Full wwPDB X-ray Structure Validation Report (i)

Jun 26, 2024 – 03:33 AM EDT

PDB ID	:	6RFT
Title	:	Crystal structure of Eis2 from Mycobacterium abscessus bound to Acetyl-CoA
Authors	:	Blaise, M.; Kremer, L.; Olieric, V.; Alsarraf, H.; Ung, K.L.
Deposited on	:	2019-04-16
Resolution	:	2.30 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:

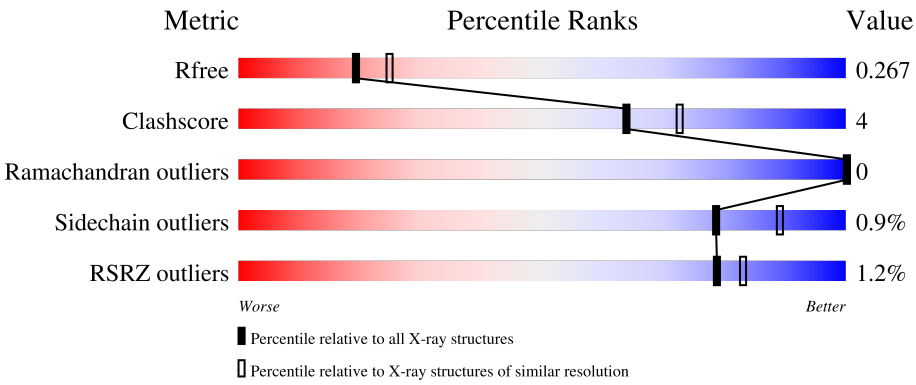
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	A	411	91% 7% •
1	B	411	88% 10% •
1	C	411	89% 9% •
1	D	411	.% 91% 6% •
1	E	411	2% 89% 9% •

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Mol	Chain	Length	Quality of chain
1	F	411	3% 84% 13%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 20077 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 Uncharacterized N-acetyltransferase D2E36_21790.

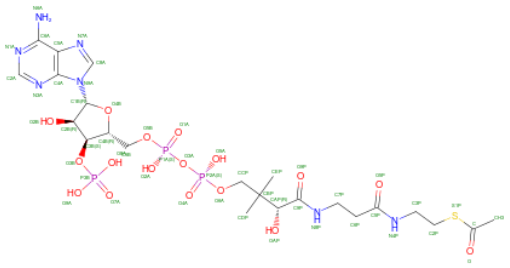
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	406	3153	1987	552	604	2	8	0	0	0
1	B	402	3117	1963	547	597	2	8	0	0	0
1	C	403	3128	1969	548	601	2	8	0	0	0
1	D	403	3126	1968	548	600	2	8	0	0	0
1	E	406	3153	1987	552	604	2	8	0	0	0
1	F	405	3147	1984	551	602	2	8	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP A0A3A1BNP8
B	1	GLY	-	expression tag	UNP A0A3A1BNP8
C	1	GLY	-	expression tag	UNP A0A3A1BNP8
D	1	GLY	-	expression tag	UNP A0A3A1BNP8
E	1	GLY	-	expression tag	UNP A0A3A1BNP8
F	1	GLY	-	expression tag	UNP A0A3A1BNP8

- Molecule 2 is ACETYL COENZYME *A (three-letter code: ACO) (formula: $C_{23}H_{38}N_7O_{17}P_3S$).

ACO



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
2	A	1	51	23	7	17	3	1	0	0
2	B	1	51	23	7	17	3	1	0	0
2	C	1	51	23	7	17	3	1	0	0
2	D	1	42	18	6	15	3		0	0
2	E	1	45	19	7	16	3		0	0
2	F	1	45	19	7	16	3		0	0

- Molecule 3 is water.

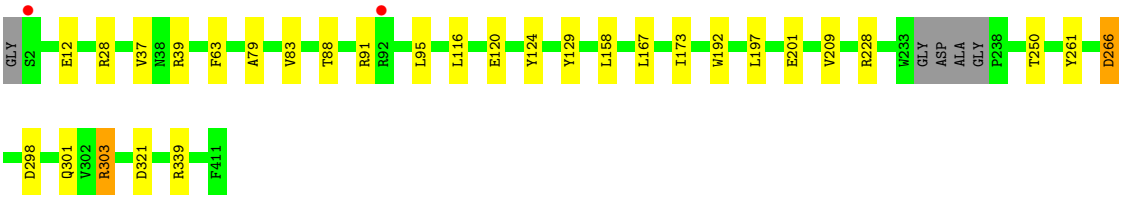
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	217	217	217	0	0
3	B	129	129	129	0	0
3	C	203	203	203	0	0
3	D	161	161	161	0	0
3	E	118	118	118	0	0
3	F	140	140	140	0	0

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.

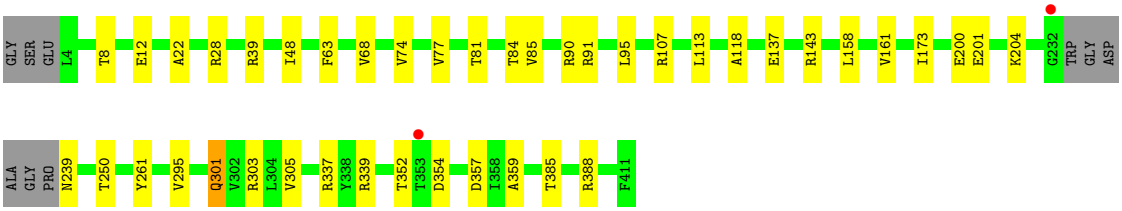
• Molecule 1: Uncharacterized N-acetyltransferase D2E36_21790

Chain A:



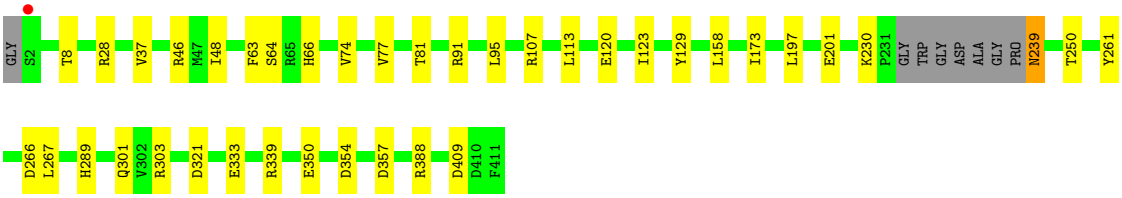
• Molecule 1: Uncharacterized N-acetyltransferase D2E36_21790

Chain B:



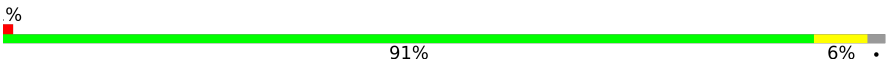
• Molecule 1: Uncharacterized N-acetyltransferase D2E36_21790

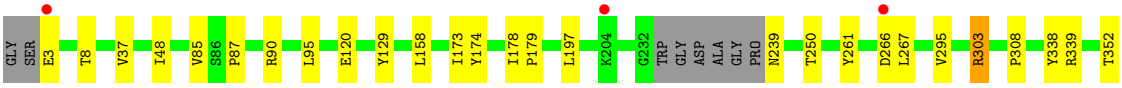
Chain C:



• Molecule 1: Uncharacterized N-acetyltransferase D2E36_21790

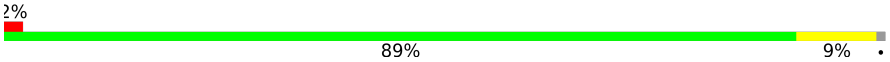
Chain D:

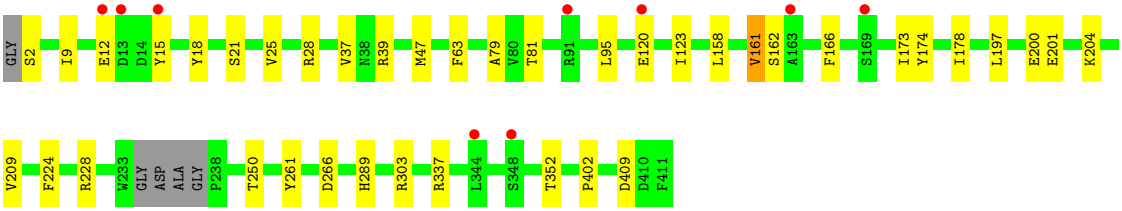




• Molecule 1: Uncharacterized N-acetyltransferase D2E36_21790

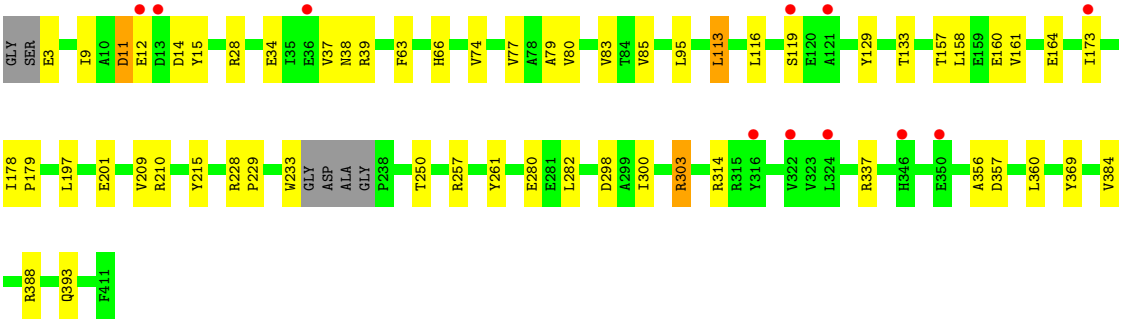
Chain E:





• Molecule 1: Uncharacterized N-acetyltransferase D2E36_21790

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	111.65Å 76.99Å 152.56Å 90.00° 90.81° 90.00°	Depositor
Resolution (Å)	48.94 – 2.30 48.94 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.94-2.30) 100.0 (48.94-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.92 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.15rc3_3435: ???)	Depositor
R, R_{free}	0.229 , 0.267 0.229 , 0.267	Depositor DCC
R_{free} test set	1996 reflections (1.73%)	wwPDB-VP
Wilson B-factor (Å^2)	30.4	Xtriage
Anisotropy	0.433	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 42.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.43$, $< L^2 > = 0.25$	Xtriage
Estimated twinning fraction	0.045 for h,-k,-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	20077	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% 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: ACO

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	0.24	0/3213	0.44	0/4355
1	B	0.24	0/3174	0.43	0/4301
1	C	0.24	0/3185	0.43	0/4316
1	D	0.24	0/3183	0.42	0/4313
1	E	0.24	0/3213	0.43	0/4355
1	F	0.23	0/3207	0.42	0/4347
All	All	0.24	0/19175	0.43	0/25987

