



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 02:00 PM UTC

PDB ID : 6HXJ / pdb_00006hxj
Title : Structure of ATP citrate lyase from *Chlorobium limicola* in complex with citrate and coenzyme A.
Authors : Verstraete, K.; Verschueren, K.
Deposited on : 2018-10-17
Resolution : 2.58 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

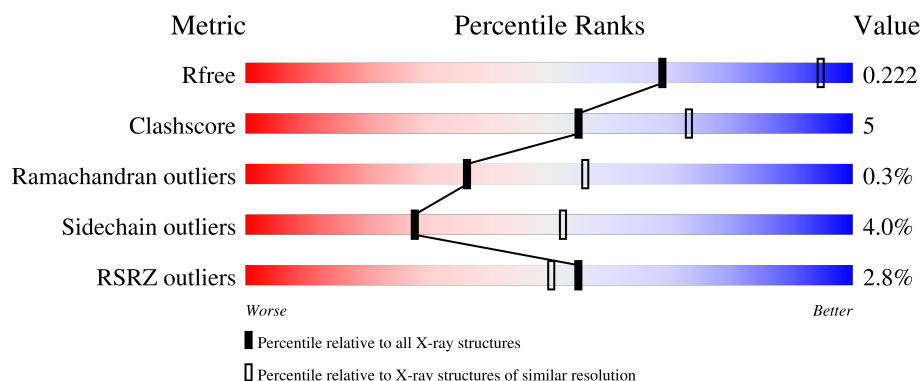
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.58 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	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (2.60-2.56)

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	398	4% 68% 15% • 16%
1	C	398	% 68% 13% • 19%
1	E	398	5% 67% 12% • 20%
1	G	398	6% 64% 15% • 19%
2	B	617	% 82% 12% • 5%

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Mol	Chain	Length	Quality of chain
2	D	617	% 83%12%••
2	F	617	% 82%13%•5%
2	H	617	2% 81%13%••

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 28715 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 ATP-citrate lyase beta-subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	0	0
			2597	1652	440	494	11			
1	C	324	Total	C	N	O	S	0	0	0
			2512	1593	426	483	10			
1	E	320	Total	C	N	O	S	0	0	0
			2480	1575	420	475	10			
1	G	322	Total	C	N	O	S	0	0	0
			2498	1583	424	481	10			

- Molecule 2 is a protein called ATP-citrate lyase alpha-subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	589	Total	C	N	O	S	0	0	0
			4464	2832	760	847	25			
2	D	591	Total	C	N	O	S	0	0	0
			4477	2840	763	849	25			
2	F	588	Total	C	N	O	S	0	0	0
			4459	2829	759	846	25			
2	H	591	Total	C	N	O	S	0	0	0
			4477	2840	763	849	25			

There are 36 discrepancies between the modelled and reference sequences:

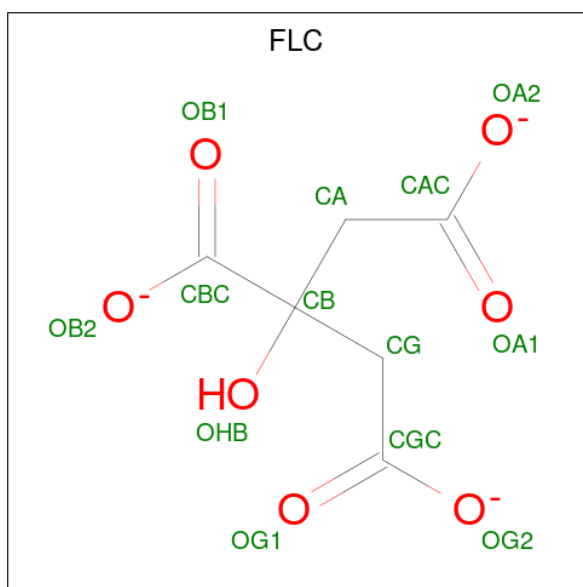
Chain	Residue	Modelled	Actual	Comment	Reference
B	609	GLY	-	expression tag	UNP Q9AJC4
B	610	GLY	-	expression tag	UNP Q9AJC4
B	611	SER	-	expression tag	UNP Q9AJC4
B	612	HIS	-	expression tag	UNP Q9AJC4
B	613	HIS	-	expression tag	UNP Q9AJC4
B	614	HIS	-	expression tag	UNP Q9AJC4
B	615	HIS	-	expression tag	UNP Q9AJC4
B	616	HIS	-	expression tag	UNP Q9AJC4

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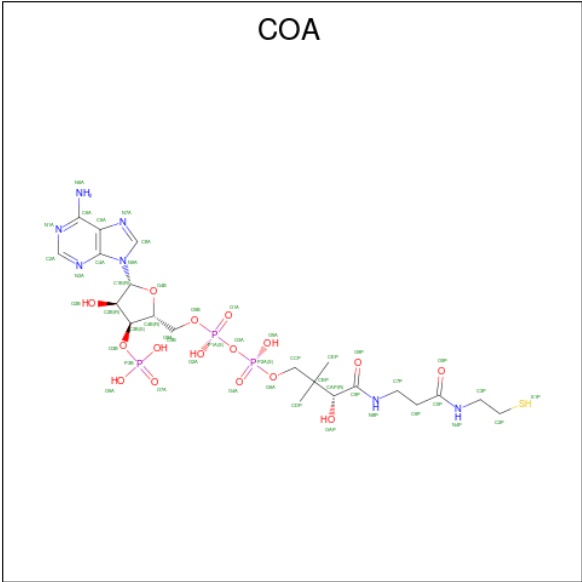
Chain	Residue	Modelled	Actual	Comment	Reference
B	617	HIS	-	expression tag	UNP Q9AJC4
D	609	GLY	-	expression tag	UNP Q9AJC4
D	610	GLY	-	expression tag	UNP Q9AJC4
D	611	SER	-	expression tag	UNP Q9AJC4
D	612	HIS	-	expression tag	UNP Q9AJC4
D	613	HIS	-	expression tag	UNP Q9AJC4
D	614	HIS	-	expression tag	UNP Q9AJC4
D	615	HIS	-	expression tag	UNP Q9AJC4
D	616	HIS	-	expression tag	UNP Q9AJC4
D	617	HIS	-	expression tag	UNP Q9AJC4
F	609	GLY	-	expression tag	UNP Q9AJC4
F	610	GLY	-	expression tag	UNP Q9AJC4
F	611	SER	-	expression tag	UNP Q9AJC4
F	612	HIS	-	expression tag	UNP Q9AJC4
F	613	HIS	-	expression tag	UNP Q9AJC4
F	614	HIS	-	expression tag	UNP Q9AJC4
F	615	HIS	-	expression tag	UNP Q9AJC4
F	616	HIS	-	expression tag	UNP Q9AJC4
F	617	HIS	-	expression tag	UNP Q9AJC4
H	609	GLY	-	expression tag	UNP Q9AJC4
H	610	GLY	-	expression tag	UNP Q9AJC4
H	611	SER	-	expression tag	UNP Q9AJC4
H	612	HIS	-	expression tag	UNP Q9AJC4
H	613	HIS	-	expression tag	UNP Q9AJC4
H	614	HIS	-	expression tag	UNP Q9AJC4
H	615	HIS	-	expression tag	UNP Q9AJC4
H	616	HIS	-	expression tag	UNP Q9AJC4
H	617	HIS	-	expression tag	UNP Q9AJC4

- Molecule 3 is CITRATE ANION (CCD ID: FLC) (formula: $C_6H_5O_7$) (labeled as "Ligand of Interest" by depositor).



