Full wwPDB X-ray Structure Validation Report (i)

Aug 16, 2023 – 01:27 PM EDT

PDB ID	:	2AF4
Title	:	Phosphotransacetylase from Methanosarcina thermophila co-crystallized with coenzyme A
Authors	:	Lawrence, S.H.; Luther, K.B.; Ferry, J.G.; Schindelin, H.
Deposited on	:	2005-07-25
Resolution	:	2.15 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 (i) 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 (i)) were used in the production of this report:

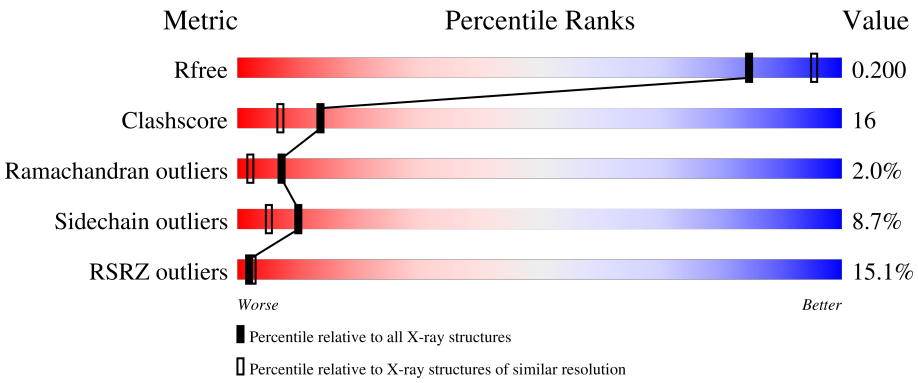
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)
RSRZ outliers	127900	2485 (2.16-2.12)

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 <=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	C	333	9%, 80%, 17%, •
1	D	333	21%, 65%, 26%, 6%, • •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5286 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.

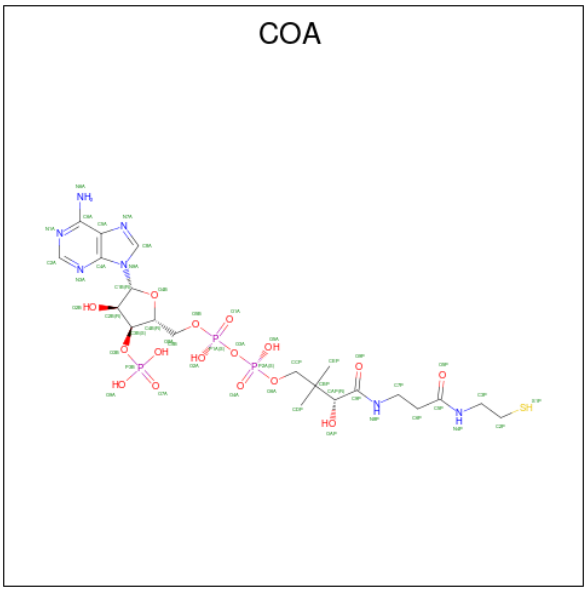
- Molecule 1 is a protein called Phosphate acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	C	332	2464	1563	404	487	10	0	0	0
1	D	331	2454	1557	402	485	10	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	159	CSO	CYS	modified residue	UNP P38503
D	159	CSO	CYS	modified residue	UNP P38503

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



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

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

- Molecule 3 is water.

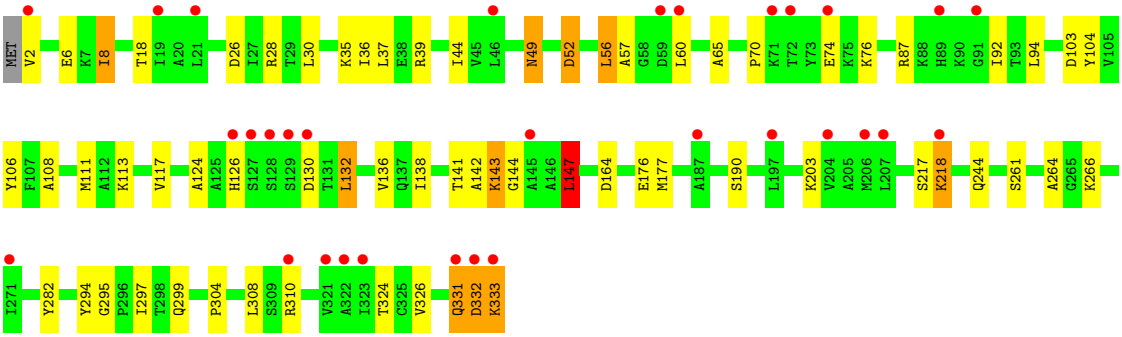
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	C	184	184	184	0	0
3	D	88	88	88	0	0

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.

