



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:42 PM UTC

PDB ID : 5ZAI / pdb_00005zai
Title : Crystal structure of 3-Hydroxypropionyl-CoA dehydratase from Metallosphaera sedula
Authors : Lee, D.; Kim, K.J.
Deposited on : 2018-02-07
Resolution : 1.80 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

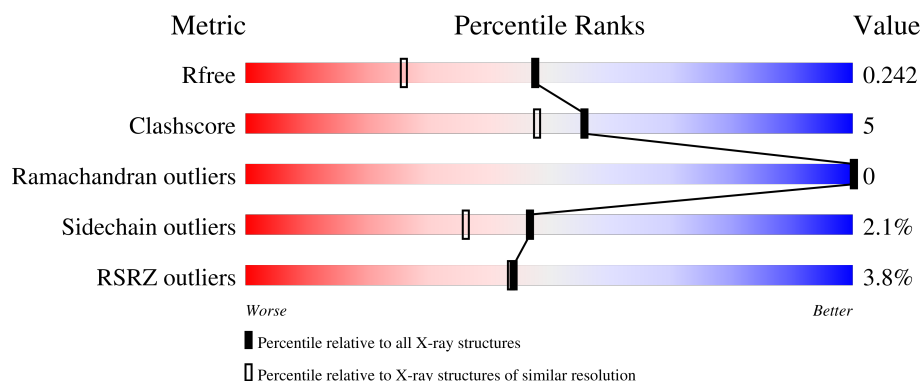
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	259	2% 90% 9% ..
1	B	259	5% 88% 10% ..
1	C	259	2% 89% 11%
1	D	259	4% 88% 11%
1	E	259	5% 88% 11% .

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Mol	Chain	Length	Quality of chain
1	F	259	5% 89% 10%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13087 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.

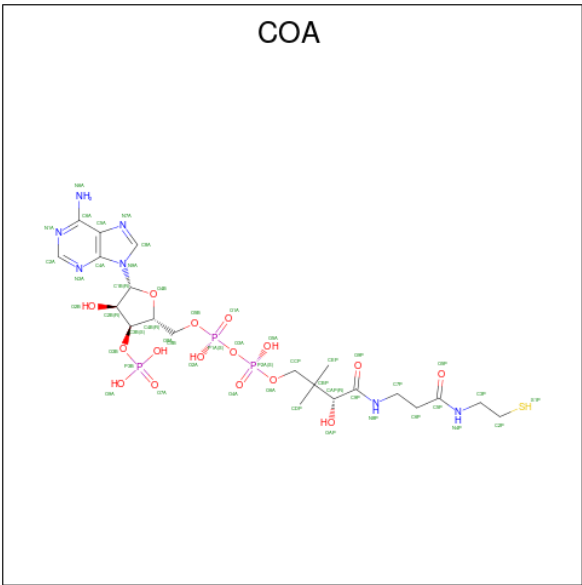
- Molecule 1 is a protein called 3-hydroxypropionyl-coenzyme A dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	257	Total	C	N	O	S	0	1	0
			1986	1262	342	374	8			
1	B	257	Total	C	N	O	S	0	3	0
			2008	1274	350	376	8			
1	C	259	Total	C	N	O	S	0	1	0
			1996	1268	343	377	8			
1	D	258	Total	C	N	O	S	0	1	0
			1990	1264	343	375	8			
1	E	257	Total	C	N	O	S	0	1	0
			1986	1262	342	374	8			
1	F	257	Total	C	N	O	S	0	0	0
			1975	1256	338	373	8			

There are 6 discrepancies between the modelled and reference sequences:

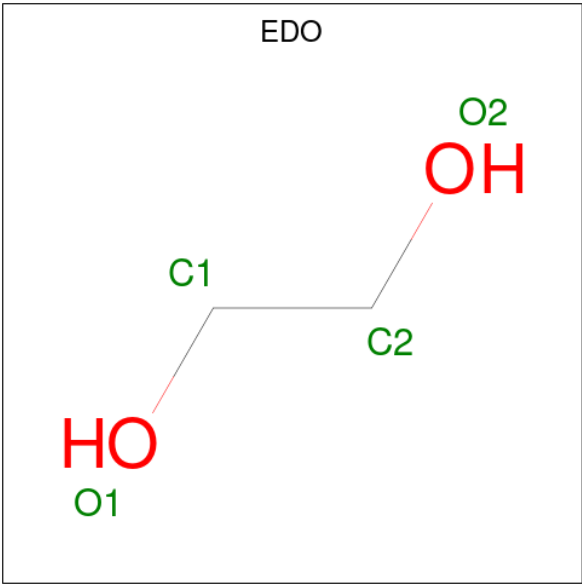
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A4YI89
B	1	MET	-	initiating methionine	UNP A4YI89
C	1	MET	-	initiating methionine	UNP A4YI89
D	1	MET	-	initiating methionine	UNP A4YI89
E	1	MET	-	initiating methionine	UNP A4YI89
F	1	MET	-	initiating methionine	UNP A4YI89

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



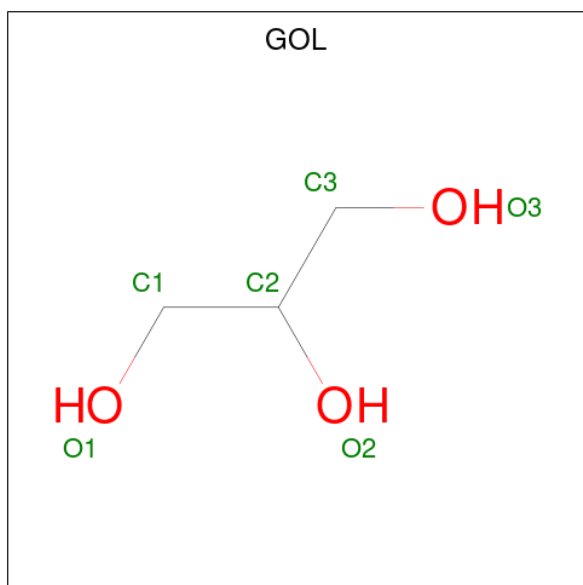
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 48	C 21	N 7	O 16	P 3	S 1	0	0
2	B	1	Total 48	C 21	N 7	O 16	P 3	S 1	0	0
2	C	1	Total 48	C 21	N 7	O 16	P 3	S 1	0	0
2	E	1	Total 48	C 21	N 7	O 16	P 3	S 1	0	0

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is water.