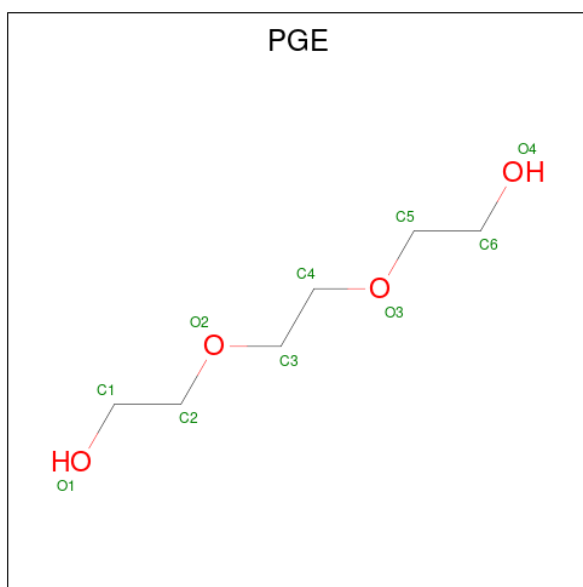
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		
3	B	1	Total	C	O	0	0
			13	6	7		
3	C	1	Total	C	O	0	0
			13	6	7		
3	D	1	Total	C	O	0	0
			13	6	7		
3	E	1	Total	C	O	0	0
			13	6	7		
3	F	1	Total	C	O	0	0
			13	6	7		
3	G	1	Total	C	O	0	0
			13	6	7		
3	H	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is COENZYME A (CCD ID: COA) (formula: $C_{21}H_{36}N_7O_{16}P_3S$) (labeled as "Ligand of Interest" by depositor).



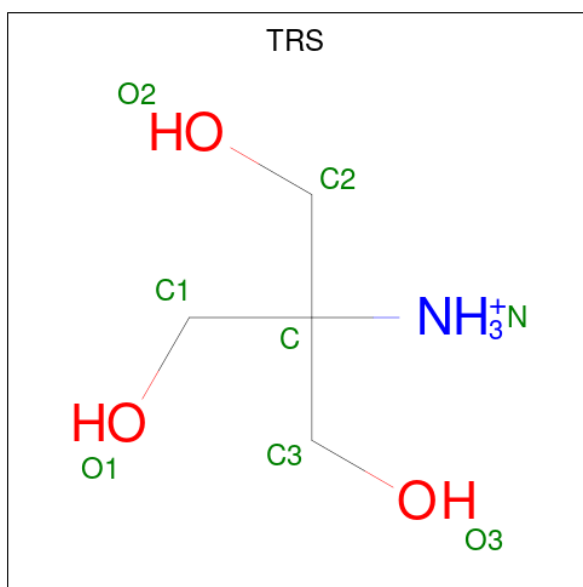
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total 37	C 15	N 5	O 14	P 3	0	0
4	B	1	Total 48	C 21	N 7	O 16	P 3 S 1	0	0
4	D	1	Total 31	C 10	N 5	O 13	P 3	0	0
4	D	1	Total 41	C 17	N 6	O 15	P 3	0	0
4	F	1	Total 31	C 10	N 5	O 13	P 3	0	0
4	F	1	Total 42	C 18	N 6	O 15	P 3	0	0
4	H	1	Total 31	C 10	N 5	O 13	P 3	0	0
4	H	1	Total 40	C 16	N 6	O 15	P 3	0	0

- Molecule 5 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: C₆H₁₄O₄).



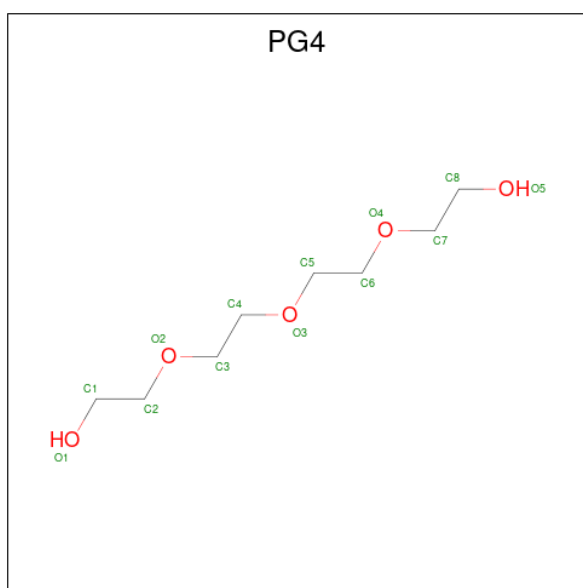
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			10	6	4		
5	C	1	Total	C	O	0	0
			10	6	4		
5	D	1	Total	C	O	0	0
			10	6	4		
5	F	1	Total	C	O	0	0
			10	6	4		
5	H	1	Total	C	O	0	0
			10	6	4		

- Molecule 6 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	N	O	0	0
			8	4	1	3		
6	D	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 7 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			13	8	5		
7	D	1	Total	C	O	0	0
			13	8	5		

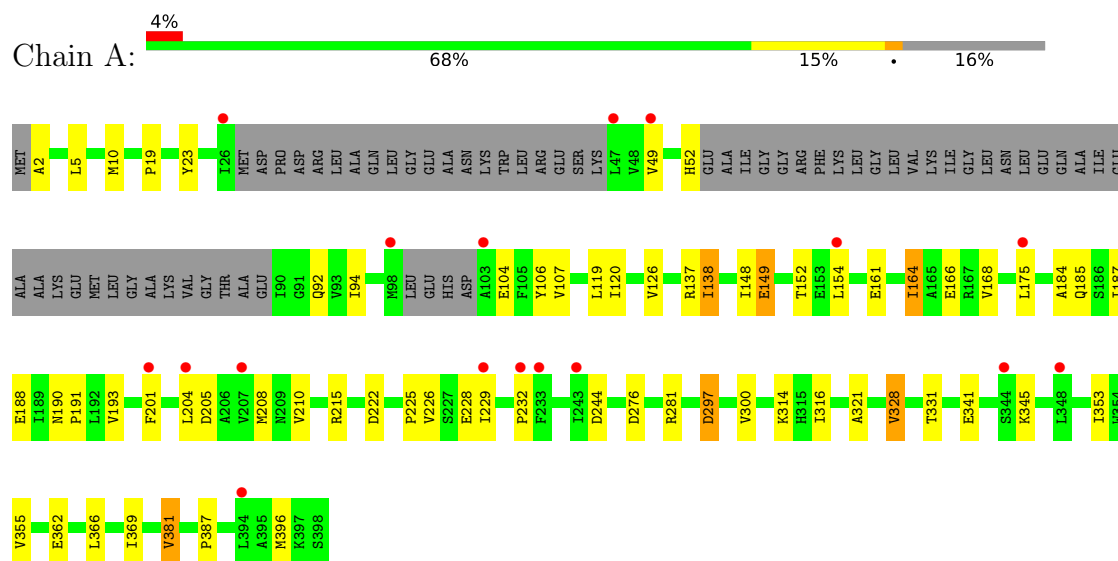
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	3	Total 3	O 3	0	0
8	B	61	Total 61	O 61	0	0
8	C	15	Total 15	O 15	0	0
8	D	58	Total 58	O 58	0	0
8	E	5	Total 5	O 5	0	0
8	F	60	Total 60	O 60	0	0
8	G	2	Total 2	O 2	0	0
8	H	50	Total 50	O 50	0	0