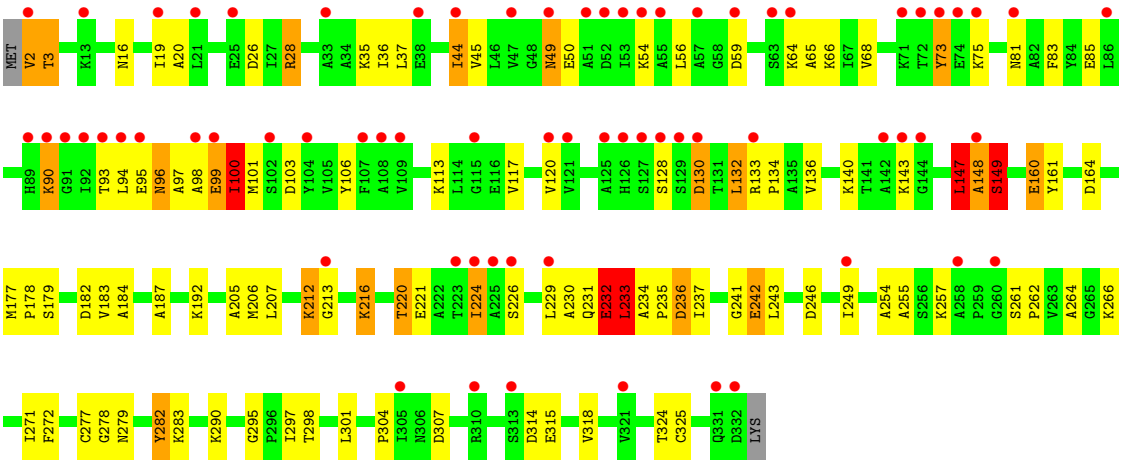
- Molecule 1: Phosphate acetyltransferase

Chain C:



- Molecule 1: Phosphate acetyltransferase

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, α, β, γ	116.49Å 116.49Å 127.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.15 19.98 – 2.15	Depositor EDS
% Data completeness (in resolution range)	98.1 (20.00-2.15) 98.1 (19.98-2.15)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	2.93 (at 2.15Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.203 , 0.272 0.216 , 0.200	Depositor DCC
R_{free} test set	2264 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	48.2	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 70.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.025 for -h,k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5286	wwPDB-VP
Average B, all atoms (Å^2)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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

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	C	0.83	0/2489	0.82	1/3368 (0.0%)
1	D	0.89	9/2479 (0.4%)	0.81	2/3357 (0.1%)
All	All	0.86	9/4968 (0.2%)	0.82	3/6725 (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	C	0	1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	231	GLN	CD-NE2	10.32	1.58	1.32
1	D	277	CYS	CB-SG	-8.82	1.67	1.82
1	D	231	GLN	CD-OE1	8.34	1.42	1.24
1	D	235	PRO	C-O	7.63	1.38	1.23
1	D	232	GLU	CD-OE2	7.55	1.33	1.25
1	D	235	PRO	C-N	7.14	1.50	1.34
1	D	232	GLU	CD-OE1	6.15	1.32	1.25
1	D	236	ASP	CG-OD2	5.79	1.38	1.25
1	D	160	GLU	CB-CG	5.60	1.62	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	232	GLU	OE1-CD-OE2	5.36	129.73	123.30
1	C	147	LEU	CB-CG-CD1	5.09	119.65	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	233	LEU	CA-CB-CG	5.02	126.84	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	144	GLY	Peptide

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	C	2464	0	2527	46	0
1	D	2454	0	2514	115	0
2	C	48	0	31	4	0
2	D	48	0	31	4	0
3	C	184	0	0	7	1
3	D	88	0	0	44	1
All	All	5286	0	5103	161	1

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 16.