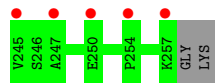
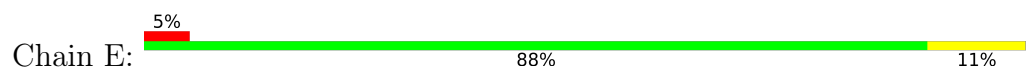
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	185	Total	O	0	0
			185	185		
5	B	129	Total	O	0	0
			129	129		
5	C	114	Total	O	0	0
			114	114		
5	D	173	Total	O	0	0
			173	173		
5	E	110	Total	O	0	0
			110	110		
5	F	139	Total	O	0	0
			139	139		

- Molecule 1: 3-hydroxypropionyl-coenzyme A dehydratase

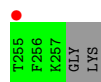
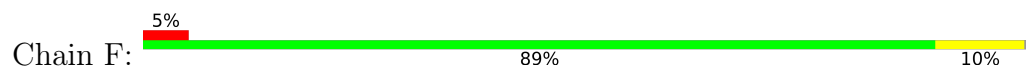




- Molecule 1: 3-hydroxypropionyl-coenzyme A dehydratase



- Molecule 1: 3-hydroxypropionyl-coenzyme A dehydratase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	84.69Å 130.17Å 84.79Å 90.00° 119.57° 90.00°	Depositor
Resolution (Å)	25.83 – 1.80 25.83 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.0 (25.83-1.80) 98.4 (25.83-1.80)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.183 , 0.229 0.197 , 0.242	Depositor DCC
R_{free} test set	7078 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	17.4	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 43.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for -h-l,k,h 0.000 for l,k,-h-l 0.016 for h,-k,-h-l 0.017 for -h-l,-k,l 0.019 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13087	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% 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: GOL, EDO, 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	0.97	3/2014 (0.1%)	1.12	1/2710 (0.0%)
1	B	0.92	1/2036 (0.0%)	1.11	0/2738
1	C	0.85	0/2024	1.10	1/2723 (0.0%)
1	D	0.97	0/2018	1.18	2/2715 (0.1%)
1	E	0.88	0/2014	1.14	2/2710 (0.1%)
1	F	0.89	1/2003 (0.0%)	1.08	1/2696 (0.0%)
All	All	0.91	5/12109 (0.0%)	1.12	7/16292 (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	A	0	4
1	B	0	2
All	All	0	6

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	149	THR	C-N	-7.23	1.23	1.33
1	A	150[A]	ARG	C-N	-6.44	1.25	1.33
1	A	150[B]	ARG	C-N	-6.44	1.25	1.33
1	B	135	ASN	N-CA	5.86	1.53	1.46
1	F	227	LEU	C-O	5.83	1.30	1.24

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	61	PHE	N-CA-C	-7.83	102.33	111.03
1	E	61	PHE	N-CA-C	-6.24	104.40	111.14
1	C	139	TYR	CB-CA-C	6.09	118.72	110.37
1	F	61	PHE	N-CA-C	-5.98	104.11	111.40
1	A	149	THR	O-C-N	-5.94	114.47	122.43
1	D	11	GLU	CB-CA-C	5.70	119.94	111.17
1	E	13	ASN	CB-CA-C	-5.18	100.69	110.01

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	149	THR	Mainchain
1	A	150[A]	ARG	Sidechain
1	A	180	ARG	Sidechain
1	B	180	ARG	Sidechain
1	B	21	ARG	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1986	0	2066	19	0
1	B	2008	0	2090	21	0
1	C	1996	0	2075	29	0
1	D	1990	0	2069	22	0
1	E	1986	0	2066	20	0
1	F	1975	0	2054	17	0
2	A	48	0	32	0	0
2	B	48	0	32	0	0
2	C	48	0	32	5	0
2	E	48	0	32	2	0
3	A	16	0	24	1	0
3	B	4	0	6	0	0
3	C	4	0	6	2	0
3	D	12	0	18	4	0
3	F	8	0	12	0	0
4	A	12	0	16	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	6	0	8	0	0
4	C	12	0	16	0	0
4	D	18	0	24	0	0
4	E	6	0	8	0	0
4	F	6	0	8	0	0
5	A	185	0	0	7	0
5	B	129	0	0	5	0
5	C	114	0	0	6	0
5	D	173	0	0	4	0
5	E	110	0	0	1	0
5	F	139	0	0	1	0
All	All	13087	0	12694	116	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 5.