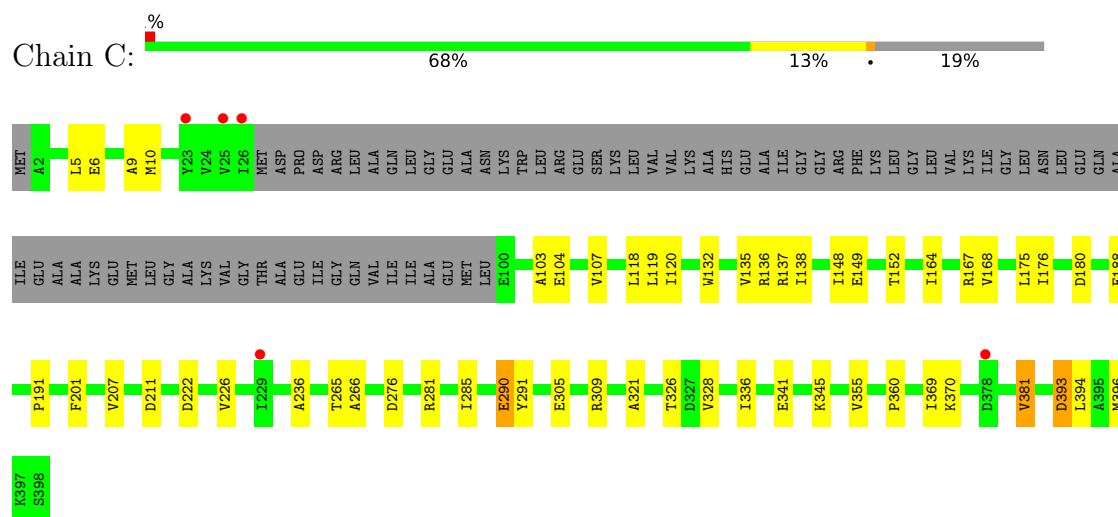
3 Residue-property plots [i](#)

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: ATP-citrate lyase beta-subunit

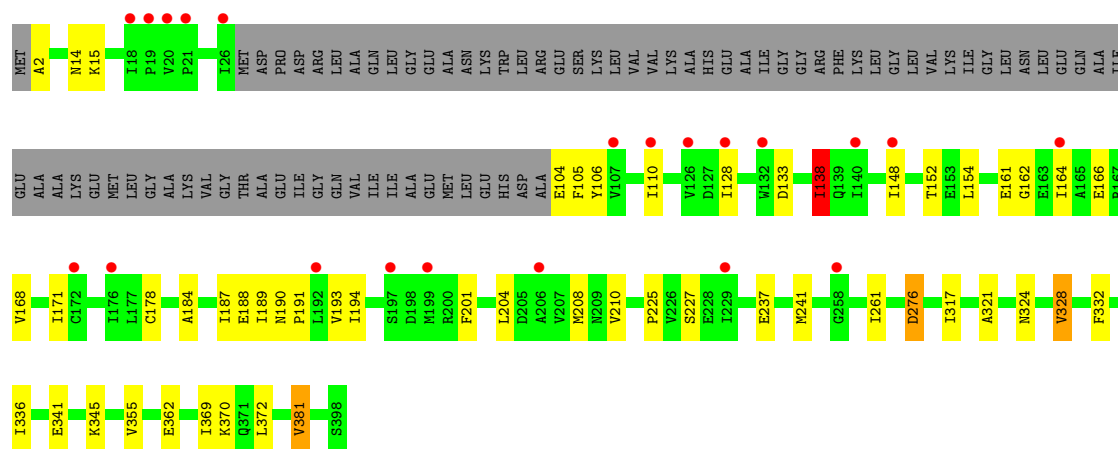


• Molecule 1: ATP-citrate lyase beta-subunit

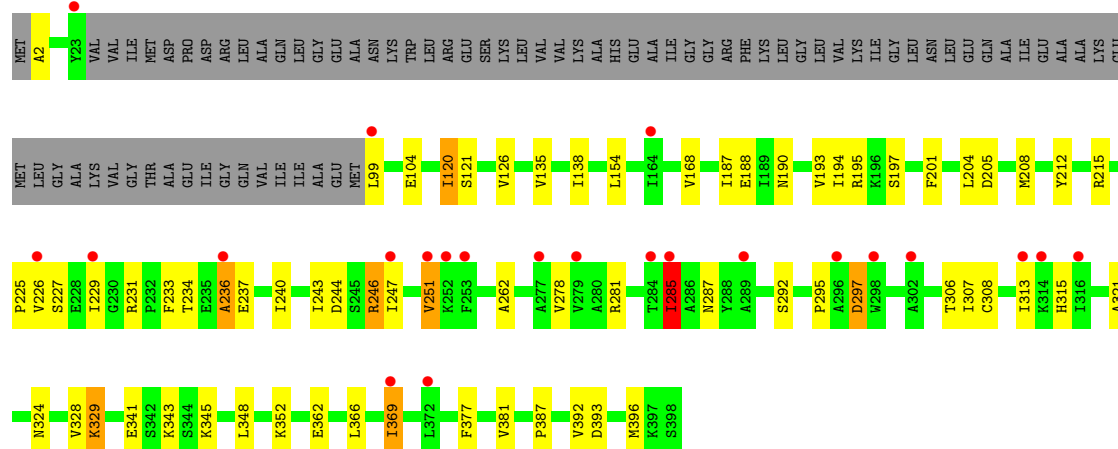


• Molecule 1: ATP-citrate lyase beta-subunit

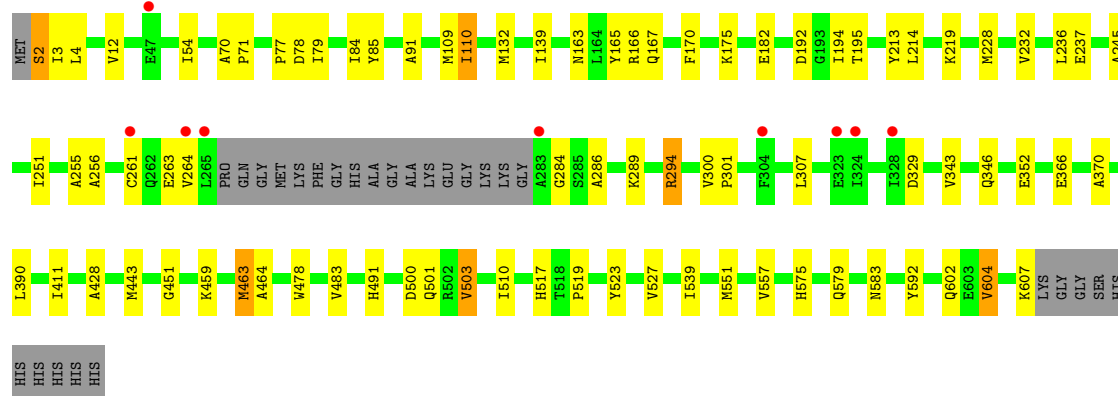
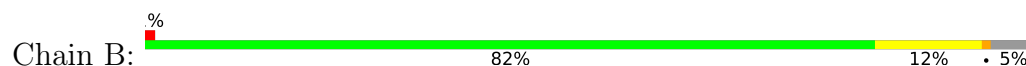