All (161) 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:206:MET:HA	3:D:555:HOH:O	1.37	1.21
1:D:230:ALA:HA	3:D:578:HOH:O	1.54	1.07
1:D:233:LEU:CA	3:D:583:HOH:O	2.00	1.07
1:C:2:VAL:N	1:C:294:TYR:HH	1.59	1.01
1:D:205:ALA:O	3:D:555:HOH:O	1.80	0.97
1:D:233:LEU:HB3	3:D:578:HOH:O	1.68	0.94
1:D:233:LEU:HA	3:D:583:HOH:O	1.57	0.94
1:D:229:LEU:HG	3:D:584:HOH:O	1.73	0.86
1:D:212:LYS:NZ	1:D:241:GLY:O	2.08	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:148:ALA:O	1:D:149:SER:HB2	1.75	0.85
1:D:179:SER:HB3	3:D:576:HOH:O	1.77	0.83
1:C:218:LYS:HD3	1:D:177:MET:SD	2.19	0.83
1:D:216:LYS:NZ	1:D:216:LYS:HB3	1.95	0.82
1:C:244:GLN:HE21	1:D:279:ASN:HD21	1.26	0.79
1:D:205:ALA:C	3:D:555:HOH:O	2.20	0.78
1:D:206:MET:CA	3:D:555:HOH:O	2.05	0.78
1:D:254:ALA:O	3:D:582:HOH:O	2.02	0.77
1:D:241:GLY:C	3:D:530:HOH:O	2.24	0.76
1:D:220:THR:HG23	3:D:516:HOH:O	1.86	0.73
1:C:36:ILE:HG21	1:C:44:ILE:HD11	1.70	0.72
1:C:177:MET:HE3	3:C:680:HOH:O	1.89	0.72
1:D:213:GLY:N	3:D:587:HOH:O	2.21	0.71
1:D:220:THR:CG2	3:D:516:HOH:O	2.37	0.70
1:D:184:ALA:HB2	3:D:585:HOH:O	1.91	0.70
1:D:2:VAL:O	1:D:3:THR:HB	1.89	0.69
2:C:501:COA:P3B	2:C:501:COA:HO2A	2.15	0.69
1:D:257:LYS:O	3:D:588:HOH:O	2.10	0.69
2:C:501:COA:O7A	2:C:501:COA:O2B	2.12	0.68
1:D:233:LEU:N	3:D:583:HOH:O	2.23	0.68
1:D:26:ASP:OD1	1:D:28:ARG:HG3	1.93	0.68
1:D:99:GLU:O	1:D:101:MET:N	2.27	0.67
1:D:242:GLU:OE1	3:D:587:HOH:O	2.13	0.66
1:D:216:LYS:HB3	1:D:216:LYS:HZ2	1.58	0.66
1:D:216:LYS:HA	1:D:220:THR:HG21	1.78	0.66
1:C:18:THR:HG22	1:C:117:VAL:HG23	1.77	0.65
1:D:230:ALA:C	1:D:232:GLU:H	2.00	0.64
2:D:501:COA:O8A	2:D:501:COA:O2B	2.16	0.64
1:D:35:LYS:NZ	1:D:315:GLU:OE1	2.26	0.63
1:D:187:ALA:HB2	1:D:206:MET:CE	2.29	0.63
1:C:142:ALA:O	1:C:143:LYS:HG2	1.99	0.62
1:D:184:ALA:CB	3:D:585:HOH:O	2.45	0.62
1:C:164:ASP:HB2	3:C:541:HOH:O	1.99	0.62
2:C:501:COA:P3B	2:C:501:COA:O2B	2.56	0.62
1:D:226:SER:HA	3:D:585:HOH:O	2.00	0.61
1:C:108:ALA:HA	1:C:111:MET:HE2	1.83	0.60
1:C:177:MET:CE	3:C:680:HOH:O	2.45	0.60
1:D:242:GLU:N	3:D:530:HOH:O	2.34	0.60
1:C:218:LYS:CD	1:D:177:MET:SD	2.91	0.58
1:D:206:MET:CE	1:D:271:ILE:HG21	2.34	0.57
1:C:108:ALA:HA	1:C:111:MET:CE	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:37:LEU:HD11	1:D:65:ALA:HB2	1.86	0.57
1:D:187:ALA:HB2	1:D:206:MET:HE1	1.86	0.57
1:D:20:ALA:HB3	1:D:120:VAL:HG22	1.85	0.56
1:D:100:ILE:HG22	1:D:106:TYR:CD2	2.40	0.56
1:D:128:SER:HB2	2:D:501:COA:H1B	1.86	0.56
1:D:272:PHE:O	3:D:580:HOH:O	2.18	0.56
1:D:230:ALA:C	1:D:232:GLU:N	2.60	0.55
1:D:234:ALA:HB1	1:D:237:ILE:HG13	1.88	0.55
1:C:132:LEU:O	1:C:136:VAL:HB	2.07	0.55
1:C:190:SER:HA	1:C:299:GLN:HE22	1.71	0.55
1:D:147:LEU:O	1:D:148:ALA:CB	2.56	0.54
1:D:233:LEU:HB2	3:D:583:HOH:O	2.03	0.54
1:C:141:THR:O	1:C:143:LYS:O	2.25	0.54
1:C:49:ASN:HD22	1:C:52:ASP:H	1.56	0.53
1:D:233:LEU:CB	3:D:583:HOH:O	2.39	0.53
1:C:36:ILE:CG2	1:C:44:ILE:HD11	2.37	0.52
1:D:241:GLY:HA2	1:D:243:LEU:HG	1.91	0.52
1:D:2:VAL:O	1:D:3:THR:CB	2.58	0.52
1:D:130:ASP:N	3:D:568:HOH:O	2.43	0.51
1:C:126:HIS:NE2	1:C:130:ASP:CB	2.74	0.51
1:D:49:ASN:HD22	1:D:50:GLU:N	2.08	0.51
1:D:184:ALA:HB2	1:D:229:LEU:HD23	1.93	0.51
1:C:295:GLY:HA2	1:C:297:ILE:HG13	1.92	0.51
1:D:314:ASP:O	1:D:318:VAL:HG23	2.10	0.51
1:C:203:LYS:HE3	3:C:676:HOH:O	2.10	0.51
1:C:2:VAL:O	1:C:6:GLU:N	2.40	0.50
1:D:221:GLU:HA	1:D:224:ILE:HD11	1.92	0.50
1:D:261:SER:HB2	1:D:264:ALA:HB3	1.94	0.50
1:C:30:LEU:HD11	1:C:56:LEU:HD23	1.94	0.50
1:C:87:ARG:HG3	1:C:92:ILE:HD13	1.94	0.50
1:D:261:SER:CB	1:D:264:ALA:HB3	2.41	0.50