All (116) 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:C:166:ARG:HH22	2:C:301:COA:CEP	1.91	0.84
5:C:511:HOH:O	1:E:74:THR:HG21	1.79	0.81
1:D:179:ASN:ND2	5:D:401:HOH:O	2.15	0.80
1:A:210:LYS:HD2	1:B:162:MET:HE1	1.62	0.79
1:A:230:VAL:HG12	1:F:230:VAL:HG12	1.64	0.79
1:F:246:SER:O	1:F:250:GLU:HG2	1.84	0.78
5:A:406:HOH:O	1:D:74:THR:HG22	1.85	0.77
1:F:40:VAL:HG13	1:F:95:LEU:HD11	1.66	0.77
1:B:210:LYS:HD3	1:C:162:MET:HE1	1.67	0.75
5:A:406:HOH:O	1:D:74:THR:CG2	2.39	0.69
1:A:214:ASN:HD21	1:B:154:LYS:NZ	1.91	0.69
1:C:166:ARG:HH22	2:C:301:COA:H143	1.58	0.68
1:A:214:ASN:HD21	1:B:154:LYS:HZ2	1.42	0.67
1:C:125:GLU:O	5:C:401:HOH:O	2.13	0.65
5:C:411:HOH:O	1:E:74:THR:HG23	1.98	0.62
1:F:179:ASN:ND2	5:F:401:HOH:O	2.34	0.60
1:D:173:GLU:OE2	5:D:402:HOH:O	2.17	0.60
1:D:173:GLU:OE1	1:D:181:VAL:HG22	2.02	0.59
1:F:106:TYR:CE1	1:F:166:ARG:NH1	2.71	0.58
1:C:160:MET:HG3	3:C:302:EDO:H21	1.85	0.58
1:D:66:ASP:OD1	1:D:68:THR:HG23	2.04	0.57
1:E:74:THR:HG22	1:E:77:GLU:H	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:166:ARG:NH2	2:C:301:COA:CEP	2.66	0.56
1:F:67:ILE:HG23	1:F:70:PHE:CD2	2.40	0.56
1:F:239:GLU:H	1:F:239:GLU:CD	2.15	0.55
3:D:301:EDO:H11	5:D:476:HOH:O	2.06	0.55
3:A:302:EDO:H21	5:A:557:HOH:O	2.07	0.54
1:C:182:VAL:HG11	1:C:190:GLU:HG3	1.90	0.54
1:C:123:ALA:O	1:C:181:VAL:HA	2.08	0.54
1:E:182:VAL:HG11	1:E:190:GLU:HG3	1.91	0.53
1:B:150[B]:ARG:NH1	5:B:401:HOH:O	2.16	0.53
1:A:210:LYS:CD	1:B:162:MET:HE1	2.35	0.52
3:C:302:EDO:C2	5:C:404:HOH:O	2.58	0.52
1:E:10:LYS:HG3	1:E:49:ILE:HD11	1.91	0.52
1:D:129:LEU:HD12	1:D:129:LEU:N	2.25	0.51
1:A:28:LEU:HD23	1:A:32:LEU:HD22	1.92	0.51
1:B:22:PRO:HD2	5:B:460:HOH:O	2.10	0.51
1:B:174:LYS:NZ	5:B:402:HOH:O	2.35	0.51
3:D:301:EDO:C1	5:D:476:HOH:O	2.58	0.51
1:C:15:PHE:CD2	1:C:43:ALA:HB2	2.46	0.50
1:C:215:ARG:CZ	1:D:222:LEU:HD23	2.42	0.49
1:C:166:ARG:HG2	5:C:494:HOH:O	2.11	0.49
1:E:166:ARG:NH1	2:E:301:COA:H141	2.27	0.49
1:C:108:LEU:HD12	2:C:301:COA:H131	1.95	0.49
1:A:28:LEU:CD2	1:A:32:LEU:HD22	2.43	0.48
1:A:10:LYS:HE2	5:A:476:HOH:O	2.13	0.48
1:E:19:LEU:HD22	1:E:32:LEU:HD21	1.96	0.48
1:C:230:VAL:CG1	1:D:231:GLY:HA2	2.44	0.48
1:C:231:GLY:HA2	1:D:230:VAL:CG1	2.44	0.48
1:D:40:VAL:HG13	1:D:95:LEU:HD11	1.95	0.48
1:A:236:PHE:CD2	1:A:241:LYS:HE3	2.49	0.48
1:B:36:LEU:O	1:B:40:VAL:HG12	2.14	0.47
1:C:21:ARG:H	1:C:26:ASN:HD22	1.63	0.47
1:E:10:LYS:HG3	1:E:49:ILE:CD1	2.45	0.47
1:C:166:ARG:NH2	2:C:301:COA:H141	2.30	0.47
1:D:37:ASP:OD1	1:D:91:LYS:CE	2.63	0.47
1:D:123:ALA:O	1:D:181:VAL:HA	2.15	0.47
1:D:159:GLU:OE2	1:F:180:ARG:NH2	2.48	0.47
1:E:166:ARG:NH1	2:E:301:COA:CEP	2.79	0.46
1:E:5:THR:OG1	1:E:32:LEU:HA	2.16	0.46
1:E:201:LYS:NZ	1:F:135:ASN:OD1	2.49	0.46
1:A:5:THR:OG1	1:A:32:LEU:HA	2.15	0.45
1:F:251:LYS:O	1:F:251:LYS:HG2	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:ALA:O	1:A:181:VAL:HA	2.16	0.45
1:D:13:ASN:HB2	1:D:50:ARG:HG3	1.99	0.45
1:D:13:ASN:OD1	3:D:302:EDO:C1	2.64	0.45
1:F:180:ARG:NH1	1:F:190:GLU:OE1	2.44	0.45
1:B:197:LYS:HD2	1:C:163:THR:HB	1.98	0.45
1:A:72:GLN:HG3	5:A:449:HOH:O	2.16	0.45
1:F:106:TYR:HE1	1:F:166:ARG:NH1	2.13	0.44
1:B:40:VAL:HG23	1:B:95:LEU:HD21	1.99	0.44
1:C:230:VAL:HG12	1:D:230:VAL:HG12	1.99	0.44
1:D:50:ARG:HD2	1:D:199:ALA:O	2.18	0.44
1:E:236:PHE:HZ	1:F:70:PHE:HA	1.83	0.44
4:A:307:GOL:H31	5:C:425:HOH:O	2.17	0.44
1:A:230:VAL:CG1	1:F:231:GLY:HA2	2.48	0.44
1:F:123:ALA:O	1:F:181:VAL:HA	2.17	0.43
1:B:123:ALA:O	1:B:181:VAL:HA	2.18	0.43
1:D:44:GLU:CD	1:D:95:LEU:HD22	2.43	0.43
1:E:123:ALA:O	1:E:181:VAL:HA	2.19	0.43
1:A:149:THR:HG23	1:A:154:LYS:HA	1.99	0.43
1:C:149:THR:HG23	1:C:154:LYS:HA	2.01	0.43
1:E:170:LYS:HG3	5:E:410:HOH:O	2.17	0.43
1:C:60:ALA:HB1	1:C:106:TYR:HB2	1.99	0.43
1:E:219:SER:HB3	1:E:220:PRO:HD2	2.01	0.43
1:F:32:LEU:C	1:F:32:LEU:HD23	2.43	0.43
1:C:13[B]:ASN:OD1	1:C:14:LEU:HD12	2.19	0.42
1:A:50:ARG:HD3	5:A:499:HOH:O	2.19	0.42
1:B:139:TYR:HB2	1:B:140:PRO:CD	2.49	0.42
1:B:210:LYS:CD	1:C:162:MET:HE1	2.43	0.42
1:E:71:ASN:ND2	1:E:72:GLN:HG2	2.34	0.42
1:E:128:GLN:HB3	1:E:166:ARG:HD2	2.01	0.42
1:B:104:ASN:ND2	1:B:104:ASN:H	2.18	0.42
1:C:13[B]:ASN:OD1	1:C:14:LEU:CD1	2.68	0.42
1:C:215:ARG:HA	1:C:215:ARG:HD3	1.90	0.41
1:B:241:LYS:O	1:B:245:VAL:HG23	2.21	0.41
1:D:13:ASN:OD1	3:D:302:EDO:H12	2.20	0.41
1:C:11:GLU:OE1	1:C:192:ARG:NH1	2.40	0.41
1:E:34:GLU:O	1:E:38:ARG:HG3	2.21	0.41
1:E:169:GLY:C	1:E:181:VAL:HG11	2.46	0.41
1:C:60:ALA:CB	1:C:106:TYR:HB2	2.50	0.41
1:C:123:ALA:HB3	1:C:181:VAL:HG12	2.02	0.41
1:A:98:PRO:HA	1:A:119:ASP:OD2	2.21	0.41
1:C:14:LEU:HD12	1:C:14:LEU:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:158:LEU:HD23	1:E:158:LEU:HA	1.92	0.41
1:A:129:LEU:N	1:A:129:LEU:HD12	2.36	0.41
1:A:150[A]:ARG:HD3	5:A:455:HOH:O	2.20	0.40
1:B:69:GLN:CD	5:B:441:HOH:O	2.64	0.40
1:B:156[A]:ARG:NH1	5:B:413:HOH:O	2.54	0.40
1:C:5:THR:O	1:C:20:ASN:N	2.43	0.40
1:D:32:LEU:C	1:D:32:LEU:HD23	2.47	0.40
1:B:215:ARG:HA	1:B:215:ARG:HD3	1.82	0.40
1:B:222:LEU:HD23	1:B:222:LEU:HA	1.94	0.40
1:A:34:GLU:OE1	1:A:38:ARG:NH2	2.55	0.40
1:B:5:THR:OG1	1:B:32:LEU:HA	2.22	0.40
1:D:156:ARG:NH1	1:F:179:ASN:O	2.41	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	256/259 (99%)	251 (98%)	5 (2%)	0	100	100
1	B	258/259 (100%)	253 (98%)	5 (2%)	0	100	100
1	C	258/259 (100%)	253 (98%)	5 (2%)	0	100	100
1	D	257/259 (99%)	254 (99%)	3 (1%)	0	100	100
1	E	256/259 (99%)	253 (99%)	3 (1%)	0	100	100
1	F	255/259 (98%)	252 (99%)	3 (1%)	0	100	100
All	All	1540/1554 (99%)	1516 (98%)	24 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	209/209 (100%)	206 (99%)	3 (1%)	59	52
1	B	211/209 (101%)	206 (98%)	5 (2%)	43	31
1	C	210/209 (100%)	209 (100%)	1 (0%)	81	80
1	D	209/209 (100%)	203 (97%)	6 (3%)	37	25
1	E	209/209 (100%)	205 (98%)	4 (2%)	50	41
1	F	208/209 (100%)	201 (97%)	7 (3%)	32	20
All	All	1256/1254 (100%)	1230 (98%)	26 (2%)	47	36