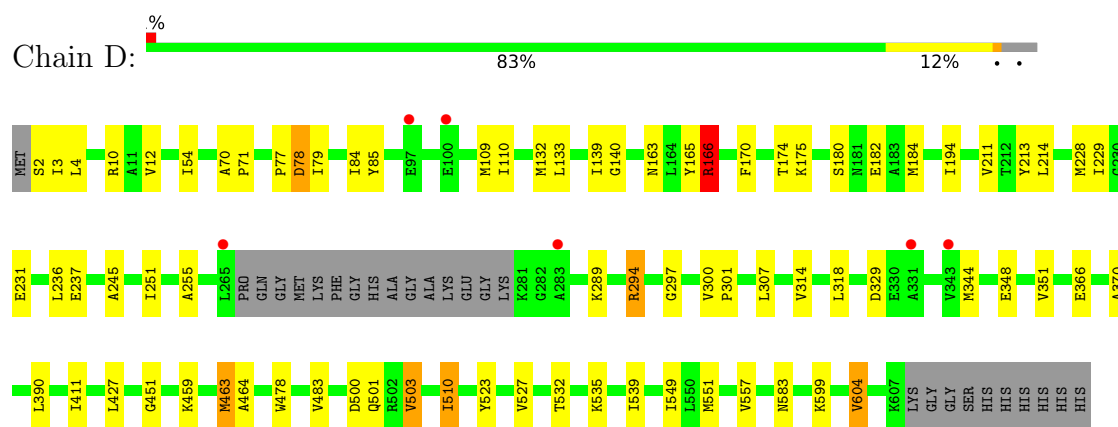
• Molecule 1: ATP-citrate lyase beta-subunit



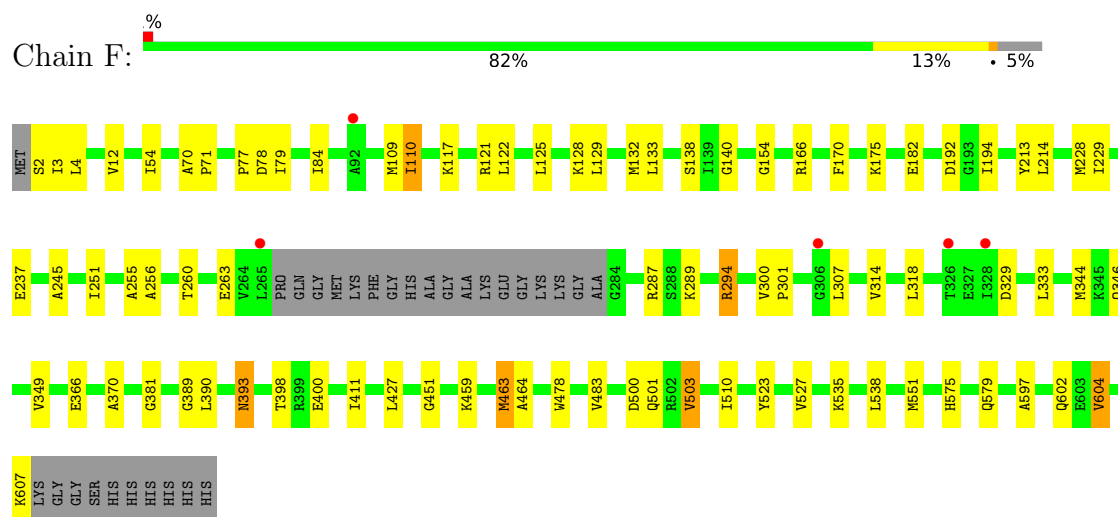
• Molecule 2: ATP-citrate lyase alpha-subunit



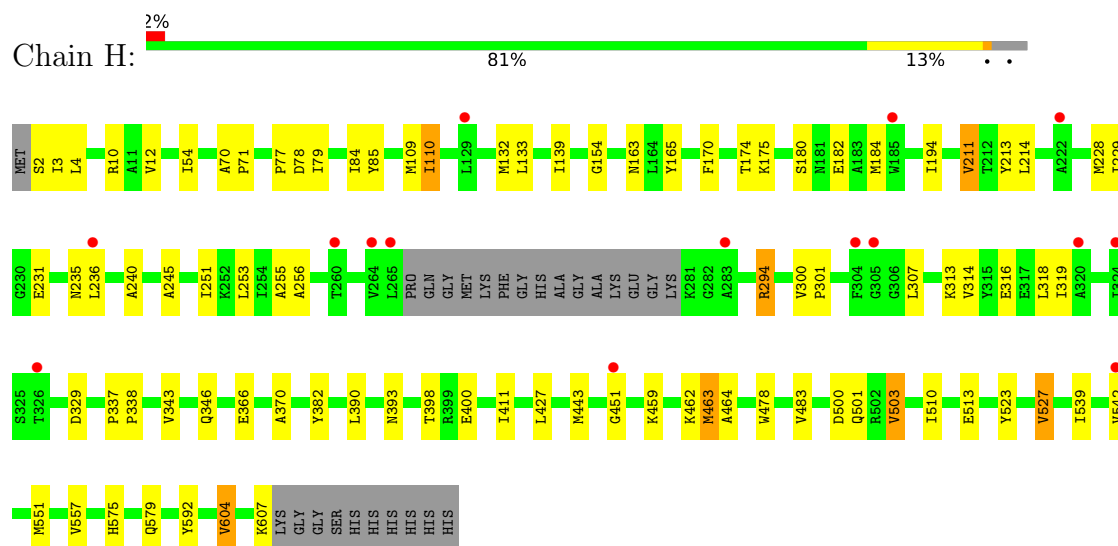
• Molecule 2: ATP-citrate lyase alpha-subunit



• Molecule 2: ATP-citrate lyase alpha-subunit



• Molecule 2: ATP-citrate lyase alpha-subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	101.67Å 134.93Å 177.71Å 90.00° 101.65° 90.00°	Depositor
Resolution (Å)	47.55 – 2.58 47.55 – 2.58	Depositor EDS
% Data completeness (in resolution range)	98.1 (47.55-2.58) 98.6 (47.55-2.58)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.02 (at 2.58Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.183 , 0.216 (Not available) , 0.222	Depositor DCC
R_{free} test set	7169 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	67.9	Xtriage
Anisotropy	0.290	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 86.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	28715	wwPDB-VP
Average B, all atoms (Å ²)	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.68% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FLC, TRS, PG4, COA, PGE

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	0.83	0/2642	1.33	9/3569 (0.3%)
1	C	0.87	0/2559	1.40	15/3460 (0.4%)
1	E	0.86	0/2526	1.40	11/3415 (0.3%)
1	G	0.88	0/2545	1.42	16/3440 (0.5%)
2	B	0.89	0/4543	1.36	19/6145 (0.3%)
2	D	0.86	0/4556	1.38	15/6161 (0.2%)
2	F	0.89	0/4538	1.37	17/6138 (0.3%)
2	H	0.89	0/4556	1.37	20/6161 (0.3%)
All	All	0.87	0/28465	1.37	122/38489 (0.3%)

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	1
1	C	0	1
2	D	0	1
2	H	0	1
All	All	0	4

There are no bond length outliers.