1:D:132:LEU:O	1:D:136:VAL:HG23	2.12	0.49
1:C:37:LEU:HD11	1:C:65:ALA:HB2	1.94	0.49
1:D:187:ALA:HB2	1:D:206:MET:HE3	1.94	0.49
1:D:19:ILE:HD13	1:D:325:CYS:SG	2.52	0.49
1:C:57:ALA:O	1:C:60:LEU:HD12	2.13	0.49
1:D:255:ALA:HA	3:D:582:HOH:O	2.12	0.49
1:D:184:ALA:CA	3:D:585:HOH:O	2.61	0.49
1:D:184:ALA:HA	3:D:585:HOH:O	2.13	0.49
1:D:304:PRO:HB2	1:D:324:THR:HG23	1.95	0.49
1:D:90:LYS:N	1:D:90:LYS:HE3	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:203:LYS:CE	3:C:676:HOH:O	2.61	0.48
1:D:81:ASN:O	1:D:85:GLU:HG2	2.14	0.48
1:D:290:LYS:NZ	3:D:586:HOH:O	2.39	0.48
1:C:126:HIS:NE2	1:C:130:ASP:HB3	2.29	0.48
1:C:304:PRO:HB2	1:C:324:THR:HG23	1.95	0.48
1:D:206:MET:HG2	3:D:555:HOH:O	2.13	0.48
1:D:206:MET:N	3:D:555:HOH:O	2.29	0.48
1:D:224:ILE:HG23	1:D:242:GLU:HG3	1.96	0.48
1:D:36:ILE:HG21	1:D:44:ILE:HD12	1.95	0.48
1:D:216:LYS:HB3	1:D:216:LYS:HZ3	1.76	0.48
1:C:113:LYS:NZ	1:C:138:ILE:O	2.38	0.47
1:C:18:THR:O	1:C:117:VAL:HG22	2.14	0.47
1:D:45:VAL:HG13	1:D:66:LYS:HG2	1.97	0.47
1:D:282:TYR:CE2	1:D:283:LYS:HE2	2.50	0.47
1:C:331:GLN:O	1:C:333:LYS:N	2.48	0.47
1:D:95:GLU:O	1:D:98:ALA:HB3	2.14	0.46
1:D:216:LYS:NZ	1:D:216:LYS:CB	2.72	0.46
1:D:83:PHE:HE2	1:D:100:ILE:HD12	1.81	0.46
1:D:179:SER:CB	3:D:576:HOH:O	2.48	0.46
1:C:147:LEU:N	1:C:147:LEU:HD12	2.31	0.45
1:C:331:GLN:O	1:C:332:ASP:C	2.53	0.45
1:D:255:ALA:CA	3:D:582:HOH:O	2.63	0.45
1:D:255:ALA:C	3:D:582:HOH:O	2.54	0.45
1:D:262:PRO:HG3	3:D:579:HOH:O	2.15	0.45
1:D:68:VAL:HG13	1:D:73:TYR:CD2	2.52	0.45
1:D:216:LYS:HZ2	1:D:216:LYS:CB	2.29	0.45
1:C:2:VAL:N	1:C:294:TYR:OH	2.35	0.45
1:C:217:SER:HB2	1:D:177:MET:CE	2.46	0.45
1:D:97:ALA:O	1:D:101:MET:HB2	2.17	0.45
2:C:501:COA:H8A	2:C:501:COA:H2B	1.82	0.45
1:D:207:LEU:HA	1:D:243:LEU:O	2.17	0.44
1:D:271:ILE:HB	3:D:555:HOH:O	2.17	0.44
1:C:331:GLN:NE2	3:C:568:HOH:O	2.50	0.44
1:D:93:THR:OG1	1:D:96:ASN:HB2	2.17	0.44
1:D:246:ASP:OD2	1:D:257:LYS:NZ	2.50	0.44
1:C:217:SER:HB2	1:D:177:MET:HE1	1.99	0.44
1:C:176:GLU:HG3	3:C:552:HOH:O	2.17	0.43
1:C:244:GLN:HE21	1:D:279:ASN:ND2	2.04	0.43
1:D:272:PHE:CG	1:D:278:GLY:HA2	2.52	0.43
1:C:26:ASP:OD1	1:C:28:ARG:HB2	2.18	0.43
1:D:161:TYR:CD1	1:D:249:ILE:HD12	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:261:SER:HB3	1:C:264:ALA:HB3	2.01	0.42
1:D:183:VAL:HG21	3:D:522:HOH:O	2.18	0.42
2:D:501:COA:O9A	3:D:581:HOH:O	2.21	0.42
1:D:49:ASN:HD22	1:D:49:ASN:C	2.23	0.42
1:D:295:GLY:HA2	1:D:297:ILE:HG13	2.01	0.42
1:C:124:ALA:HB2	1:C:308:LEU:HD13	2.01	0.42
1:D:178:PRO:HB2	1:D:183:VAL:HG23	2.00	0.42
1:D:133:ARG:N	1:D:134:PRO:HD2	2.34	0.42
1:D:182:ASP:O	1:D:183:VAL:C	2.54	0.42
1:D:224:ILE:HG23	1:D:242:GLU:CD	2.40	0.42
1:C:35:LYS:O	1:C:39:ARG:HG3	2.20	0.42
1:C:103:ASP:HB3	1:C:106:TYR:HB2	2.01	0.42
1:D:212:LYS:HD3	3:D:531:HOH:O	2.20	0.42
1:C:8:ILE:HG13	1:C:326:VAL:HG21	2.02	0.41
1:D:147:LEU:O	1:D:148:ALA:HB2	2.20	0.41
1:D:130:ASP:O	1:D:134:PRO:CD	2.68	0.41
1:D:236:ASP:N	3:D:502:HOH:O	2.37	0.41
1:D:233:LEU:CB	3:D:578:HOH:O	2.46	0.41
1:D:226:SER:CA	3:D:585:HOH:O	2.64	0.41
1:D:16:ASN:ND2	3:D:513:HOH:O	2.51	0.41
1:D:207:LEU:HD12	1:D:272:PHE:CE2	2.56	0.41
1:D:307:ASP:HB3	2:D:501:COA:C2A	2.51	0.41
1:C:70:PRO:HG2	1:C:104:TYR:CD2	2.55	0.41
1:D:83:PHE:CE2	1:D:100:ILE:HD12	2.55	0.41
1:D:272:PHE:CD1	1:D:278:GLY:HA2	2.56	0.41
1:D:206:MET:HE3	1:D:271:ILE:HG13	2.03	0.40
1:D:206:MET:HE2	1:D:271:ILE:HG21	2.04	0.40
1:D:68:VAL:HG13	1:D:73:TYR:CG	2.57	0.40
1:D:298:THR:HG21	1:D:301:LEU:HD11	2.02	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:685:HOH:O	3:D:553:HOH:O[3_655]	2.07	0.13