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	3153	0	3090	21	0
1	B	3117	0	3061	26	0
1	C	3128	0	3069	26	0
1	D	3126	0	3067	17	0
1	E	3153	0	3090	24	0
1	F	3147	0	3085	35	0
2	A	51	0	34	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	51	0	34	6	0
2	C	51	0	34	7	0
2	D	42	0	24	5	0
2	E	45	0	26	3	0
2	F	45	0	26	5	0
3	A	217	0	0	0	0
3	B	129	0	0	3	0
3	C	203	0	0	2	0
3	D	161	0	0	2	0
3	E	118	0	0	1	0
3	F	140	0	0	2	0
All	All	20077	0	18640	157	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (157) 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)
2:E:501:ACO:H131	2:E:501:ACO:HN8	1.43	0.81
1:F:12:GLU:HA	1:F:15:TYR:HB3	1.66	0.79
1:F:34:GLU:O	1:F:38:ASN:ND2	2.27	0.67
1:F:95:LEU:HD22	2:F:501:ACO:H133	1.77	0.66
1:F:85:VAL:HB	2:F:501:ACO:H10	1.75	0.66
1:B:28:ARG:NH2	1:B:201:GLU:OE2	2.28	0.64
1:B:337:ARG:NH1	1:B:354:ASP:O	2.30	0.64
1:C:91:ARG:HH12	2:C:501:ACO:H143	1.63	0.63
1:D:85:VAL:HB	2:D:501:ACO:H122	1.80	0.63
1:F:337:ARG:HD2	1:F:356:ALA:HB2	1.80	0.62
1:A:91:ARG:HH12	2:A:501:ACO:H143	1.64	0.62
1:A:266:ASP:OD1	1:A:266:ASP:N	2.22	0.61
1:B:143:ARG:NH1	3:B:611:HOH:O	2.33	0.61
2:A:501:ACO:N7A	2:A:501:ACO:H142	2.15	0.61
1:F:3:GLU:N	3:F:606:HOH:O	2.33	0.61
2:C:501:ACO:H142	2:C:501:ACO:N7A	2.17	0.60
2:F:501:ACO:HN8	2:F:501:ACO:H131	1.66	0.60
1:E:37:VAL:HG11	1:E:197:LEU:HD22	1.83	0.59
1:C:107:ARG:NH1	1:C:333:GLU:OE2	2.35	0.59
1:F:28:ARG:NH2	1:F:201:GLU:OE1	2.35	0.59
1:C:239:ASN:N	3:C:611:HOH:O	2.36	0.59
1:D:3:GLU:N	3:D:611:HOH:O	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:63:PHE:HB2	1:F:79:ALA:HB3	1.84	0.58
1:D:239:ASN:N	3:D:612:HOH:O	2.36	0.58
1:A:116:LEU:HD22	1:A:301:GLN:HE21	1.69	0.58
1:F:12:GLU:HG2	1:F:39:ARG:HE	1.68	0.58
2:B:501:ACO:N7A	2:B:501:ACO:H142	2.19	0.58
1:C:266:ASP:OD1	1:C:267:LEU:N	2.36	0.57
1:C:120:GLU:OE1	2:C:501:ACO:N6A	2.37	0.57
1:E:12:GLU:OE2	1:E:39:ARG:NE	2.36	0.57
1:E:402:PRO:HG2	1:F:393:GLN:HG3	1.87	0.57
2:F:501:ACO:H8A	2:F:501:ACO:H52A	1.86	0.57
1:C:28:ARG:NH2	1:C:201:GLU:OE1	2.38	0.56
1:D:95:LEU:HD22	2:D:501:ACO:H133	1.88	0.55
1:D:158:LEU:HD13	1:D:261:TYR:HB2	1.88	0.55
1:A:120:GLU:OE1	2:A:501:ACO:N6A	2.39	0.55
1:B:91:ARG:HH12	2:B:501:ACO:H143	1.70	0.55
1:C:129:TYR:HB3	1:C:301:GLN:HE21	1.72	0.55
1:C:321:ASP:OD1	1:C:339:ARG:NH1	2.38	0.55
1:A:91:ARG:NH1	2:A:501:ACO:H143	2.20	0.55
1:F:9:ILE:HG21	1:F:15:TYR:HB2	1.89	0.54
1:A:158:LEU:HD13	1:A:261:TYR:HB2	1.88	0.54
1:B:158:LEU:HD13	1:B:261:TYR:HB2	1.90	0.54
1:A:28:ARG:NH2	1:A:201:GLU:OE1	2.40	0.53
1:A:83:VAL:HB	2:A:501:ACO:HH33	1.91	0.53
1:C:239:ASN:N	1:C:239:ASN:HD22	2.06	0.53
1:C:123:ILE:HG12	2:C:501:ACO:N7A	2.24	0.53
1:C:8:THR:HG22	1:C:48:ILE:HG22	1.90	0.53
2:D:501:ACO:H131	2:D:501:ACO:HN8	1.74	0.53
1:B:91:ARG:NH1	2:B:501:ACO:H143	2.24	0.52
1:E:28:ARG:NH2	1:E:201:GLU:OE1	2.42	0.52
1:F:158:LEU:HD13	1:F:261:TYR:HB2	1.92	0.52
1:F:11:ASP:O	1:F:15:TYR:N	2.43	0.52
1:F:129:TYR:CE1	1:F:303:ARG:HB2	2.45	0.52
1:B:8:THR:HG22	1:B:48:ILE:HG22	1.92	0.52
1:F:314:ARG:NH1	1:F:369:TYR:O	2.42	0.52
1:C:173:ILE:HG23	1:C:250:THR:HG23	1.92	0.51
1:A:321:ASP:OD1	1:A:339:ARG:NH1	2.42	0.51
1:F:178:ILE:HG13	1:F:179:PRO:HD3	1.93	0.51
1:B:118:ALA:HB2	1:B:301:GLN:HE21	1.74	0.51
1:D:266:ASP:OD1	1:D:267:LEU:N	2.44	0.51
1:F:173:ILE:HG23	1:F:250:THR:HG23	1.93	0.51
1:E:158:LEU:HD13	1:E:261:TYR:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:83:VAL:O	2:F:501:ACO:H62	2.11	0.50
1:C:46:ARG:NH1	1:C:64:SER:OG	2.42	0.50
1:D:37:VAL:HG11	1:D:197:LEU:HD22	1.93	0.50
1:F:209:VAL:HG22	1:F:228:ARG:NE	2.27	0.50
1:B:295:VAL:HG22	1:D:295:VAL:HG22	1.95	0.49
1:F:37:VAL:HG11	1:F:197:LEU:HD22	1.95	0.49
1:B:12:GLU:OE2	1:B:39:ARG:NH2	2.34	0.49
1:C:230:LYS:NZ	3:C:622:HOH:O	2.45	0.49
1:E:173:ILE:HG23	1:E:250:THR:HG23	1.94	0.49
1:C:409:ASP:N	1:C:409:ASP:OD1	2.45	0.49
1:F:80:VAL:HB	1:F:116:LEU:HB3	1.94	0.49
1:F:257:ARG:NH2	3:F:626:HOH:O	2.47	0.48
1:C:158:LEU:HD13	1:C:261:TYR:HB2	1.97	0.47
1:E:63:PHE:HB2	1:E:79:ALA:HB3	1.96	0.47
1:A:173:ILE:HG23	1:A:250:THR:HG23	1.97	0.47
1:A:37:VAL:HG11	1:A:197:LEU:HD22	1.96	0.47
1:E:12:GLU:HA	1:E:15:TYR:HB3	1.95	0.47
1:F:357:ASP:OD1	1:F:388:ARG:HD3	2.15	0.47
1:D:173:ILE:HG23	1:D:250:THR:HG23	1.95	0.47
1:F:133:THR:HB	1:F:300:ILE:HB	1.97	0.46
1:B:173:ILE:HG23	1:B:250:THR:HG23	1.98	0.46
1:C:37:VAL:HG11	1:C:197:LEU:HD22	1.98	0.46
1:F:164:GLU:OE1	1:F:164:GLU:N	2.45	0.46
1:A:298:ASP:OD2	1:C:289:HIS:HB3	2.16	0.46
1:B:85:VAL:HB	2:B:501:ACO:H10	1.97	0.45
1:B:90:ARG:NH2	1:E:266:ASP:OD1	2.48	0.45
1:E:2:SER:N	3:E:625:HOH:O	2.50	0.45
2:A:501:ACO:H31	2:A:501:ACO:H62	1.65	0.45
1:E:337:ARG:HB2	1:E:352:THR:O	2.15	0.45
1:E:209:VAL:HG22	1:E:228:ARG:NE	2.32	0.45
1:B:22:ALA:HA	1:B:84:THR:HG21	1.97	0.44
2:B:501:ACO:H62	2:B:501:ACO:H31	1.70	0.44
1:C:339:ARG:NH2	1:C:354:ASP:OD2	2.47	0.44
1:E:200:GLU:O	1:E:204:LYS:HG3	2.17	0.44
1:F:360:LEU:HB3	1:F:384:VAL:HG13	1.99	0.44
1:E:409:ASP:OD1	1:E:409:ASP:N	2.45	0.44
1:A:12:GLU:OE2	1:A:39:ARG:NH2	2.39	0.44
1:D:120:GLU:OE1	2:D:501:ACO:N6A	2.49	0.44
1:C:301:GLN:HE21	1:C:301:GLN:HB3	1.62	0.44
1:C:357:ASP:OD1	1:C:388:ARG:HD3	2.17	0.44
1:A:124:TYR:HB2	1:A:301:GLN:HE22	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:63:PHE:CE2	1:B:81:THR:HG21	2.53	0.44
1:E:95:LEU:HD22	2:E:501:ACO:H133	1.99	0.43
1:F:66:HIS:HB3	1:F:74:VAL:HG12	2.00	0.43
2:D:501:ACO:HN8	2:D:501:ACO:H141	1.84	0.43
1:E:18:TYR:CE1	1:E:47:MSE:HE3	2.54	0.43
1:A:209:VAL:HG22	1:A:228:ARG:NE	2.33	0.43
1:B:68:VAL:HG22	1:B:74:VAL:HG22	2.00	0.43
1:C:91:ARG:NH1	2:C:501:ACO:H143	2.32	0.43
1:B:107:ARG:HB2	1:B:305:VAL:CG1	2.49	0.43
1:D:8:THR:HG22	1:D:48:ILE:HG22	2.00	0.43
1:E:63:PHE:CE2	1:E:81:THR:HG21	2.54	0.43
1:B:200:GLU:O	1:B:204:LYS:HG3	2.19	0.43
1:C:95:LEU:HD22	2:C:501:ACO:H121	2.01	0.43
1:D:129:TYR:CE2	1:D:303:ARG:HB2	2.54	0.43
1:F:210:ARG:HD3	1:F:229:PRO:HD3	2.01	0.43
1:A:63:PHE:HB2	1:A:79:ALA:HB3	2.00	0.43
1:A:129:TYR:CE2	1:A:303:ARG:HB2	2.53	0.43
1:B:95:LEU:HD22	2:B:501:ACO:H121	2.00	0.43
1:A:83:VAL:H	2:A:501:ACO:CH3	2.31	0.43
1:F:77:VAL:HG23	1:F:113:LEU:HD13	2.00	0.42
1:B:359:ALA:HB3	1:B:385:THR:HB	2.00	0.42
1:B:118:ALA:HB2	1:B:301:GLN:NE2	2.34	0.42
2:C:501:ACO:H62	2:C:501:ACO:H31	1.67	0.42
1:E:120:GLU:OE1	1:E:123:ILE:HD11	2.20	0.42
1:E:289:HIS:HB2	1:F:298:ASP:OD2	2.19	0.42
1:F:280:GLU:HG3	1:F:282:LEU:H	1.84	0.42
2:A:501:ACO:H8A	2:A:501:ACO:H51A	2.01	0.42
1:E:166:PHE:HE1	1:E:224:PHE:HB2	1.84	0.42
2:E:501:ACO:N8P	2:E:501:ACO:H141	2.35	0.42
2:A:501:ACO:H22	2:A:501:ACO:HH32	1.76	0.41
1:C:63:PHE:CE2	1:C:81:THR:HG21	2.55	0.41
1:F:11:ASP:OD1	1:F:14:ASP:N	2.46	0.41
1:B:137:GLU:OE2	3:B:601:HOH:O	2.22	0.41
1:B:339:ARG:HB2	1:B:352:THR:HG21	2.02	0.41
1:B:77:VAL:HG23	1:B:113:LEU:HG	2.01	0.41
1:E:9:ILE:HG21	1:E:15:TYR:HB2	2.03	0.41
1:D:174:TYR:CE2	1:D:178:ILE:HD13	2.56	0.41
1:F:12:GLU:CG	1:F:39:ARG:HE	2.31	0.41
1:B:357:ASP:OD1	1:B:388:ARG:HD3	2.21	0.41
1:B:239:ASN:N	3:B:635:HOH:O	2.54	0.41
1:D:339:ARG:HB2	1:D:352:THR:HG21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:LEU:HD22	1:A:192:TRP:HB3	2.01	0.41
1:C:66:HIS:HB3	1:C:74:VAL:HG12	2.02	0.41
1:A:95:LEU:HD22	2:A:501:ACO:H121	2.04	0.40
1:D:87:PRO:HA	1:D:90:ARG:HD2	2.04	0.40
1:D:308:PRO:HG3	1:D:338:TYR:CE2	2.56	0.40
1:E:174:TYR:CE2	1:E:178:ILE:HD13	2.56	0.40
1:C:77:VAL:HG23	1:C:113:LEU:HG	2.03	0.40
1:A:88:THR:HG21	1:F:160:GLU:H	1.86	0.40
1:E:161:VAL:HG13	1:E:162:SER:O	2.21	0.40
1:F:157:THR:HG23	1:F:215:TYR:HB2	2.04	0.40
1:D:178:ILE:HG13	1:D:179:PRO:HD3	2.04	0.40
1:E:21:SER:O	1:E:25:VAL:HG23	2.22	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	402/411 (98%)	394 (98%)	8 (2%)	0	100	100
1	B	398/411 (97%)	391 (98%)	7 (2%)	0	100	100
1	C	399/411 (97%)	392 (98%)	7 (2%)	0	100	100
1	D	399/411 (97%)	391 (98%)	8 (2%)	0	100	100
1	E	402/411 (98%)	394 (98%)	8 (2%)	0	100	100
1	F	401/411 (98%)	388 (97%)	13 (3%)	0	100	100
All	All	2401/2466 (97%)	2350 (98%)	51 (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	331/324 (102%)	329 (99%)	2 (1%)	86	94
1	B	327/324 (101%)	324 (99%)	3 (1%)	78	89
1	C	329/324 (102%)	326 (99%)	3 (1%)	78	89
1	D	328/324 (101%)	327 (100%)	1 (0%)	92	97
1	E	331/324 (102%)	329 (99%)	2 (1%)	86	94
1	F	330/324 (102%)	324 (98%)	6 (2%)	59	75
All	All	1976/1944 (102%)	1959 (99%)	17 (1%)	78	89