All (122) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	77	PRO	CA-C-N	11.60	136.27	120.38
2	F	77	PRO	C-N-CA	11.60	136.27	120.38
2	B	77	PRO	CA-C-N	11.21	135.74	120.38
2	B	77	PRO	C-N-CA	11.21	135.74	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	77	PRO	CA-C-N	11.12	135.62	120.38
2	D	77	PRO	C-N-CA	11.12	135.62	120.38
2	H	77	PRO	CA-C-N	11.05	135.52	120.38
2	H	77	PRO	C-N-CA	11.05	135.52	120.38
2	D	604	VAL	N-CA-CB	8.17	118.97	110.23
2	B	175	LYS	CA-C-N	7.54	131.50	120.95
2	B	175	LYS	C-N-CA	7.54	131.50	120.95
2	B	604	VAL	N-CA-CB	7.42	118.17	110.23
2	B	3	ILE	N-CA-CB	7.29	117.62	111.64
1	C	211	ASP	CA-CB-CG	7.29	119.89	112.60
1	E	227	SER	CB-CA-C	7.24	121.05	109.61
2	F	3	ILE	N-CA-CB	7.23	117.57	111.64
2	H	236	LEU	N-CA-C	-7.21	105.10	114.04
2	H	235	ASN	CA-CB-CG	7.20	119.80	112.60
2	D	3	ILE	N-CA-CB	7.19	117.54	111.64
2	D	2	SER	CA-C-N	-6.85	115.90	123.16
2	D	2	SER	C-N-CA	-6.85	115.90	123.16
2	H	3	ILE	N-CA-CB	6.85	117.26	111.64
2	F	2	SER	CA-C-N	-6.82	115.93	123.16
2	F	2	SER	C-N-CA	-6.82	115.93	123.16
2	D	78	ASP	CA-CB-CG	6.79	119.39	112.60
2	D	175	LYS	CA-C-N	6.76	130.42	120.95
2	D	175	LYS	C-N-CA	6.76	130.42	120.95
2	F	604	VAL	N-CA-CB	6.76	117.46	110.23
2	F	175	LYS	CA-C-N	6.51	130.07	120.95
2	F	175	LYS	C-N-CA	6.51	130.07	120.95
2	H	2	SER	CA-C-N	-6.44	116.33	123.16
2	H	2	SER	C-N-CA	-6.44	116.33	123.16
2	B	352	GLU	CB-CG-CD	6.44	123.55	112.60
2	F	78	ASP	CA-CB-CG	6.27	118.87	112.60
1	A	185	GLN	N-CA-C	-6.22	105.82	113.41
1	E	227	SER	N-CA-C	-6.17	101.71	110.35
2	B	428	ALA	CA-C-N	6.13	128.50	120.28
2	B	428	ALA	C-N-CA	6.13	128.50	120.28
1	G	285	ILE	N-CA-CB	6.12	117.20	110.53
1	E	138	ILE	N-CA-CB	6.06	119.78	111.41
2	B	78	ASP	CA-CB-CG	6.05	118.66	112.60
1	A	222	ASP	CA-CB-CG	6.05	118.65	112.60
2	H	604	VAL	N-CA-CB	6.04	116.69	110.23
1	E	276	ASP	CA-CB-CG	6.02	118.62	112.60
1	G	377	PHE	N-CA-C	6.00	118.28	110.43
1	A	276	ASP	CA-CB-CG	5.95	118.55	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	236	ALA	CA-C-N	5.92	128.13	120.44
1	G	236	ALA	C-N-CA	5.92	128.13	120.44
1	C	222	ASP	CA-CB-CG	5.88	118.48	112.60
2	B	2	SER	CA-C-N	-5.84	116.97	123.16
2	B	2	SER	C-N-CA	-5.84	116.97	123.16
1	E	14	ASN	CA-CB-CG	5.84	118.44	112.60
1	C	276	ASP	CA-CB-CG	5.79	118.39	112.60
2	H	175	LYS	CA-C-N	5.75	128.99	120.95
2	H	175	LYS	C-N-CA	5.75	128.99	120.95
2	D	175	LYS	N-CA-C	-5.74	103.77	112.04
2	H	393	ASN	CA-CB-CG	5.73	118.33	112.60
1	A	232	PRO	CA-C-N	5.70	128.80	120.71
1	A	232	PRO	C-N-CA	5.70	128.80	120.71
2	H	78	ASP	CA-CB-CG	5.67	118.27	112.60
2	H	3	ILE	CA-C-O	-5.66	115.76	120.80
2	F	597	ALA	CA-C-N	5.66	129.04	120.95
2	F	597	ALA	C-N-CA	5.66	129.04	120.95
1	C	5	LEU	CA-C-N	5.65	128.17	120.54
1	C	5	LEU	C-N-CA	5.65	128.17	120.54
1	G	329	LYS	CA-C-N	5.64	128.11	120.44
1	G	329	LYS	C-N-CA	5.64	128.11	120.44
2	D	140	GLY	CA-C-N	5.63	130.81	122.99
2	D	140	GLY	C-N-CA	5.63	130.81	122.99
1	G	387	PRO	CB-CA-C	5.57	118.63	111.56
2	H	175	LYS	N-CA-C	-5.56	104.03	112.04
1	E	178	CYS	CA-C-N	5.55	128.04	120.54
1	E	178	CYS	C-N-CA	5.55	128.04	120.54
1	E	105	PHE	CA-CB-CG	5.55	119.35	113.80
2	F	175	LYS	N-CA-C	-5.54	104.07	112.04
1	C	285	ILE	N-CA-CB	5.49	116.71	110.72
1	C	9	ALA	CA-C-N	5.44	127.57	120.28
1	C	9	ALA	C-N-CA	5.44	127.57	120.28
2	H	527	VAL	N-CA-CB	5.43	117.92	110.54
2	B	175	LYS	N-CA-C	-5.43	104.22	112.04
1	C	226	VAL	CA-C-N	5.41	128.39	120.71
1	C	226	VAL	C-N-CA	5.41	128.39	120.71
2	D	3	ILE	CA-C-O	-5.35	116.04	120.80
1	A	226	VAL	CA-C-N	5.34	128.35	120.82
1	A	226	VAL	C-N-CA	5.34	128.35	120.82
1	G	369	ILE	CA-C-N	5.34	127.43	120.28
1	G	369	ILE	C-N-CA	5.34	127.43	120.28
2	B	3	ILE	CA-C-O	-5.33	116.05	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	244	ASP	CA-CB-CG	5.29	117.89	112.60
1	G	126	VAL	CA-C-N	5.28	129.53	120.72
1	G	126	VAL	C-N-CA	5.28	129.53	120.72
1	A	244	ASP	CA-CB-CG	5.27	117.87	112.60
2	H	542	VAL	N-CA-CB	5.26	117.69	110.54
1	G	246	ARG	N-CA-C	-5.26	108.63	114.62
2	B	284	GLY	CA-C-N	5.25	128.16	120.71
2	B	284	GLY	C-N-CA	5.25	128.16	120.71
1	C	393	ASP	CA-CB-CG	5.24	117.84	112.60
1	C	236	ALA	CA-C-N	5.22	127.55	120.44
1	C	236	ALA	C-N-CA	5.22	127.55	120.44
1	E	133	ASP	CA-CB-CG	5.21	117.81	112.60
1	E	171	ILE	CA-C-N	5.21	127.51	120.38
1	E	171	ILE	C-N-CA	5.21	127.51	120.38
2	H	245	ALA	CA-C-N	5.18	127.48	120.38
2	H	245	ALA	C-N-CA	5.18	127.48	120.38
2	F	3	ILE	CA-C-O	-5.17	116.20	120.80
2	D	245	ALA	CA-C-N	5.13	127.41	120.38
2	D	245	ALA	C-N-CA	5.13	127.41	120.38
1	G	393	ASP	CA-C-N	5.13	127.15	120.28
1	G	393	ASP	C-N-CA	5.13	127.15	120.28
1	A	387	PRO	CB-CA-C	5.12	118.06	111.56
2	B	245	ALA	CA-C-N	5.11	127.37	120.38
2	B	245	ALA	C-N-CA	5.11	127.37	120.38
2	H	3	ILE	N-CA-C	5.10	115.65	111.62
1	C	207	VAL	CA-C-N	-5.10	115.96	123.00
1	C	207	VAL	C-N-CA	-5.10	115.96	123.00
2	F	245	ALA	CA-C-N	5.10	127.36	120.38
2	F	245	ALA	C-N-CA	5.10	127.36	120.38
2	B	263	GLU	N-CA-C	-5.09	107.75	114.31
2	F	333	LEU	N-CA-C	5.07	116.46	110.07
2	H	211	VAL	N-CA-CB	5.05	117.41	110.54
1	G	233	PHE	CA-CB-CG	5.04	118.84	113.80
2	F	140	GLY	N-CA-C	5.04	117.53	110.38