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	C	329/333 (99%)	310 (94%)	16 (5%)	3 (1%)	17 10
1	D	328/333 (98%)	293 (89%)	25 (8%)	10 (3%)	4 1
All	All	657/666 (99%)	603 (92%)	41 (6%)	13 (2%)	7 2

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	74	GLU
1	D	3	THR
1	D	99	GLU
1	D	100	ILE
1	D	148	ALA
1	D	149	SER
1	D	73	TYR
1	D	140	LYS
1	C	310	ARG
1	C	332	ASP
1	D	147	LEU
1	D	212	LYS
1	D	143	LYS

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	C	259/260 (100%)	245 (95%)	14 (5%)	22 17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	D	258/260 (99%)	227 (88%)	31 (12%)	5 2
All	All	517/520 (99%)	472 (91%)	45 (9%)	10 5

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	8	ILE
1	C	49	ASN
1	C	52	ASP
1	C	56	LEU
1	C	76	LYS
1	C	94	LEU
1	C	132	LEU
1	C	143	LYS
1	C	147	LEU
1	C	218	LYS
1	C	266	LYS
1	C	282	TYR
1	C	331	GLN
1	C	333	LYS
1	D	2	VAL
1	D	28	ARG
1	D	44	ILE
1	D	49	ASN
1	D	54	LYS
1	D	56	LEU
1	D	59	ASP
1	D	64	LYS
1	D	75	LYS
1	D	90	LYS
1	D	94	LEU
1	D	96	ASN
1	D	100	ILE
1	D	103	ASP
1	D	113	LYS
1	D	117	VAL
1	D	130	ASP
1	D	132	LEU
1	D	147	LEU
1	D	149	SER
1	D	160	GLU
1	D	164	ASP

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Mol	Chain	Res	Type
1	D	192	LYS
1	D	216	LYS
1	D	220	THR
1	D	224	ILE
1	D	232	GLU
1	D	233	LEU
1	D	242	GLU
1	D	266	LYS
1	D	282	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	49	ASN
1	C	96	ASN
1	C	299	GLN
1	D	49	ASN
1	D	279	ASN
1	D	299	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)

2 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	CSO	D	159	1	3,6,7	0.57	0	0,6,8	-	-
1	CSO	C	159	1	3,6,7	0.61	0	0,6,8	-	-

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	CSO	D	159	1	-	0/1/5/7	-
1	CSO	C	159	1	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	COA	D	501	1	41,50,50	1.76	4 (9%)	52,75,75	1.40	5 (9%)
2	COA	C	501	1	41,50,50	1.86	4 (9%)	52,75,75	1.94	15 (28%)

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
2	COA	D	501	1	-	10/44/64/64	0/3/3/3
2	COA	C	501	1	-	18/44/64/64	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	501	COA	O9P-C9P	8.63	1.40	1.23
2	C	501	COA	O9P-C9P	8.10	1.39	1.23
2	C	501	COA	P3B-O3B	4.28	1.67	1.59
2	C	501	COA	C2A-N3A	4.23	1.38	1.32
2	D	501	COA	C2A-N3A	3.81	1.38	1.32
2	C	501	COA	C2A-N1A	3.49	1.40	1.33
2	D	501	COA	P3B-O3B	3.47	1.65	1.59
2	D	501	COA	C2A-N1A	3.07	1.39	1.33

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	501	COA	N3A-C2A-N1A	-7.09	117.59	128.68
2	D	501	COA	N3A-C2A-N1A	-5.73	119.73	128.68
2	C	501	COA	C7P-C6P-C5P	-5.52	103.17	112.36
2	D	501	COA	P2A-O3A-P1A	-4.25	118.24	132.83
2	C	501	COA	C3B-C2B-C1B	3.31	107.21	99.89
2	C	501	COA	CDP-CBP-CAP	3.29	114.52	108.82
2	C	501	COA	N6A-C6A-N1A	3.02	124.85	118.57
2	D	501	COA	CEP-CBP-CAP	2.86	113.78	108.82
2	C	501	COA	CEP-CBP-CAP	2.85	113.77	108.82
2	C	501	COA	C5A-C6A-N6A	-2.61	116.39	120.35
2	C	501	COA	C3P-N4P-C5P	-2.39	118.40	122.84
2	C	501	COA	O5P-C5P-C6P	-2.35	117.71	122.02
2	C	501	COA	O3B-C3B-C4B	2.26	118.27	110.08
2	C	501	COA	O2A-P1A-O1A	2.24	123.33	112.24
2	D	501	COA	C1B-N9A-C4A	-2.13	122.90	126.64
2	C	501	COA	O5A-P2A-O6A	-2.12	97.91	107.75
2	C	501	COA	O4B-C4B-C3B	2.08	109.33	104.87
2	D	501	COA	O4B-C4B-C3B	2.07	109.31	104.87
2	C	501	COA	C2A-N1A-C6A	2.02	122.22	118.75
2	C	501	COA	OAP-CAP-CBP	2.01	114.98	110.25

