE	2.1
1	A	192	ASP	2.1
1	D	49	VAL	2.1
1	D	161	ALA	2.1
1	D	264	ALA	2.1
1	A	203	ILE	2.1
1	C	336	ILE	2.1
1	C	40	GLU	2.1
1	D	220	ARG	2.1
1	A	324	CYS	2.1
1	C	237	LYS	2.1
1	D	205	LYS	2.1
1	D	157	MET	2.1
1	D	321	ALA	2.1
1	D	162	GLU	2.1
1	C	214	ASP	2.1
1	D	152	PHE	2.1
1	D	308	GLY	2.1
1	C	314	GLU	2.1
1	B	346	ILE	2.1
1	C	150	ASP	2.1
1	B	167	GLN	2.0
1	D	270	GLN	2.0
1	D	6	VAL	2.0
1	B	240	THR	2.0
1	D	191	LYS	2.0
1	B	180	VAL	2.0
1	D	323	ALA	2.0
1	D	280	THR	2.0
1	B	332	TRP	2.0
1	A	197	ASP	2.0

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

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
1	SCY	D	89	9/10	0.86	0.14	46,53,71,73	0
1	SCY	C	89	9/10	0.88	0.16	41,55,59,63	0
1	SCY	B	89	9/10	0.91	0.16	24,32,62,64	0
1	SCY	A	89	9/10	0.93	0.11	23,44,57,63	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

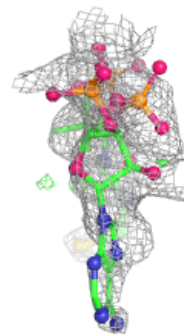
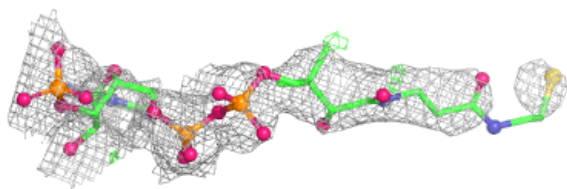
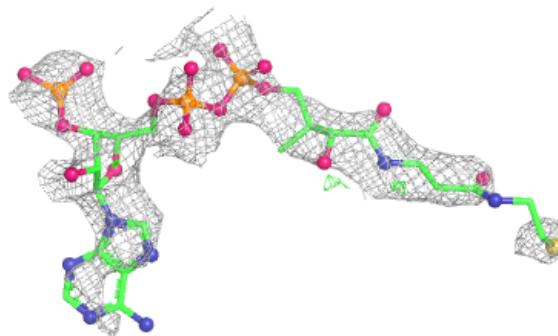
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	COA	D	401	48/48	0.73	0.20	71,105,115,116	48
2	SO4	C	403	5/5	0.77	0.10	96,96,98,99	0
2	SO4	D	402	5/5	0.80	0.14	93,94,94,94	0
2	SO4	A	401	5/5	0.80	0.15	69,76,77,78	0
3	COA	C	401	48/48	0.81	0.17	49,72,97,100	48
2	SO4	B	403	5/5	0.81	0.20	74,76,76,78	0
3	COA	A	404	48/48	0.84	0.15	34,47,66,70	48
3	COA	B	404	48/48	0.84	0.14	17,46,82,85	48
2	SO4	B	401	5/5	0.84	0.11	81,81,82,84	0
2	SO4	C	402	5/5	0.84	0.15	89,90,92,93	0
2	SO4	A	403	5/5	0.85	0.20	75,77,78,79	0
2	SO4	D	403	5/5	0.85	0.14	85,85,87,89	0
2	SO4	A	402	5/5	0.88	0.13	61,65,67,72	0
2	SO4	B	402	5/5	0.91	0.14	60,63,64,67	0

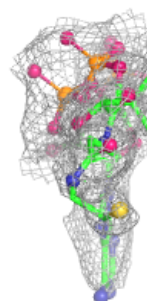
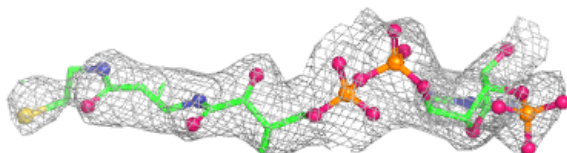
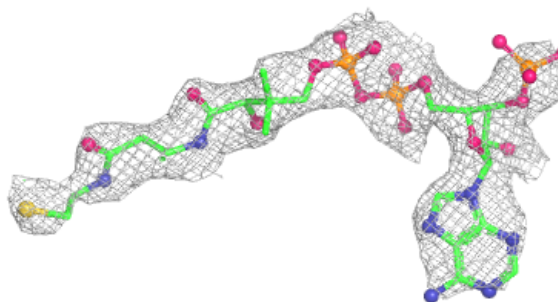
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around COA D 401:

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

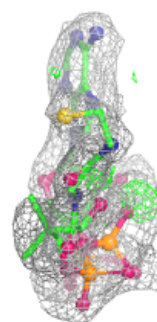
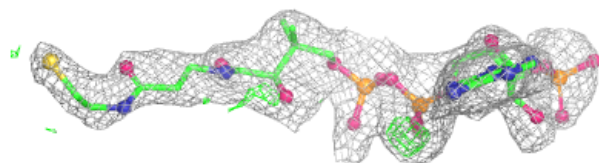
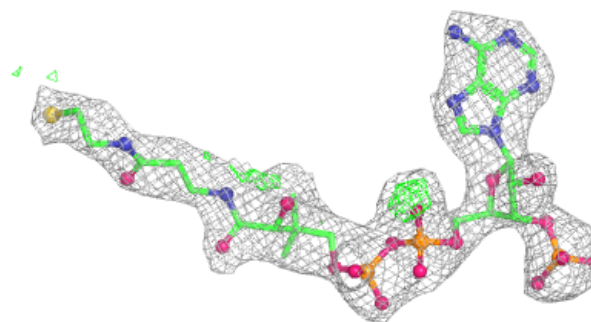
**Electron density around COA C 401:**

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

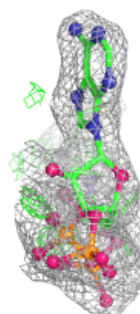
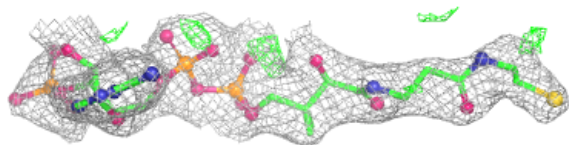
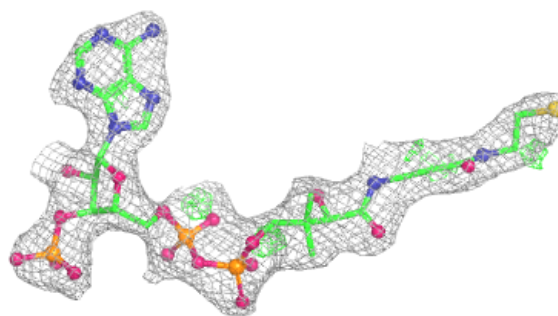


Electron density around COA A 404:

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

**Electron density around COA B 404:**

$2mF_o-DF_c$ (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.