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	215	ARG	Sidechain
1	C	136	ARG	Sidechain
2	D	166	ARG	Sidechain

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Mol	Chain	Res	Type	Group
2	H	10	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	2597	0	2584	33	0
1	C	2512	0	2476	24	0
1	E	2480	0	2454	23	0
1	G	2498	0	2458	41	0
2	B	4464	0	4524	43	0
2	D	4477	0	4540	45	0
2	F	4459	0	4519	44	0
2	H	4477	0	4540	40	0
3	A	13	0	5	0	0
3	B	13	0	5	0	0
3	C	13	0	5	0	0
3	D	13	0	5	0	0
3	E	13	0	5	0	0
3	F	13	0	5	0	0
3	G	13	0	5	0	0
3	H	13	0	5	0	0
4	B	85	0	52	2	0
4	D	72	0	33	0	0
4	F	73	0	35	0	0
4	H	71	0	32	0	0
5	B	10	0	14	2	0
5	C	10	0	14	0	0
5	D	10	0	14	1	0
5	F	10	0	14	0	0
5	H	10	0	14	2	0
6	B	8	0	12	0	0
6	D	8	0	12	0	0
7	C	13	0	18	1	0
7	D	13	0	18	1	0
8	A	3	0	0	0	0
8	B	61	0	0	1	0
8	C	15	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	D	58	0	0	0	0
8	E	5	0	0	0	0
8	F	60	0	0	0	0
8	G	2	0	0	0	0
8	H	50	0	0	0	0
All	All	28715	0	28417	274	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 (274) 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:D:163:ASN:HB3	2:D:166:ARG:NH2	1.67	1.10
2:D:163:ASN:CB	2:D:166:ARG:NH2	2.22	1.01
1:G:231:ARG:HH12	1:G:234:THR:HG23	1.26	0.98
2:B:166:ARG:NH2	2:B:192:ASP:O	1.97	0.95
2:B:607:LYS:NZ	8:B:1101:HOH:O	1.57	0.95
2:B:592:TYR:HB2	2:D:344:MET:SD	2.10	0.91
2:F:166:ARG:NH1	2:F:192:ASP:O	2.10	0.82
2:F:166:ARG:HD2	2:F:166:ARG:O	1.82	0.79
2:B:163:ASN:HA	2:B:165:TYR:CE1	2.21	0.76
1:G:231:ARG:NH1	1:G:234:THR:HG23	2.00	0.74
2:B:219:LYS:HZ3	5:B:1004:PGE:H32	1.54	0.73
1:G:281:ARG:HB2	1:G:396:MET:HE1	1.71	0.73
1:E:138:ILE:HG12	1:E:154:LEU:HD22	1.71	0.72
2:D:163:ASN:CB	2:D:166:ARG:HH21	2.04	0.71
1:G:308:CYS:O	1:G:313:ILE:HD13	1.89	0.71
1:G:328:VAL:CG2	1:G:362:GLU:HA	2.21	0.70
1:A:316:ILE:HD12	1:A:353:ILE:HG12	1.74	0.69
2:B:219:LYS:NZ	5:B:1004:PGE:H32	2.08	0.69
2:B:214:LEU:HD11	2:B:228:MET:HE1	1.76	0.68
2:D:163:ASN:HB3	2:D:166:ARG:HH21	1.51	0.67
2:F:344:MET:SD	2:H:592:TYR:HB2	2.35	0.67
1:E:2:ALA:HB1	1:E:225:PRO:HB3	1.78	0.66
1:G:226:VAL:HG12	1:G:227:SER:N	2.11	0.66
1:G:328:VAL:HG21	1:G:362:GLU:HA	1.78	0.66
2:D:163:ASN:CB	2:D:166:ARG:HH22	2.10	0.65
2:B:91:ALA:HB1	2:B:109:MET:HE3	1.78	0.64
2:D:599:LYS:HZ2	7:D:1005:PG4:H72	1.63	0.63
2:H:462:LYS:HE3	5:H:1004:PGE:H12	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:462:LYS:HE3	5:H:1004:PGE:C1	2.29	0.63
2:D:4:LEU:HD11	2:D:213:TYR:CE1	2.35	0.62
1:A:107:VAL:HG11	1:A:175:LEU:HD22	1.81	0.62
2:B:232:VAL:HG13	2:B:286:ALA:HB2	1.81	0.62
2:H:398:THR:HG22	2:H:400:GLU:H	1.62	0.62
1:G:138:ILE:HG23	1:G:154:LEU:HD13	1.80	0.62
1:A:148:ILE:O	1:A:152:THR:HG23	2.00	0.61
2:F:110:ILE:HG22	2:F:138:SER:O	2.01	0.60
1:G:226:VAL:HG12	1:G:227:SER:H	1.66	0.60
1:A:138:ILE:HG12	1:A:154:LEU:HD22	1.83	0.60
2:D:109:MET:HE2	2:D:133:LEU:HD11	1.83	0.60
2:F:166:ARG:HD2	2:F:166:ARG:C	2.26	0.59
2:F:214:LEU:HD11	2:F:228:MET:HE1	1.83	0.59
2:D:4:LEU:HD11	2:D:213:TYR:HE1	1.66	0.59
1:E:321:ALA:HB1	2:F:182:GLU:HB2	1.83	0.59
1:A:297:ASP:N	1:A:297:ASP:OD1	2.34	0.59
2:F:109:MET:HE2	2:F:133:LEU:HD11	1.85	0.59
2:H:214:LEU:HD11	2:H:228:MET:HE1	1.83	0.59
1:A:321:ALA:HB1	2:B:182:GLU:HB2	1.85	0.59
2:D:366:GLU:HB3	2:F:501:GLN:HB3	1.85	0.58
2:H:4:LEU:HD11	2:H:213:TYR:HE1	1.67	0.58
2:F:398:THR:HG22	2:F:400:GLU:H	1.68	0.58
1:G:308:CYS:O	1:G:313:ILE:CD1	2.51	0.58
2:H:4:LEU:HD11	2:H:213:TYR:CE1	2.39	0.58
1:C:167:ARG:HG2	1:C:201:PHE:CE1	2.38	0.58
1:C:118:LEU:HB3	1:C:138:ILE:CG2	2.33	0.58