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	501	COA	CCP-O6A-P2A-O3A
2	C	501	COA	CCP-O6A-P2A-O4A
2	C	501	COA	CCP-O6A-P2A-O5A
2	C	501	COA	OAP-CAP-CBP-CCP
2	C	501	COA	C9P-CAP-CBP-CCP
2	C	501	COA	OAP-CAP-CBP-CDP
2	C	501	COA	C9P-CAP-CBP-CDP
2	C	501	COA	OAP-CAP-CBP-CEP
2	C	501	COA	C9P-CAP-CBP-CEP
2	C	501	COA	S1P-C2P-C3P-N4P
2	D	501	COA	C9P-CAP-CBP-CCP
2	D	501	COA	C9P-CAP-CBP-CDP
2	D	501	COA	C9P-CAP-CBP-CEP
2	C	501	COA	C2B-C3B-O3B-P3B
2	D	501	COA	C2B-C3B-O3B-P3B
2	C	501	COA	C4B-C3B-O3B-P3B
2	D	501	COA	C4B-C3B-O3B-P3B
2	C	501	COA	CEP-CBP-CCP-O6A
2	D	501	COA	OAP-CAP-CBP-CDP
2	D	501	COA	OAP-CAP-CBP-CEP
2	C	501	COA	C2P-C3P-N4P-C5P
2	D	501	COA	C4B-C5B-O5B-P1A
2	C	501	COA	C4B-C5B-O5B-P1A
2	D	501	COA	OAP-CAP-CBP-CCP
2	C	501	COA	CDP-CBP-CCP-O6A
2	C	501	COA	N8P-C9P-CAP-CBP
2	C	501	COA	C3B-C4B-C5B-O5B
2	D	501	COA	CCP-O6A-P2A-O4A

There are no ring outliers.

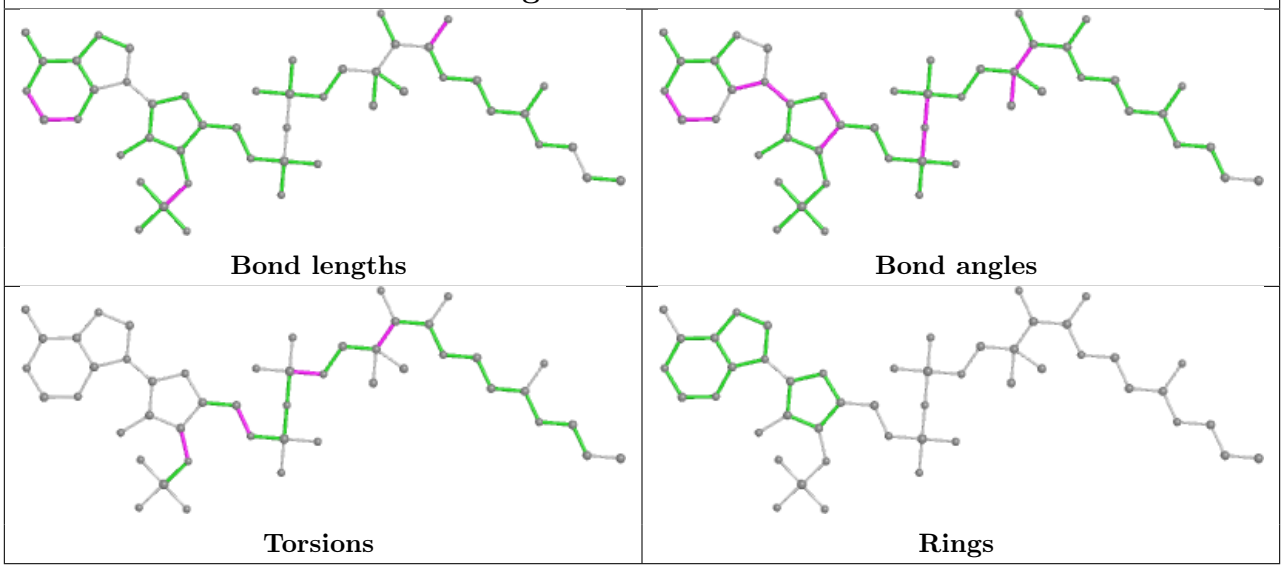
2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	501	COA	4	0
2	C	501	COA	4	0