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	266	ASP
1	A	303	ARG
1	B	161	VAL
1	B	301	GLN
1	B	303	ARG
1	C	239	ASN
1	C	303	ARG
1	C	350	GLU
1	D	303	ARG
1	E	161	VAL
1	E	303	ARG
1	F	11	ASP
1	F	113	LEU
1	F	119	SER
1	F	161	VAL
1	F	233	TRP
1	F	303	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	301	GLN
1	B	301	GLN
1	C	301	GLN
1	D	301	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

6 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	ACO	E	501	-	39,47,53	0.62	0	49,72,79	0.85	3 (6%)
2	ACO	D	501	-	36,44,53	0.55	0	45,68,79	0.69	0
2	ACO	A	501	-	45,53,53	0.54	0	56,79,79	0.68	0
2	ACO	B	501	-	45,53,53	0.48	0	56,79,79	0.62	0
2	ACO	F	501	-	39,47,53	0.56	0	49,72,79	0.66	0
2	ACO	C	501	-	45,53,53	0.47	0	56,79,79	0.61	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
2	ACO	E	501	-	-	11/40/60/67	0/3/3/3
2	ACO	D	501	-	-	12/37/57/67	0/3/3/3
2	ACO	A	501	-	-	22/47/67/67	0/3/3/3
2	ACO	B	501	-	-	20/47/67/67	0/3/3/3
2	ACO	F	501	-	-	7/40/60/67	0/3/3/3
2	ACO	C	501	-	-	22/47/67/67	0/3/3/3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	501	ACO	C7P-N8P-C9P	2.39	126.84	122.59
2	E	501	ACO	CDP-CBP-CAP	2.16	112.56	108.82
2	E	501	ACO	C6P-C7P-N8P	-2.03	107.80	111.90

There are no chirality outliers.

All (94) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	ACO	C5B-O5B-P1A-O3A
2	A	501	ACO	CCP-O6A-P2A-O3A
2	A	501	ACO	CCP-O6A-P2A-O5A
2	A	501	ACO	CDP-CBP-CCP-O6A
2	A	501	ACO	CAP-CBP-CCP-O6A
2	A	501	ACO	S1P-C2P-C3P-N4P
2	A	501	ACO	C3P-C2P-S1P-C
2	A	501	ACO	O-C-S1P-C2P
2	A	501	ACO	CH3-C-S1P-C2P
2	B	501	ACO	O4B-C4B-C5B-O5B
2	B	501	ACO	CCP-O6A-P2A-O3A
2	B	501	ACO	CDP-CBP-CCP-O6A
2	B	501	ACO	CAP-CBP-CCP-O6A
2	B	501	ACO	O9P-C9P-CAP-OAP
2	B	501	ACO	S1P-C2P-C3P-N4P
2	B	501	ACO	C3P-C2P-S1P-C
2	B	501	ACO	O-C-S1P-C2P
2	B	501	ACO	CH3-C-S1P-C2P
2	C	501	ACO	C5B-O5B-P1A-O1A
2	C	501	ACO	C5B-O5B-P1A-O2A

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Mol	Chain	Res	Type	Atoms
2	C	501	ACO	CCP-O6A-P2A-O3A
2	C	501	ACO	CCP-O6A-P2A-O4A
2	C	501	ACO	CCP-O6A-P2A-O5A
2	C	501	ACO	CAP-CBP-CCP-O6A
2	C	501	ACO	O9P-C9P-CAP-OAP
2	C	501	ACO	S1P-C2P-C3P-N4P
2	C	501	ACO	C3P-C2P-S1P-C
2	C	501	ACO	O-C-S1P-C2P
2	C	501	ACO	CH3-C-S1P-C2P
2	D	501	ACO	C3B-O3B-P3B-O7A
2	D	501	ACO	C5B-O5B-P1A-O1A
2	D	501	ACO	C5B-O5B-P1A-O2A
2	D	501	ACO	C5B-O5B-P1A-O3A
2	D	501	ACO	O9P-C9P-CAP-CBP
2	D	501	ACO	N8P-C9P-CAP-CBP
2	D	501	ACO	O9P-C9P-CAP-OAP
2	E	501	ACO	C5B-O5B-P1A-O1A
2	E	501	ACO	C5B-O5B-P1A-O2A
2	E	501	ACO	C5B-O5B-P1A-O3A
2	E	501	ACO	O9P-C9P-CAP-CBP
2	E	501	ACO	N8P-C9P-CAP-CBP
2	F	501	ACO	C5B-O5B-P1A-O1A
2	F	501	ACO	C5B-O5B-P1A-O2A
2	F	501	ACO	C5B-O5B-P1A-O3A
2	F	501	ACO	O9P-C9P-CAP-CBP
2	F	501	ACO	N8P-C9P-CAP-CBP
2	A	501	ACO	C6P-C5P-N4P-C3P
2	B	501	ACO	C6P-C5P-N4P-C3P
2	C	501	ACO	C6P-C5P-N4P-C3P
2	A	501	ACO	O4B-C4B-C5B-O5B
2	A	501	ACO	O5P-C5P-N4P-C3P
2	B	501	ACO	O5P-C5P-N4P-C3P
2	C	501	ACO	O5P-C5P-N4P-C3P
2	A	501	ACO	C3B-C4B-C5B-O5B
2	A	501	ACO	CEP-CBP-CCP-O6A
2	B	501	ACO	CEP-CBP-CCP-O6A
2	C	501	ACO	CDP-CBP-CCP-O6A
2	C	501	ACO	CEP-CBP-CCP-O6A
2	A	501	ACO	C5P-C6P-C7P-N8P
2	B	501	ACO	C5P-C6P-C7P-N8P
2	A	501	ACO	O9P-C9P-CAP-OAP
2	B	501	ACO	OAP-CAP-CBP-CDP