2:F:4:LEU:HD11	2:F:213:TYR:HE1	1.68	0.58
2:B:517:HIS:CE1	2:B:519:PRO:HD3	2.39	0.58
2:D:163:ASN:HB2	2:D:166:ARG:HH22	1.67	0.57
1:E:261:ILE:HD11	1:E:317:ILE:HD11	1.86	0.57
2:H:109:MET:HE2	2:H:133:LEU:HD11	1.86	0.57
2:D:551:MET:HE3	2:D:551:MET:HA	1.86	0.57
1:A:5:LEU:HD13	1:A:52:HIS:ND1	2.18	0.57
1:A:138:ILE:HG23	1:A:154:LEU:HD13	1.86	0.57
2:B:4:LEU:HD11	2:B:213:TYR:HE1	1.68	0.57
2:F:4:LEU:HD11	2:F:213:TYR:CE1	2.39	0.57
2:B:551:MET:HE3	2:B:551:MET:HA	1.87	0.57
2:B:4:LEU:HD11	2:B:213:TYR:CE1	2.40	0.57
1:A:2:ALA:HB1	1:A:225:PRO:HB3	1.86	0.56
1:E:328:VAL:CG2	1:E:362:GLU:HA	2.34	0.56
2:F:125:LEU:HA	2:F:128:LYS:HG2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:297:ASP:OD1	1:G:297:ASP:N	2.38	0.56
2:B:366:GLU:HB3	2:H:501:GLN:HB3	1.88	0.55
2:F:117:LYS:HE3	2:F:121:ARG:NH2	2.21	0.55
1:C:281:ARG:HD2	1:C:393:ASP:OD1	2.07	0.54
2:B:575:HIS:O	2:B:579:GLN:HG2	2.07	0.54
1:A:119:LEU:HG	1:A:137:ARG:HB3	1.90	0.54
1:C:321:ALA:HB1	2:D:182:GLU:HB2	1.90	0.54
2:H:551:MET:HE3	2:H:551:MET:HA	1.90	0.54
1:A:366:LEU:HA	1:A:369:ILE:HG22	1.90	0.53
1:C:148:ILE:O	1:C:152:THR:HG23	2.08	0.53
1:C:103:ALA:HB2	7:C:1002:PG4:H32	1.91	0.52
2:D:214:LEU:HD11	2:D:228:MET:HE1	1.90	0.52
1:A:19:PRO:HB3	1:A:201:PHE:O	2.09	0.52
2:H:294:ARG:HD3	2:H:300:VAL:HB	1.92	0.52
2:F:381:GLY:O	2:H:607:LYS:HE2	2.08	0.52
1:G:287:ASN:HD21	1:G:307:ILE:HG12	1.74	0.52
1:A:187:ILE:HG12	1:A:208:MET:HG3	1.92	0.52
1:A:52:HIS:HB2	1:A:92:GLN:HB3	1.92	0.52
1:A:149:GLU:CD	1:A:149:GLU:H	2.17	0.52
2:D:501:GLN:HB3	2:F:366:GLU:HB3	1.91	0.51
2:B:294:ARG:HD3	2:B:300:VAL:HB	1.91	0.51
1:E:148:ILE:O	1:E:152:THR:HG23	2.09	0.51
1:G:392:VAL:CG1	1:G:396:MET:HE2	2.40	0.51
2:F:464:ALA:HB1	2:F:523:TYR:CE1	2.46	0.51
2:F:535:LYS:HB2	2:F:538:LEU:HG	1.92	0.51
2:F:551:MET:HE3	2:F:551:MET:HA	1.92	0.51
1:A:341:GLU:O	1:A:345:LYS:HG2	2.11	0.51
1:G:341:GLU:O	1:G:345:LYS:HG2	2.11	0.51
2:D:10:ARG:HD3	2:D:78:ASP:CG	2.36	0.50
2:D:163:ASN:CG	2:D:166:ARG:HH21	2.19	0.50
2:D:294:ARG:HD3	2:D:300:VAL:HB	1.92	0.50
1:A:107:VAL:CG1	1:A:175:LEU:HD22	2.41	0.50
1:E:328:VAL:O	1:E:332:PHE:HB2	2.12	0.50
1:G:281:ARG:HB2	1:G:396:MET:CE	2.42	0.50
1:G:321:ALA:HB1	2:H:182:GLU:HB2	1.93	0.50
2:B:12:VAL:HB	2:B:79:ILE:HD13	1.93	0.50
2:F:12:VAL:HB	2:F:79:ILE:HD13	1.94	0.50
2:H:12:VAL:HB	2:H:79:ILE:HD13	1.93	0.50
1:C:341:GLU:O	1:C:345:LYS:HG2	2.12	0.49
2:F:294:ARG:HD3	2:F:300:VAL:HB	1.93	0.49
2:F:70:ALA:HB3	2:F:71:PRO:HD3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:226:VAL:CG1	1:G:227:SER:H	2.25	0.49
1:E:328:VAL:HG21	1:E:362:GLU:HA	1.94	0.49
1:A:106:TYR:HD1	1:A:190:ASN:HB2	1.78	0.49
2:F:166:ARG:C	2:F:166:ARG:CD	2.85	0.49
2:B:464:ALA:HB1	2:B:523:TYR:CE1	2.47	0.49
1:G:121:SER:HB2	1:G:135:VAL:HG22	1.94	0.49
1:A:10:MET:HB3	1:A:23:TYR:CE2	2.48	0.49
1:C:167:ARG:HG2	1:C:201:PHE:HE1	1.78	0.49
1:G:2:ALA:HB1	1:G:225:PRO:HB3	1.95	0.49
2:H:85:TYR:CD1	2:H:110:ILE:HG12	2.48	0.49
1:C:355:VAL:HB	1:C:381:VAL:HB	1.94	0.48
2:F:229:ILE:HD11	2:F:307:LEU:HD21	1.95	0.48
2:D:532:THR:HA	2:D:535:LYS:O	2.13	0.48
2:F:132:MET:HE2	2:F:132:MET:HB2	1.79	0.48
1:G:392:VAL:HG12	1:G:396:MET:HE2	1.95	0.48
2:D:211:VAL:HA	2:D:214:LEU:HD12	1.94	0.48
2:B:443:MET:HE1	2:H:443:MET:HE1	1.95	0.48
2:D:464:ALA:HB1	2:D:523:TYR:CE1	2.49	0.48
2:D:229:ILE:HD11	2:D:307:LEU:HD21	1.95	0.48
2:H:464:ALA:HB1	2:H:523:TYR:CE1	2.48	0.48
1:E:341:GLU:O	1:E:345:LYS:HG2	2.14	0.48
1:G:240:ILE:HG23	1:G:251:VAL:HG22	1.96	0.48
1:E:138:ILE:HG12	1:E:154:LEU:CD2	2.39	0.47