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	80	LYS
1	A	222	LEU
1	A	232	TRP
1	B	40	VAL
1	B	181	VAL
1	B	197	LYS
1	B	232	TRP
1	B	249	LEU
1	C	232	TRP
1	D	59	LYS
1	D	95	LEU
1	D	166	ARG
1	D	218	ASP
1	D	232	TRP
1	D	246	SER
1	E	57	LYS
1	E	74	THR
1	E	189	GLN
1	E	218	ASP
1	F	66	ASP
1	F	128	GLN
1	F	197	LYS

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Mol	Chain	Res	Type
1	F	222	LEU
1	F	236	PHE
1	F	239	GLU
1	F	253	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	ASN
1	A	69	GLN
1	A	72	GLN
1	A	179	ASN
1	A	186	ASN
1	A	214	ASN
1	B	71	ASN
1	B	104	ASN
1	C	26	ASN
1	C	186	ASN
1	D	42	GLN
1	D	179	ASN
1	D	186	ASN
1	D	189	GLN
1	E	13	ASN
1	E	26	ASN
1	E	71	ASN
1	E	72	GLN
1	E	179	ASN
1	F	179	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

25 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$
4	GOL	D	306	-	5,5,5	0.36	0	5,5,5	0.63	0
2	COA	E	301	-	47,50,50	1.25	6 (12%)	69,75,75	1.71	15 (21%)
4	GOL	B	303	-	5,5,5	0.57	0	5,5,5	1.00	0
3	EDO	F	301	-	3,3,3	0.57	0	2,2,2	0.42	0
3	EDO	A	303	-	3,3,3	0.34	0	2,2,2	0.32	0
3	EDO	A	305	-	3,3,3	0.50	0	2,2,2	0.08	0
2	COA	C	301	-	47,50,50	1.33	5 (10%)	69,75,75	1.73	14 (20%)
4	GOL	C	304	-	5,5,5	0.27	0	5,5,5	0.30	0
4	GOL	F	303	-	5,5,5	0.58	0	5,5,5	0.71	0
4	GOL	D	304	-	5,5,5	0.47	0	5,5,5	0.53	0
2	COA	B	301	-	47,50,50	1.36	6 (12%)	69,75,75	2.82	17 (24%)
2	COA	A	301	-	47,50,50	1.27	5 (10%)	69,75,75	1.59	13 (18%)
3	EDO	A	304	-	3,3,3	0.33	0	2,2,2	0.24	0
4	GOL	C	303	-	5,5,5	0.51	0	5,5,5	0.84	0
4	GOL	A	307	-	5,5,5	0.66	0	5,5,5	1.46	1 (20%)
3	EDO	D	303	-	3,3,3	0.45	0	2,2,2	0.51	0
3	EDO	F	302	-	3,3,3	0.66	0	2,2,2	0.15	0
3	EDO	D	302	-	3,3,3	0.36	0	2,2,2	0.30	0
4	GOL	A	306	-	5,5,5	0.59	0	5,5,5	0.44	0
4	GOL	D	305	-	5,5,5	0.44	0	5,5,5	0.65	0
3	EDO	C	302	-	3,3,3	0.38	0	2,2,2	0.35	0
3	EDO	D	301	-	3,3,3	0.70	0	2,2,2	0.52	0
3	EDO	B	302	-	3,3,3	0.37	0	2,2,2	0.50	0
4	GOL	E	302	-	5,5,5	0.63	0	5,5,5	0.49	0
3	EDO	A	302	-	3,3,3	0.80	0	2,2,2	0.56	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
4	GOL	D	306	-	-	2/4/4/4	-
2	COA	E	301	-	-	22/48/64/64	0/3/3/3
4	GOL	B	303	-	-	2/4/4/4	-
3	EDO	F	301	-	-	0/1/1/1	-
3	EDO	A	303	-	-	1/1/1/1	-
3	EDO	A	305	-	-	1/1/1/1	-
2	COA	C	301	-	-	4/48/64/64	0/3/3/3
4	GOL	C	304	-	-	2/4/4/4	-
4	GOL	F	303	-	-	4/4/4/4	-
4	GOL	D	304	-	-	0/4/4/4	-
2	COA	B	301	-	-	3/48/64/64	0/3/3/3
2	COA	A	301	-	-	1/48/64/64	0/3/3/3
3	EDO	A	304	-	-	1/1/1/1	-
4	GOL	C	303	-	-	2/4/4/4	-
4	GOL	A	307	-	-	2/4/4/4	-
3	EDO	D	303	-	-	1/1/1/1	-
3	EDO	F	302	-	-	0/1/1/1	-
3	EDO	D	302	-	-	1/1/1/1	-
4	GOL	A	306	-	-	2/4/4/4	-
4	GOL	D	305	-	-	2/4/4/4	-
3	EDO	C	302	-	-	1/1/1/1	-
3	EDO	D	301	-	-	0/1/1/1	-
3	EDO	B	302	-	-	1/1/1/1	-
4	GOL	E	302	-	-	2/4/4/4	-
3	EDO	A	302	-	-	1/1/1/1	-

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	COA	C5A-C4A	4.94	1.47	1.39
2	A	301	COA	C5A-C4A	4.91	1.47	1.39
2	B	301	COA	C5A-C4A	4.89	1.47	1.39
2	E	301	COA	C5A-C4A	4.80	1.47	1.39
2	A	301	COA	P3B-O3B	3.46	1.65	1.59
2	C	301	COA	C5A-C6A	3.17	1.49	1.41
2	C	301	COA	P1A-O3A	3.00	1.62	1.59
2	B	301	COA	P2A-O3A	2.87	1.62	1.59
2	B	301	COA	P1A-O3A	2.84	1.62	1.59
2	B	301	COA	C5A-C6A	2.80	1.48	1.41
2	C	301	COA	P2A-O3A	2.72	1.62	1.59
2	A	301	COA	C4A-N9A	-2.70	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	301	COA	C5A-C6A	2.51	1.48	1.41
2	E	301	COA	P1A-O3A	2.45	1.62	1.59
2	C	301	COA	C8A-N7A	2.40	1.36	1.31
2	E	301	COA	P2A-O3A	2.38	1.62	1.59
2	A	301	COA	C2A-N1A	2.29	1.38	1.33
2	E	301	COA	C8A-N7A	2.26	1.36	1.31
2	A	301	COA	C5A-C6A	2.23	1.47	1.41
2	B	301	COA	C8A-N7A	2.13	1.35	1.31
2	B	301	COA	C5A-N7A	-2.11	1.35	1.39
2	E	301	COA	C5A-N7A	-2.09	1.35	1.39