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Mol	Chain	Res	Type	Atoms
2	B	501	ACO	OAP-CAP-CBP-CEP
2	C	501	ACO	P2A-O3A-P1A-O1A
2	A	501	ACO	C5B-O5B-P1A-O1A
2	A	501	ACO	C5B-O5B-P1A-O2A
2	A	501	ACO	CCP-O6A-P2A-O4A
2	B	501	ACO	CCP-O6A-P2A-O4A
2	B	501	ACO	CCP-O6A-P2A-O5A
2	B	501	ACO	OAP-CAP-CBP-CCP
2	C	501	ACO	OAP-CAP-CBP-CCP
2	A	501	ACO	OAP-CAP-CBP-CEP
2	C	501	ACO	OAP-CAP-CBP-CEP
2	D	501	ACO	CDP-CBP-CCP-O6A
2	D	501	ACO	O4B-C4B-C5B-O5B
2	A	501	ACO	C3B-O3B-P3B-O7A
2	C	501	ACO	N8P-C9P-CAP-OAP
2	E	501	ACO	N8P-C9P-CAP-OAP
2	F	501	ACO	N8P-C9P-CAP-OAP
2	D	501	ACO	CEP-CBP-CCP-O6A
2	E	501	ACO	C5P-C6P-C7P-N8P
2	B	501	ACO	C9P-CAP-CBP-CDP
2	A	501	ACO	C3B-O3B-P3B-O8A
2	C	501	ACO	C5B-O5B-P1A-O3A
2	C	501	ACO	OAP-CAP-CBP-CDP
2	E	501	ACO	C3B-O3B-P3B-O8A
2	E	501	ACO	CCP-O6A-P2A-O3A
2	E	501	ACO	O4B-C4B-C5B-O5B
2	C	501	ACO	P2A-O3A-P1A-O2A
2	D	501	ACO	P2A-O3A-P1A-O1A
2	D	501	ACO	CCP-O6A-P2A-O4A
2	E	501	ACO	CCP-O6A-P2A-O4A
2	F	501	ACO	O4B-C4B-C5B-O5B
2	B	501	ACO	C9P-CAP-CBP-CCP

There are no ring outliers.

6 monomers are involved in 36 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	501	ACO	3	0
2	D	501	ACO	5	0
2	A	501	ACO	10	0
2	B	501	ACO	6	0
2	F	501	ACO	5	0

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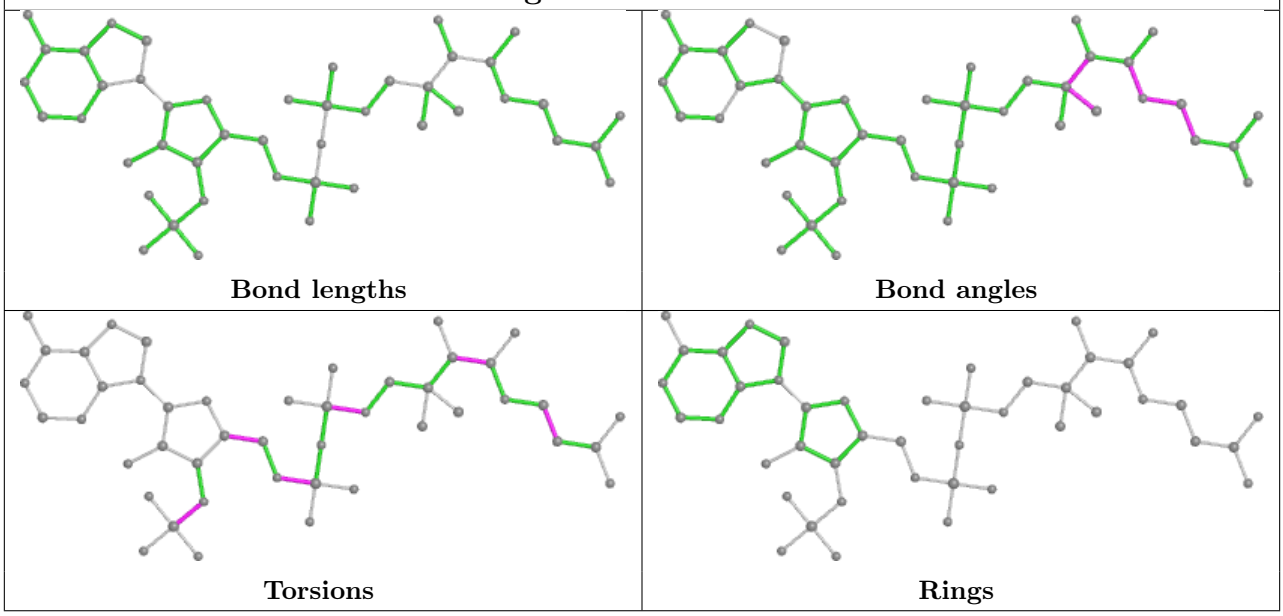
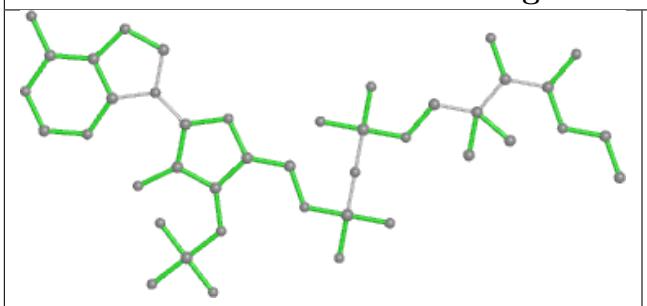
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	501	ACO	7	0

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.