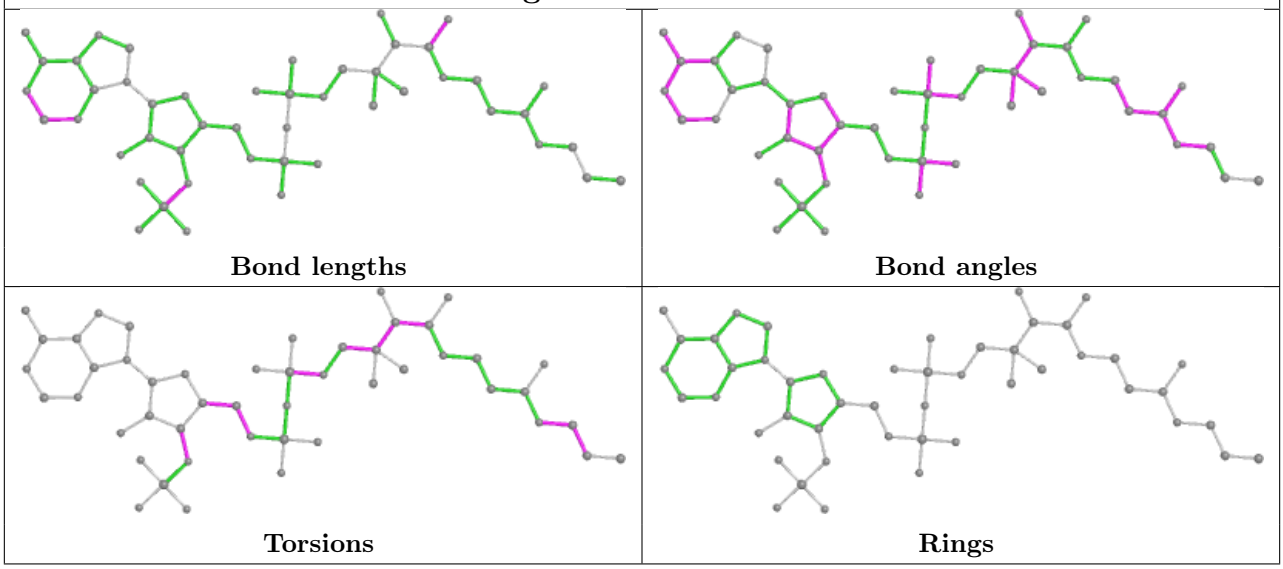
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.

Ligand COA D 501



Ligand COA C 501



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	C	331/333 (99%)	0.35	31 (9%) 8 11	40, 61, 94, 118	0
1	D	330/333 (99%)	1.13	69 (20%) 1 1	42, 86, 153, 184	0
All	All	661/666 (99%)	0.74	100 (15%) 2 2	40, 71, 137, 184	0

All (100) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	2	VAL	9.5
1	D	55	ALA	8.7
1	D	89	HIS	7.4
1	D	129	SER	6.0
1	D	59	ASP	6.0
1	D	332	ASP	5.8
1	D	72	THR	5.5
1	D	126	HIS	5.3
1	D	51	ALA	5.0
1	D	86	LEU	4.9
1	C	333	LYS	4.8
1	D	94	LEU	4.7
1	D	104	TYR	4.7
1	D	331	GLN	4.7
1	D	125	ALA	4.6
1	D	54	LYS	4.5
1	D	71	LYS	4.5
1	D	74	GLU	4.5
1	C	59	ASP	4.3
1	D	143	LYS	4.2
1	D	130	ASP	4.1
1	D	91	GLY	3.9
1	D	21	LEU	3.8
1	D	305	ILE	3.8

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Mol	Chain	Res	Type	RSRZ
1	D	127	SER	3.7
1	D	2	VAL	3.7
1	D	92	ILE	3.7
1	C	72	THR	3.6
1	C	21	LEU	3.6
1	D	90	LYS	3.6
1	C	310	ARG	3.5
1	C	60	LEU	3.5
1	D	57	ALA	3.4
1	C	321	VAL	3.4
1	D	121	VAL	3.4
1	D	148	ALA	3.4
1	D	109	VAL	3.4
1	D	260	GLY	3.4
1	D	128	SER	3.4
1	D	38	GLU	3.3
1	D	142	ALA	3.3
1	D	120	VAL	3.1
1	D	144	GLY	3.1
1	D	81	ASN	3.1
1	D	49	ASN	3.1
1	D	93	THR	3.1
1	D	310	ARG	3.1
1	D	225	ALA	3.1
1	D	73	TYR	3.1
1	C	129	SER	3.0
1	C	271	ILE	2.9
1	C	128	SER	2.9
1	D	108	ALA	2.9
1	D	258	ALA	2.9
1	D	224	ILE	2.8
1	D	33	ALA	2.8
1	C	91	GLY	2.7
1	D	133	ARG	2.7
1	D	19	ILE	2.6
1	D	52	ASP	2.6
1	D	95	GLU	2.6
1	D	249	ILE	2.6
1	D	44	ILE	2.5
1	D	25	GLU	2.5
1	D	102	SER	2.5
1	D	229	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	187	ALA	2.4
1	D	98	ALA	2.4
1	D	63	SER	2.4
1	D	213	GLY	2.4
1	C	207	LEU	2.4
1	C	126	HIS	2.4
1	C	74	GLU	2.3
1	D	115	GLY	2.3
1	D	53	ILE	2.3
1	C	322	ALA	2.3
1	C	89	HIS	2.3
1	D	107	PHE	2.3
1	C	127	SER	2.3
1	D	75	LYS	2.3
1	C	331	GLN	2.3
1	C	204	VAL	2.3
1	D	223	THR	2.3
1	D	47	VAL	2.2
1	D	99	GLU	2.2
1	C	46	LEU	2.2
1	C	197	LEU	2.2
1	D	313	SER	2.2
1	C	130	ASP	2.2
1	C	332	ASP	2.1
1	D	226	SER	2.1
1	C	206	MET	2.1
1	C	145	ALA	2.1
1	C	218	LYS	2.1
1	C	19	ILE	2.0
1	C	71	LYS	2.0
1	D	321	VAL	2.0
1	D	13	LYS	2.0
1	D	64	LYS	2.0
1	C	323	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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
1	CSO	D	159	7/8	0.85	0.13	61,64,66,69	0
1	CSO	C	159	7/8	0.89	0.09	58,61,63,67	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