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	COA	CEP-CBP-CAP	-11.89	88.49	108.77
2	B	301	COA	CDP-CBP-CAP	-9.90	91.89	108.77
2	B	301	COA	CEP-CBP-CDP	7.89	124.94	109.20
2	B	301	COA	CEP-CBP-CCP	5.66	117.56	108.22
2	B	301	COA	CDP-CBP-CCP	5.46	117.23	108.22
2	B	301	COA	C5A-C4A-N3A	-5.41	119.27	126.72
2	C	301	COA	C5A-C4A-N3A	-5.33	119.38	126.72
2	E	301	COA	C5A-C4A-N3A	-4.96	119.89	126.72
2	B	301	COA	N3A-C4A-N9A	4.84	135.40	127.17
2	E	301	COA	N3A-C4A-N9A	4.42	134.69	127.17
2	C	301	COA	N3A-C4A-N9A	4.13	134.20	127.17
2	E	301	COA	N3A-C2A-N1A	-4.12	122.35	128.58
2	A	301	COA	N3A-C2A-N1A	-4.05	122.45	128.58
2	B	301	COA	N3A-C2A-N1A	-4.00	122.53	128.58
2	B	301	COA	C2A-N3A-C4A	3.91	121.39	111.83
2	C	301	COA	C4A-C5A-N7A	-3.89	106.13	110.58
2	C	301	COA	C2A-N3A-C4A	3.79	121.08	111.83
2	E	301	COA	C7P-N8P-C9P	-3.72	115.87	122.55
2	A	301	COA	N3A-C4A-N9A	3.71	133.49	127.17
2	A	301	COA	C4A-N9A-C8A	3.67	109.59	105.74
2	E	301	COA	C2A-N3A-C4A	3.65	120.75	111.83
2	A	301	COA	C5A-C4A-N3A	-3.63	121.72	126.72
2	C	301	COA	N3A-C2A-N1A	-3.60	123.14	128.58
2	B	301	COA	C4A-N9A-C8A	3.55	109.46	105.74
2	A	301	COA	O9A-P3B-O8A	3.29	120.12	107.80
2	A	301	COA	O5A-P2A-O4A	3.27	127.64	112.44
2	E	301	COA	C4A-N9A-C8A	3.24	109.14	105.74
2	C	301	COA	C3P-N4P-C5P	3.16	128.71	122.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	301	COA	C6P-C5P-N4P	3.16	122.11	116.34
2	B	301	COA	O6A-CCP-CBP	3.16	115.62	110.55
2	A	301	COA	C2A-N3A-C4A	3.07	119.32	111.83
2	C	301	COA	O4B-C1B-N9A	3.05	113.95	108.09
2	E	301	COA	C2A-N1A-C6A	3.03	123.71	118.73
2	B	301	COA	C4A-C5A-N7A	-3.02	107.12	110.58
2	C	301	COA	C4A-N9A-C8A	3.01	108.90	105.74
2	A	301	COA	O3A-P2A-O4A	-2.90	101.99	110.70
2	C	301	COA	C5A-N7A-C8A	2.82	107.88	103.45
2	E	301	COA	O4B-C1B-N9A	2.77	113.42	108.09
2	E	301	COA	C6P-C7P-N8P	-2.74	106.17	112.00
2	A	301	COA	O3B-P3B-O7A	-2.72	99.65	109.33
4	A	307	GOL	C3-C2-C1	-2.69	101.93	111.80
2	E	301	COA	C4A-C5A-N7A	-2.68	107.52	110.58
2	B	301	COA	C5A-N7A-C8A	2.55	107.45	103.45
2	C	301	COA	C6A-C5A-N7A	2.54	137.00	132.09
2	A	301	COA	C4A-C5A-N7A	-2.40	107.83	110.58
2	C	301	COA	O5P-C5P-C6P	-2.36	117.73	122.02
2	A	301	COA	O2B-C2B-C3B	2.35	117.77	111.19
2	A	301	COA	C2A-N1A-C6A	2.34	122.58	118.73
2	B	301	COA	N9A-C8A-N7A	-2.33	110.63	113.94
2	C	301	COA	N9A-C8A-N7A	-2.30	110.67	113.94
2	E	301	COA	C5A-N7A-C8A	2.27	107.01	103.45
2	A	301	COA	C6A-C5A-N7A	2.26	136.44	132.09
2	B	301	COA	C6A-C5A-N7A	2.21	136.35	132.09
2	E	301	COA	N9A-C8A-N7A	-2.14	110.90	113.94
2	E	301	COA	O5P-C5P-C6P	-2.09	118.23	122.02
2	E	301	COA	CAP-C9P-N8P	-2.08	112.53	116.48
2	B	301	COA	O5A-P2A-O4A	2.08	122.10	112.44
2	C	301	COA	C2A-N1A-C6A	2.02	122.05	118.73
2	E	301	COA	N6A-C6A-N1A	2.02	122.87	118.38
2	B	301	COA	O4B-C1B-N9A	2.01	111.96	108.09

There are no chirality outliers.

All (58) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	301	COA	CEP-CBP-CCP-O6A
2	B	301	COA	S1P-C2P-C3P-N4P
2	E	301	COA	O4B-C4B-C5B-O5B
2	E	301	COA	C5B-O5B-P1A-O1A
2	E	301	COA	C5B-O5B-P1A-O3A

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Mol	Chain	Res	Type	Atoms
2	E	301	COA	CDP-CBP-CCP-O6A
2	E	301	COA	CEP-CBP-CCP-O6A
2	E	301	COA	CAP-CBP-CCP-O6A
2	E	301	COA	O9P-C9P-CAP-CBP
2	E	301	COA	CAP-C9P-N8P-C7P
2	E	301	COA	C5P-C6P-C7P-N8P
4	A	306	GOL	O1-C1-C2-C3
4	A	307	GOL	C1-C2-C3-O3
4	A	307	GOL	O2-C2-C3-O3
4	D	305	GOL	C1-C2-C3-O3
4	D	306	GOL	C1-C2-C3-O3
4	E	302	GOL	C1-C2-C3-O3
4	F	303	GOL	C1-C2-C3-O3
2	C	301	COA	C6P-C5P-N4P-C3P
2	C	301	COA	O5P-C5P-N4P-C3P
2	E	301	COA	O9P-C9P-N8P-C7P
4	D	305	GOL	O2-C2-C3-O3
2	E	301	COA	C3B-C4B-C5B-O5B
4	B	303	GOL	C1-C2-C3-O3
4	C	303	GOL	C1-C2-C3-O3
4	C	304	GOL	C1-C2-C3-O3
4	F	303	GOL	O1-C1-C2-C3
4	A	306	GOL	O1-C1-C2-O2
4	B	303	GOL	O2-C2-C3-O3
4	C	303	GOL	O2-C2-C3-O3
4	E	302	GOL	O2-C2-C3-O3
4	F	303	GOL	O1-C1-C2-O2
4	F	303	GOL	O2-C2-C3-O3
3	B	302	EDO	O1-C1-C2-O2
4	C	304	GOL	O2-C2-C3-O3
4	D	306	GOL	O2-C2-C3-O3
2	E	301	COA	O9P-C9P-CAP-OAP
3	A	302	EDO	O1-C1-C2-O2
3	A	303	EDO	O1-C1-C2-O2
3	C	302	EDO	O1-C1-C2-O2
2	E	301	COA	OAP-CAP-CBP-CDP
2	E	301	COA	OAP-CAP-CBP-CEP
2	E	301	COA	N8P-C9P-CAP-OAP
3	A	305	EDO	O1-C1-C2-O2
3	D	303	EDO	O1-C1-C2-O2
2	E	301	COA	P1A-O3A-P2A-O6A
3	D	302	EDO	O1-C1-C2-O2