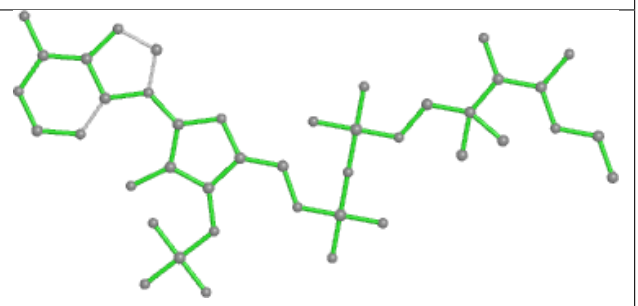
Ligand ACO E 501



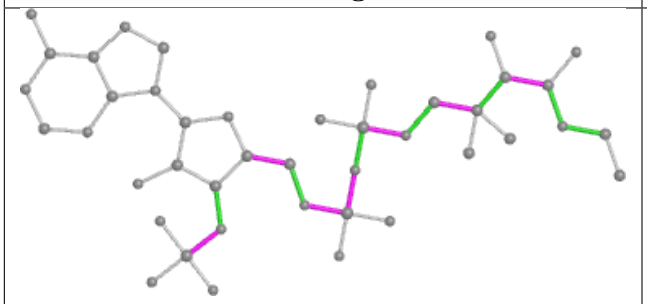
Ligand ACO D 501



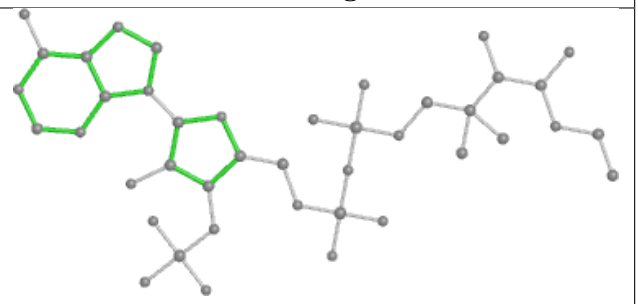
Bond lengths



Bond angles

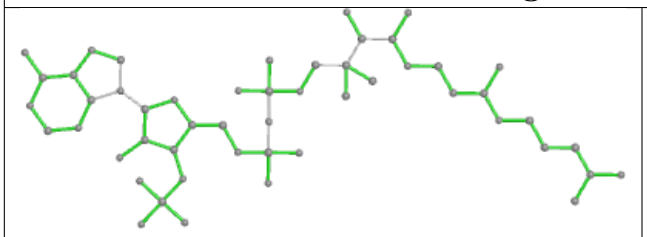


Torsions

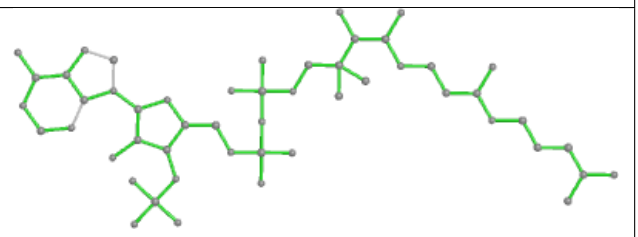


Rings

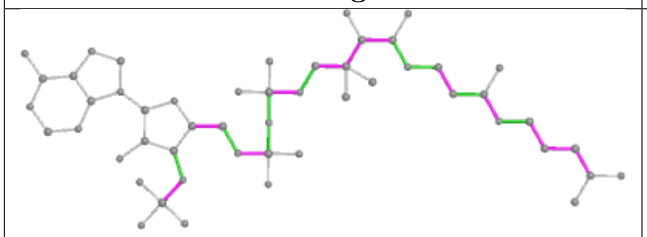
Ligand ACO A 501



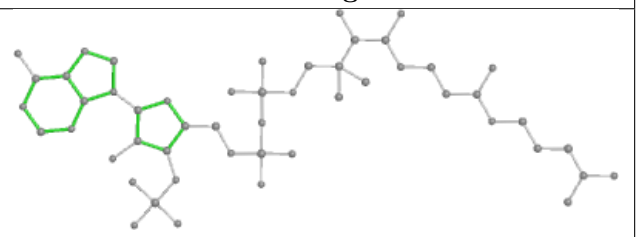
Bond lengths



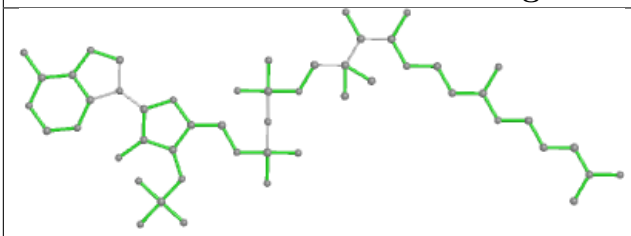
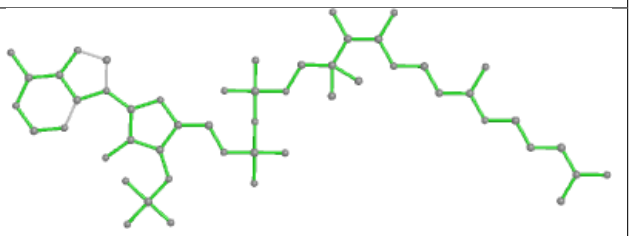
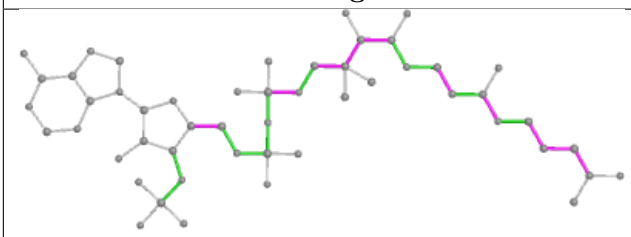
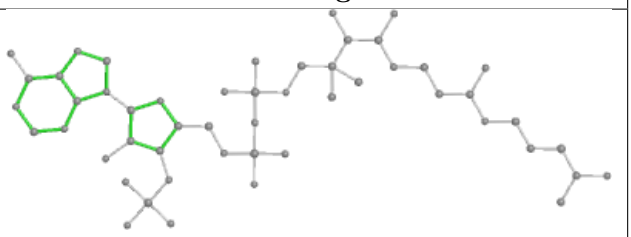
Bond angles

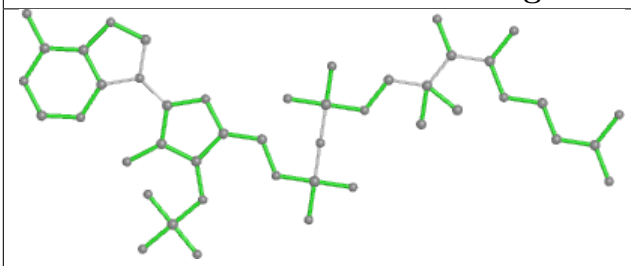
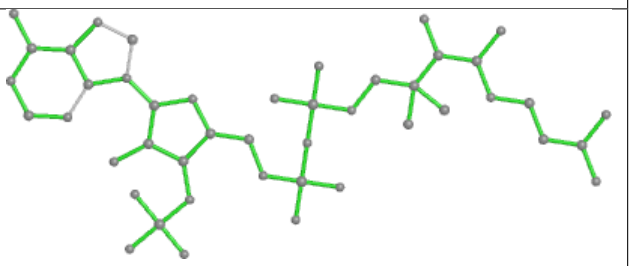
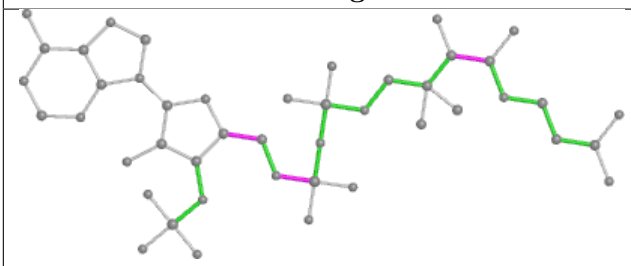
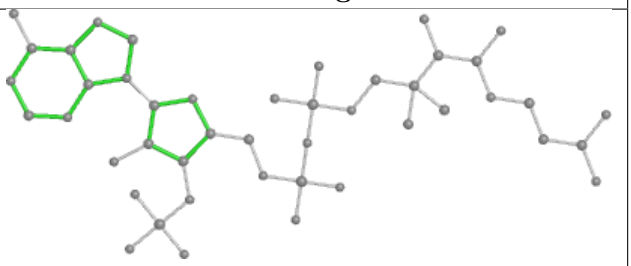


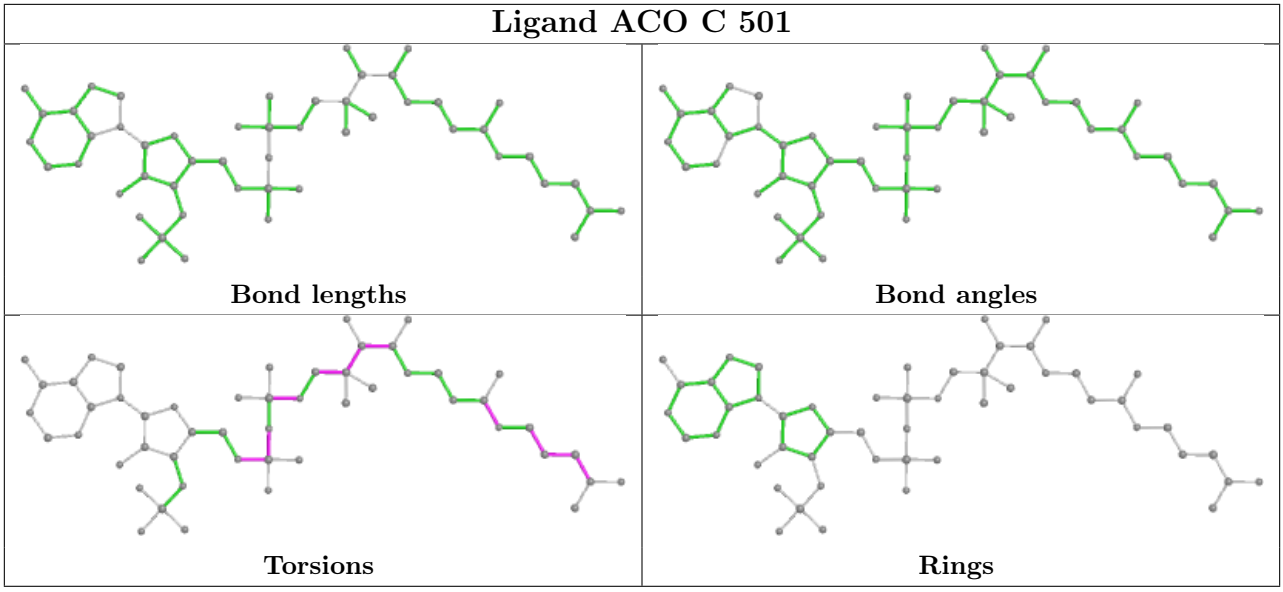
Torsions



Rings

Ligand ACO B 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand ACO F 501	
 Bond lengths	 Bond angles
 Torsions	 Rings