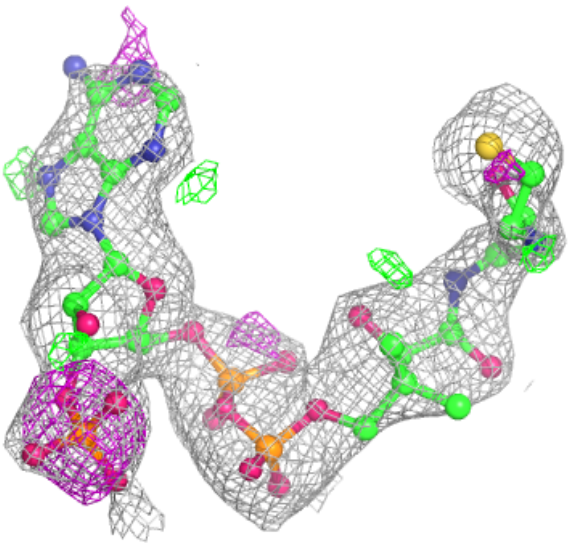
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

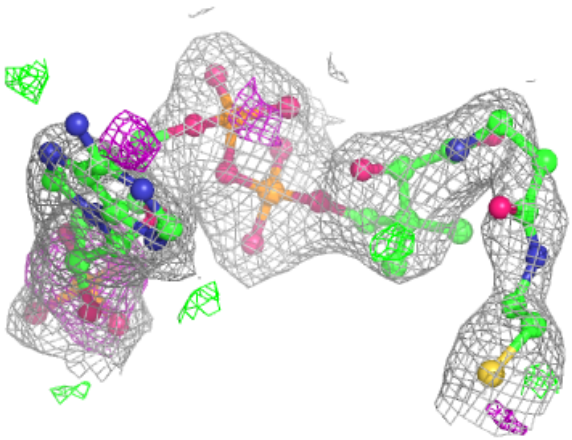
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	COA	D	501	48/48	0.91	0.18	61,81,96,99	0
2	COA	C	501	48/48	0.92	0.12	46,63,92,96	0

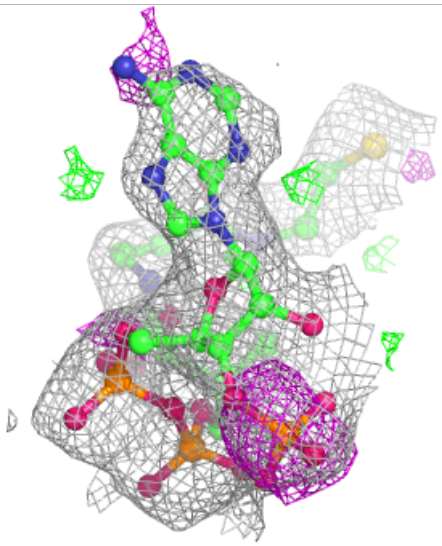
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around COA D 501:

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

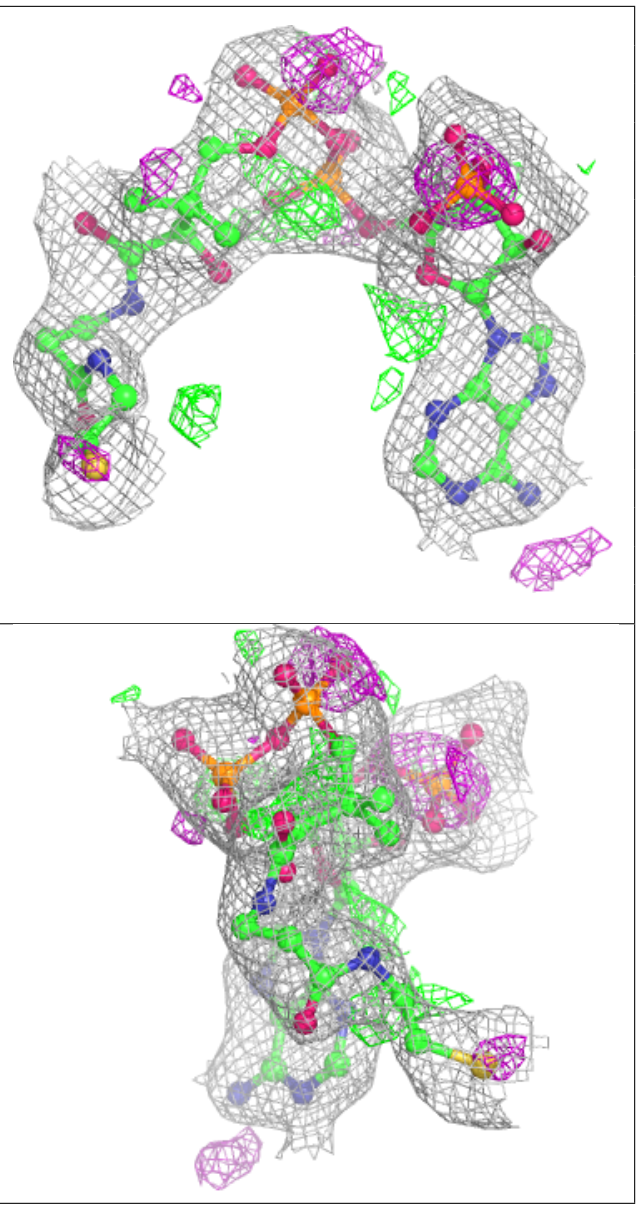






Electron density around COA C 501:

$2mF_o$-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.