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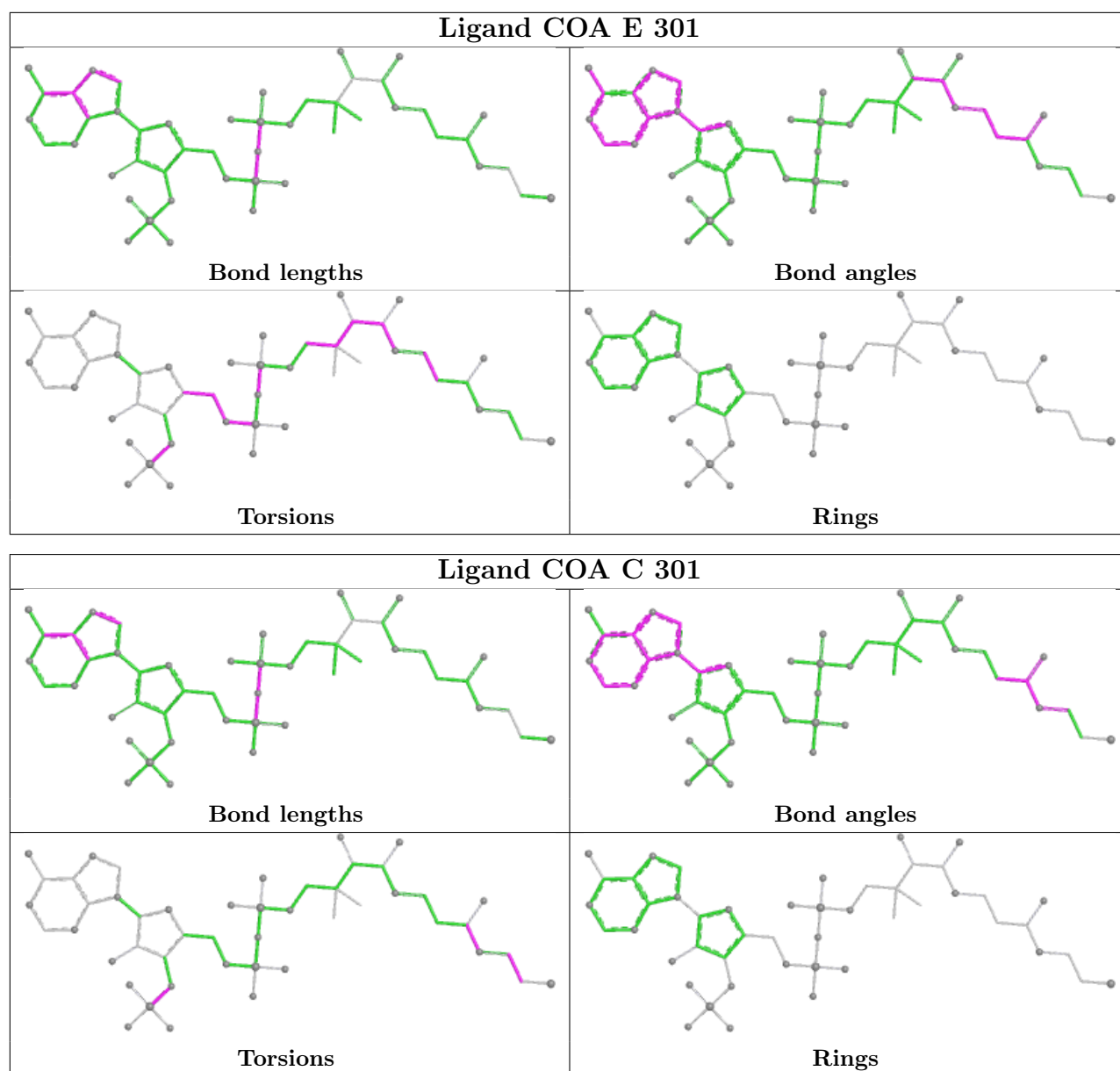
Mol	Chain	Res	Type	Atoms
2	E	301	COA	C3B-O3B-P3B-O7A
2	B	301	COA	CAP-CBP-CCP-O6A
2	C	301	COA	S1P-C2P-C3P-N4P
3	A	304	EDO	O1-C1-C2-O2
2	E	301	COA	C5B-O5B-P1A-O2A
2	E	301	COA	OAP-CAP-CBP-CCP
2	A	301	COA	C3B-O3B-P3B-O7A
2	E	301	COA	C4B-C5B-O5B-P1A
2	E	301	COA	C9P-CAP-CBP-CDP
2	C	301	COA	C3B-O3B-P3B-O9A
2	E	301	COA	C9P-CAP-CBP-CCP

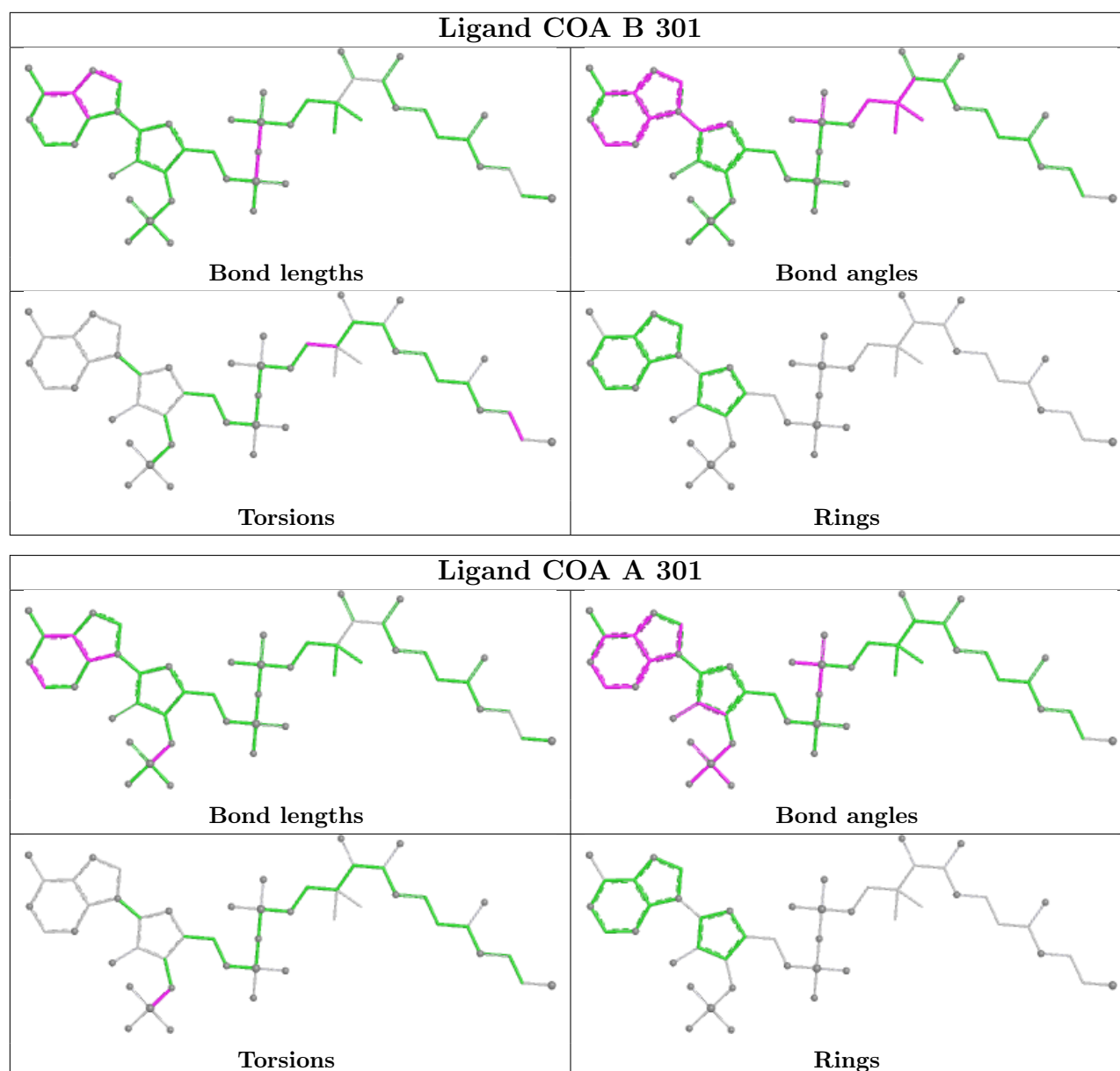
There are no ring outliers.