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	398/411 (96%)	-0.11	2 (0%)	91	94	18, 31, 46, 63	0
1	B	394/411 (95%)	0.17	2 (0%)	91	94	28, 46, 60, 76	0
1	C	395/411 (96%)	-0.06	1 (0%)	94	96	18, 31, 48, 66	0
1	D	395/411 (96%)	0.04	3 (0%)	86	89	29, 42, 57, 76	0
1	E	398/411 (96%)	0.22	9 (2%)	60	67	27, 46, 65, 81	0
1	F	397/411 (96%)	0.27	11 (2%)	53	60	27, 46, 67, 96	0
All	All	2377/2466 (96%)	0.09	28 (1%)	79	83	18, 41, 61, 96	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	232	GLY	5.2
1	C	2	SER	4.3
1	D	3	GLU	3.5
1	F	12	GLU	3.3
1	E	344	LEU	3.2
1	F	13	ASP	2.9
1	F	324	LEU	2.7
1	D	204	LYS	2.7
1	F	119	SER	2.4
1	D	266	ASP	2.4
1	B	353	THR	2.4
1	E	91	ARG	2.3
1	E	15	TYR	2.3
1	F	322	VAL	2.2
1	E	12	GLU	2.2
1	F	316	TYR	2.2
1	E	169	SER	2.2
1	E	348	SER	2.1
1	E	13	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	2	SER	2.1
1	F	173	ILE	2.1
1	F	121	ALA	2.1
1	E	163	ALA	2.1
1	F	36	GLU	2.1
1	F	350	GLU	2.0
1	F	346	HIS	2.0
1	A	92	ARG	2.0
1	E	120	GLU	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 monosaccharides in this entry.

6.4 Ligands (i)

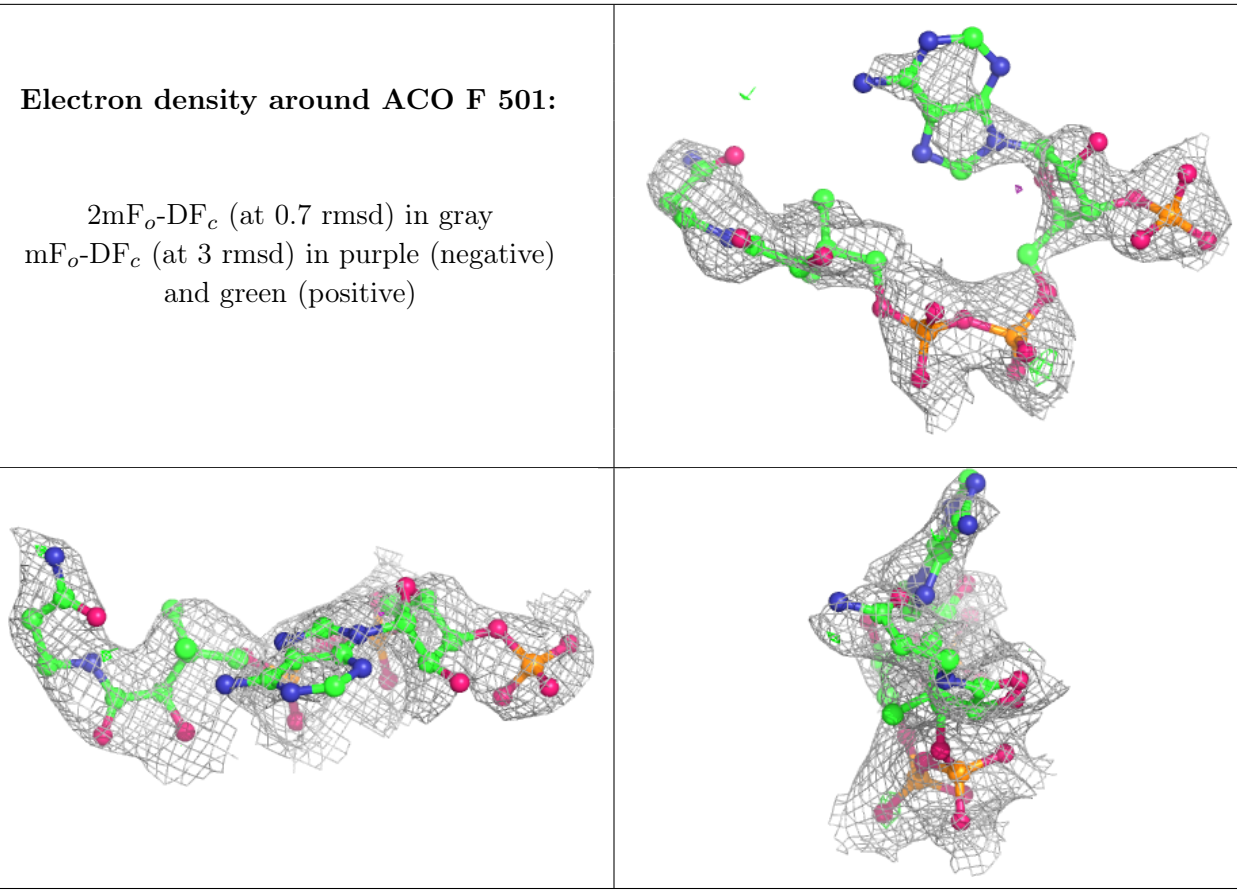
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	ACO	F	501	45/51	0.79	0.25	81,96,118,119	0
2	ACO	B	501	51/51	0.83	0.23	50,66,83,86	0
2	ACO	E	501	45/51	0.84	0.22	64,74,93,94	0
2	ACO	C	501	51/51	0.88	0.19	37,59,74,78	0
2	ACO	D	501	42/51	0.89	0.18	45,66,74,76	0
2	ACO	A	501	51/51	0.94	0.13	27,45,50,54	0

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

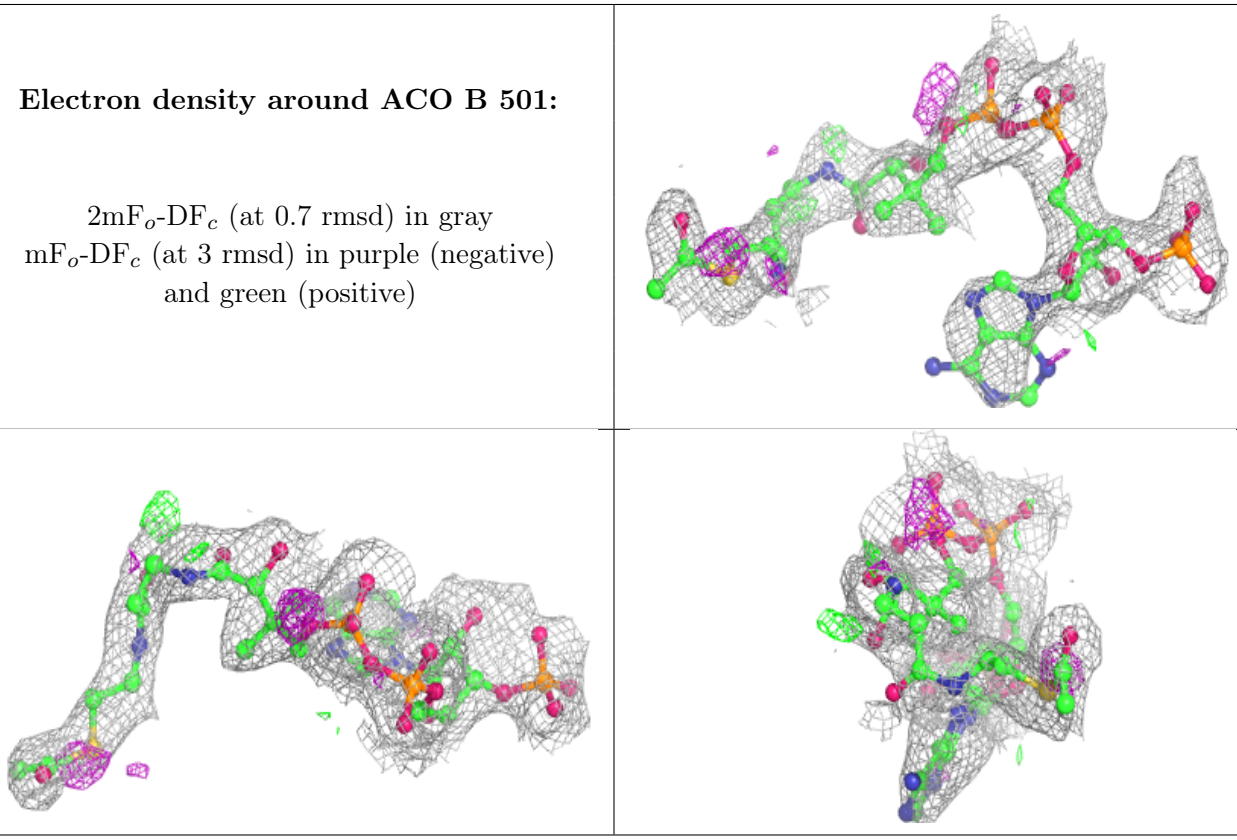
Electron density around ACO F 501:

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



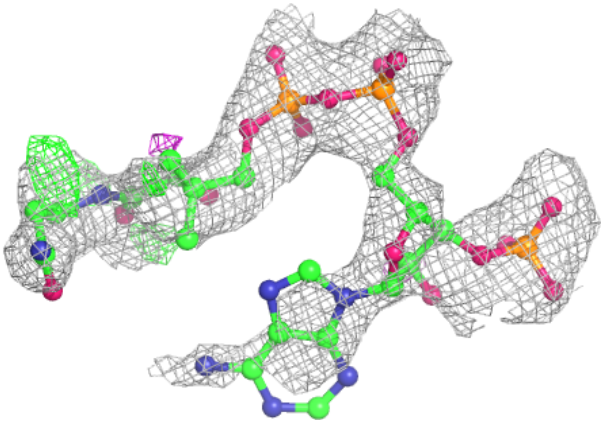
Electron density around ACO B 501:

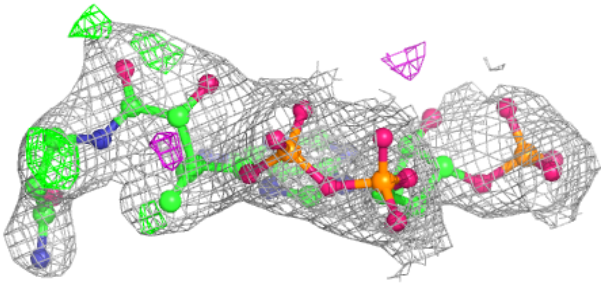
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

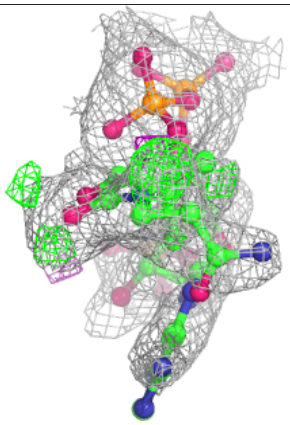


Electron density around ACO E 501:

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







Electron density around ACO C 501:

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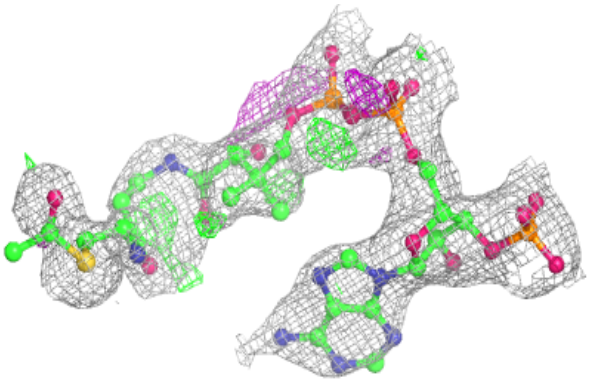
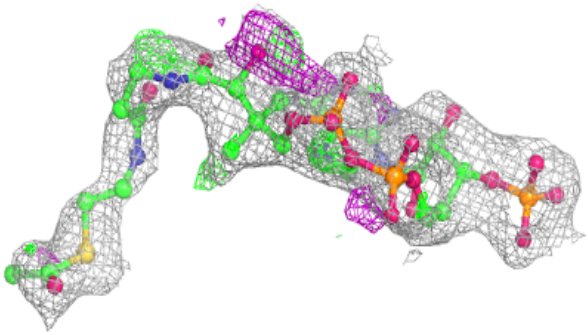
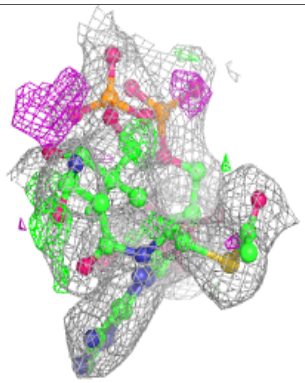
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







Electron density around ACO D 501:

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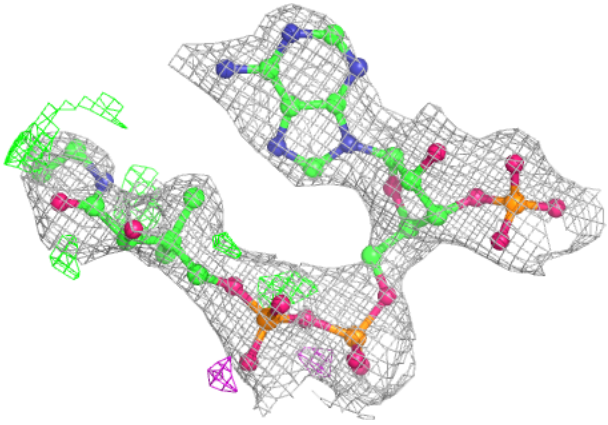
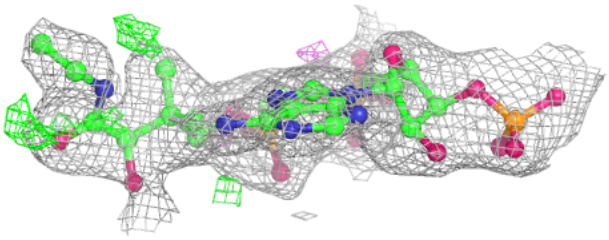
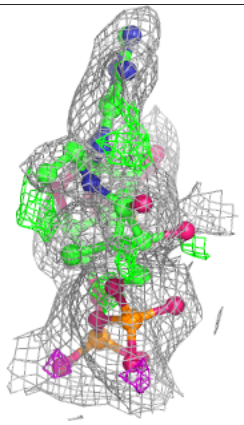
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







Electron density around ACO A 501:

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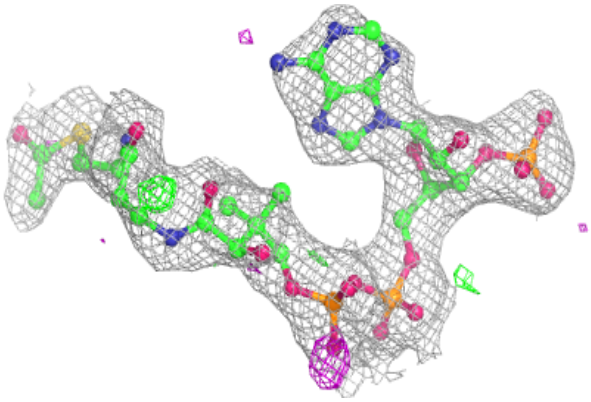
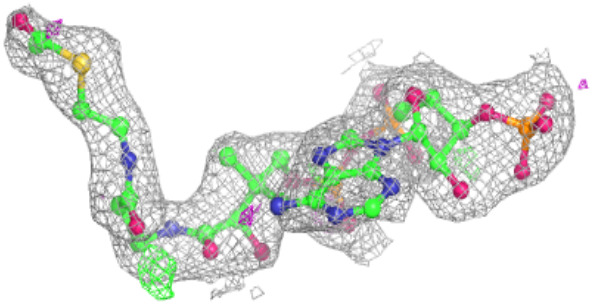
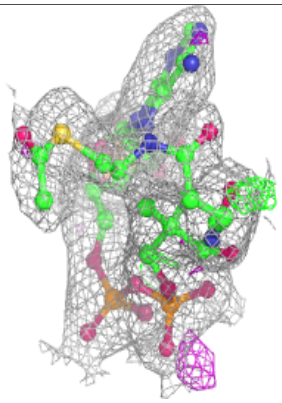
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







6.5 Other polymers (i)

There are no such residues in this entry.