7 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	301	COA	2	0
2	C	301	COA	5	0
4	A	307	GOL	1	0
3	D	302	EDO	2	0
3	C	302	EDO	2	0
3	D	301	EDO	2	0
3	A	302	EDO	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	257/259 (99%)	-0.15	6 (2%) 61 61	7, 18, 46, 75	1 (0%)
1	B	257/259 (99%)	0.16	12 (4%) 36 35	8, 23, 52, 76	3 (1%)
1	C	259/259 (100%)	0.18	6 (2%) 61 61	10, 24, 53, 82	1 (0%)
1	D	258/259 (99%)	-0.05	10 (3%) 43 43	8, 19, 49, 72	1 (0%)
1	E	257/259 (99%)	0.27	12 (4%) 36 35	8, 27, 49, 83	1 (0%)
1	F	257/259 (99%)	0.29	12 (4%) 36 35	11, 26, 59, 77	0
All	All	1545/1554 (99%)	0.12	58 (3%) 44 44	7, 23, 52, 83	7 (0%)

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	1	MET	5.2
1	D	1	MET	5.0
1	B	249	LEU	4.3
1	B	68	THR	3.8
1	E	1	MET	3.8
1	B	247	ALA	3.7
1	F	45	SER	3.2
1	A	1	MET	3.2
1	F	23	ASP	3.2
1	F	71	ASN	3.1
1	F	254	PRO	3.1
1	D	71	ASN	3.0
1	F	67	ILE	3.0
1	E	72	GLN	2.9
1	E	23	ASP	2.9
1	C	71	ASN	2.9
1	D	258	GLY	2.7
1	F	247	ALA	2.6
1	D	68	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	249	LEU	2.6
1	B	1	MET	2.6
1	D	247	ALA	2.6
1	E	257	LYS	2.6
1	B	248	PHE	2.6
1	C	1	MET	2.5
1	F	249	LEU	2.5
1	D	2	GLU	2.4
1	E	63	ALA	2.4
1	E	247	ALA	2.4
1	E	71	ASN	2.4
1	A	253	GLU	2.4
1	E	65	ALA	2.4
1	E	64	GLY	2.4
1	F	68	THR	2.4
1	C	58	GLY	2.4
1	F	251	LYS	2.4
1	F	255	THR	2.3
1	B	71	ASN	2.3
1	B	251	LYS	2.3
1	B	64	GLY	2.2
1	C	23	ASP	2.2
1	B	70	PHE	2.2
1	D	23	ASP	2.2
1	F	2	GLU	2.2
1	B	66	ASP	2.2
1	E	254	PRO	2.2
1	D	251	LYS	2.2
1	A	2	GLU	2.1
1	C	65	ALA	2.1
1	D	246	SER	2.1
1	B	250	GLU	2.1
1	E	245	VAL	2.1
1	A	247	ALA	2.1
1	A	252	ARG	2.1
1	E	250	GLU	2.0
1	C	259	LYS	2.0
1	D	67	ILE	2.0
1	B	72	GLN	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.

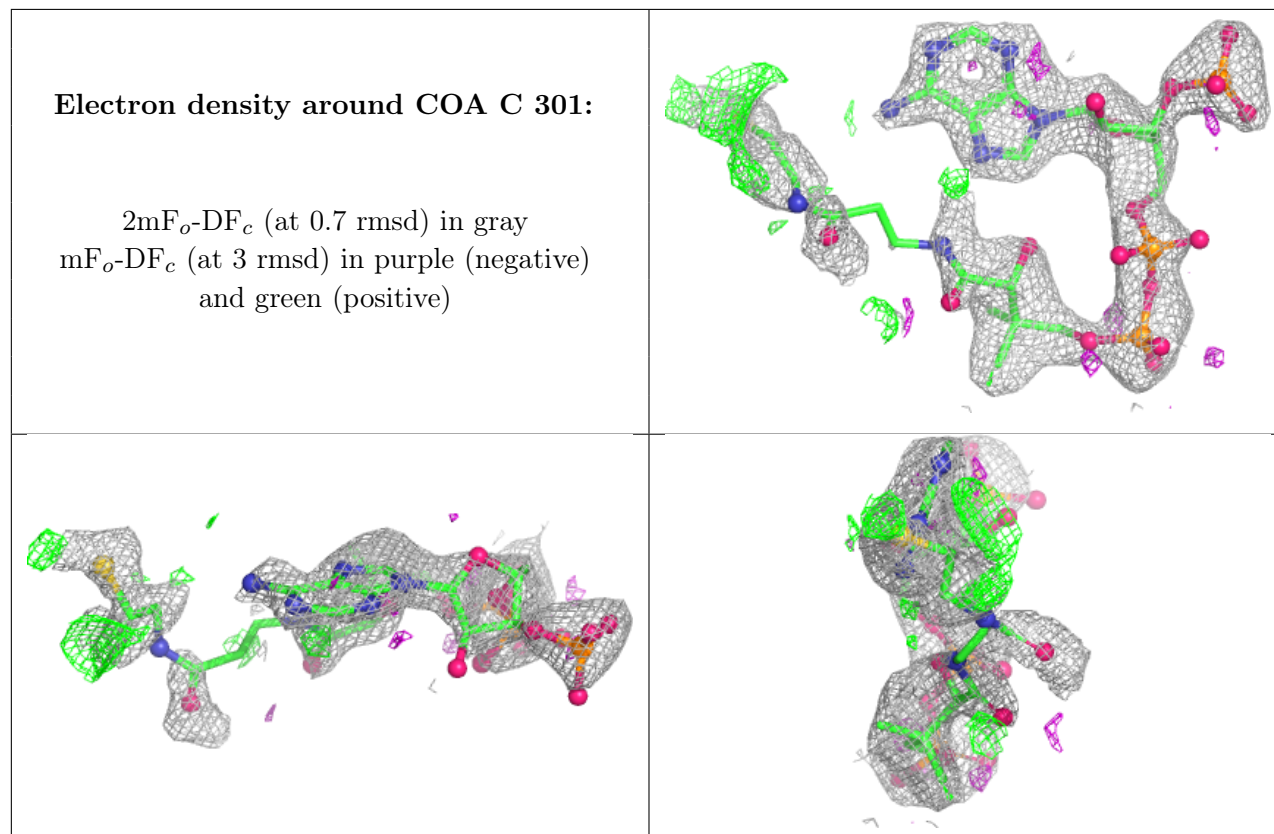
6.4 Ligands [i](#)

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
2	COA	C	301	48/48	0.68	0.17	60,74,83,85	0
4	GOL	C	304	6/6	0.74	0.16	53,55,56,57	0
2	COA	E	301	48/48	0.75	0.16	67,80,88,96	0
2	COA	B	301	48/48	0.75	0.14	57,68,80,84	0
4	GOL	A	307	6/6	0.76	0.15	41,42,44,45	0
4	GOL	B	303	6/6	0.80	0.13	41,47,47,48	0
3	EDO	F	302	4/4	0.80	0.15	47,50,50,50	0
4	GOL	D	304	6/6	0.81	0.12	35,40,41,43	0
3	EDO	D	303	4/4	0.82	0.10	31,33,37,41	0
4	GOL	D	305	6/6	0.83	0.12	42,44,45,46	0
4	GOL	F	303	6/6	0.84	0.12	38,43,45,46	0
3	EDO	B	302	4/4	0.85	0.13	41,43,45,47	0
3	EDO	A	303	4/4	0.86	0.17	47,47,50,51	0
4	GOL	C	303	6/6	0.86	0.11	42,45,50,51	0
3	EDO	A	304	4/4	0.86	0.11	29,33,35,38	0
4	GOL	A	306	6/6	0.87	0.11	40,43,44,46	0
3	EDO	F	301	4/4	0.88	0.12	39,39,41,41	0
4	GOL	D	306	6/6	0.89	0.10	38,45,46,47	0
4	GOL	E	302	6/6	0.89	0.11	26,30,34,40	0
3	EDO	A	302	4/4	0.89	0.10	33,33,36,37	0
3	EDO	D	302	4/4	0.90	0.13	40,43,44,46	0
3	EDO	A	305	4/4	0.90	0.11	30,33,37,42	0
3	EDO	C	302	4/4	0.91	0.10	36,37,37,40	0
3	EDO	D	301	4/4	0.92	0.09	24,27,28,30	0
2	COA	A	301	48/48	0.96	0.06	16,23,27,37	0

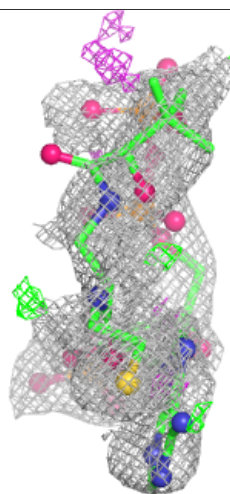
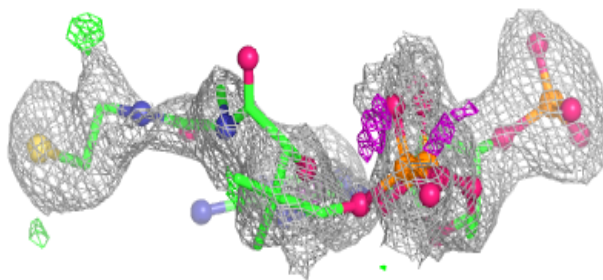
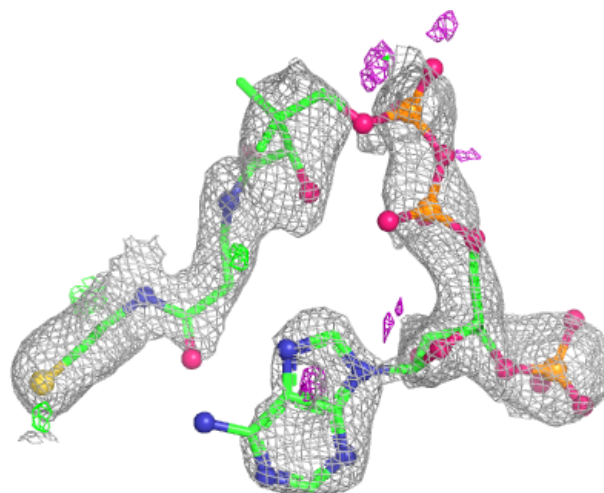
The following is a graphical depiction of the model fit to experimental electron density of all

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.



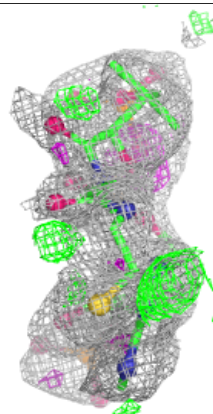
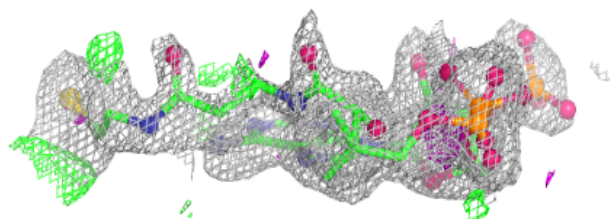
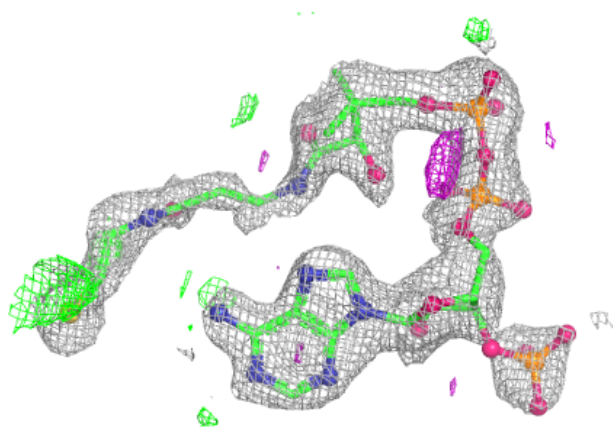
Electron density around COA E 301:

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



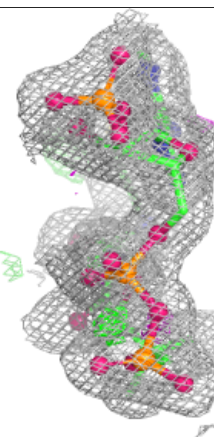
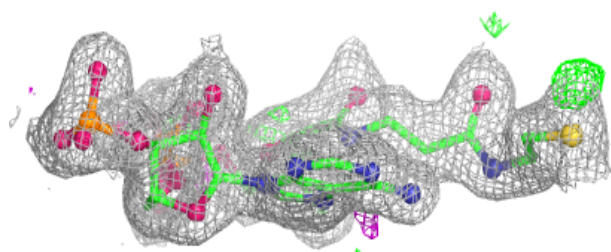
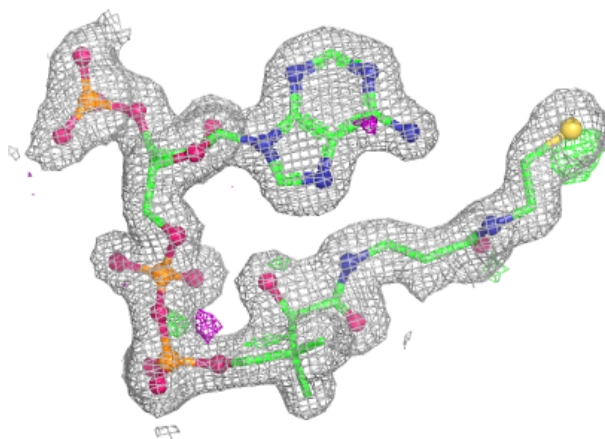
Electron density around COA B 301:

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



Electron density around COA A 301:

$2mF_o-DF_c$ (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.