1:E:355:VAL:HB	1:E:381:VAL:HB	1.95	0.47
2:B:2:SER:N	2:B:167:GLN:HE22	2.12	0.47
1:G:226:VAL:CG1	1:G:227:SER:N	2.77	0.47
1:C:305:GLU:O	1:C:309:ARG:HG2	2.15	0.47
2:D:12:VAL:HB	2:D:79:ILE:HD13	1.96	0.47
1:E:104:GLU:HB3	1:E:193:VAL:HG12	1.97	0.47
2:B:163:ASN:HA	2:B:165:TYR:HE1	1.75	0.47
1:E:194:ILE:HD13	1:E:201:PHE:CE1	2.49	0.47
1:E:187:ILE:HG12	1:E:208:MET:HG3	1.97	0.47
1:G:366:LEU:HA	1:G:369:ILE:HG22	1.97	0.47
1:A:328:VAL:CG2	1:A:362:GLU:HA	2.45	0.46
1:G:194:ILE:HD13	1:G:201:PHE:CE1	2.49	0.46
2:D:510:ILE:HD13	2:D:549:ILE:CD1	2.46	0.46
2:B:261:CYS:HB3	2:B:264:VAL:HG12	1.97	0.46
2:D:85:TYR:CD2	2:D:110:ILE:HG12	2.50	0.46
1:G:243:ILE:HA	1:G:246:ARG:HD2	1.97	0.46
2:B:85:TYR:CD2	2:B:110:ILE:HG12	2.50	0.46
1:C:336:ILE:HG12	1:C:369:ILE:HD12	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:287:ASN:ND2	1:G:307:ILE:HG12	2.30	0.46
2:B:237:GLU:HB2	2:B:289:LYS:HD3	1.98	0.46
1:C:120:ILE:HD11	1:C:168:VAL:CG1	2.46	0.46
1:E:237:GLU:O	1:E:241:MET:HG3	2.16	0.46
2:H:500:ASP:HB3	2:H:503:VAL:HG13	1.97	0.46
1:A:190:ASN:O	1:A:205:ASP:HB2	2.15	0.45
1:E:328:VAL:HG22	1:E:362:GLU:HA	1.97	0.45
2:B:500:ASP:HB3	2:B:503:VAL:HG13	1.97	0.45
2:B:501:GLN:HB3	2:H:366:GLU:HB3	1.96	0.45
1:E:184:ALA:HA	1:E:210:VAL:HA	1.97	0.45
2:F:370:ALA:HB3	2:F:390:LEU:HD22	1.98	0.45
2:F:575:HIS:O	2:F:579:GLN:HG2	2.16	0.45
1:G:292:SER:O	1:G:295:PRO:HG3	2.16	0.45
2:B:343:VAL:HG21	2:F:349:VAL:HG23	1.98	0.45
1:G:104:GLU:HG2	1:G:193:VAL:HG12	1.98	0.45
2:D:500:ASP:HB3	2:D:503:VAL:HG13	1.98	0.45
1:E:161:GLU:O	1:E:164:ILE:HG13	2.17	0.45
2:F:389:GLY:O	2:F:393:ASN:HB2	2.17	0.45
1:G:99:LEU:HD21	1:G:195:ARG:CZ	2.46	0.45
2:H:70:ALA:HB3	2:H:71:PRO:HD3	1.98	0.45
2:F:314:VAL:O	2:F:318:LEU:HG	2.17	0.45
2:D:370:ALA:HB3	2:D:390:LEU:HD22	1.98	0.45
1:G:120:ILE:HD11	1:G:168:VAL:HG11	1.99	0.44
1:C:119:LEU:HD23	1:C:135:VAL:HG11	1.98	0.44
2:F:170:PHE:O	2:F:194:ILE:HA	2.18	0.44
2:H:132:MET:HB2	2:H:132:MET:HE2	1.75	0.44
2:D:70:ALA:HB3	2:D:71:PRO:HD3	1.98	0.44
2:B:84:ILE:HB	2:B:109:MET:HG2	2.00	0.44
2:F:125:LEU:HD12	2:F:128:LYS:HD2	1.98	0.44
2:H:255:ALA:O	2:H:301:PRO:HD2	2.18	0.44
1:A:328:VAL:HG22	1:A:362:GLU:HA	1.99	0.44
1:E:324:ASN:O	2:F:154:GLY:HA2	2.18	0.44
1:G:240:ILE:HD13	1:G:243:ILE:HD11	1.99	0.44
1:G:324:ASN:O	2:H:154:GLY:HA2	2.18	0.44
2:H:170:PHE:O	2:H:194:ILE:HA	2.18	0.44
2:D:348:GLU:C	2:H:337:PRO:HB3	2.42	0.44
2:H:84:ILE:HB	2:H:109:MET:HG2	2.00	0.44
1:G:315:HIS:HE1	1:G:352:LYS:HD2	1.82	0.44
2:H:575:HIS:O	2:H:579:GLN:HG2	2.18	0.44
1:G:343:LYS:HG3	1:G:348:LEU:HB2	2.00	0.44
2:H:463:MET:HE1	2:H:478:TRP:CZ3	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:592:TYR:HD1	2:D:351:VAL:HG11	1.82	0.43
1:G:190:ASN:O	1:G:205:ASP:HB3	2.18	0.43
2:H:370:ALA:HB3	2:H:390:LEU:HD22	1.99	0.43
2:B:70:ALA:HB3	2:B:71:PRO:HD3	2.00	0.43
1:C:107:VAL:HG11	1:C:175:LEU:HD22	2.01	0.43
2:B:256:ALA:HB2	2:B:307:LEU:HD13	2.00	0.43
1:G:236:ALA:HB1	1:G:306:THR:HG23	2.00	0.43
1:G:262:ALA:HB1	1:G:307:ILE:HG23	1.99	0.43
2:H:163:ASN:HA	2:H:165:TYR:CE1	2.54	0.43
2:D:84:ILE:HB	2:D:109:MET:HG2	2.00	0.43
2:D:237:GLU:HB2	2:D:289:LYS:HD3	1.99	0.43
1:G:187:ILE:HG12	1:G:208:MET:HG3	2.00	0.43
2:H:174:THR:HG22	2:H:229:ILE:HB	2.00	0.43
2:B:110:ILE:HD11	4:B:1002:COA:H133	1.99	0.43
2:B:463:MET:HE1	2:B:478:TRP:CZ3	2.54	0.43
2:F:255:ALA:O	2:F:301:PRO:HD2	2.18	0.43
1:A:107:VAL:CG1	1:A:175:LEU:CD2	2.96	0.43
2:D:132:MET:HE2	2:D:132:MET:HB2	1.83	0.43
2:D:255:ALA:O	2:D:301:PRO:HD2	2.19	0.43
2:D:463:MET:HE1	2:D:478:TRP:CZ3	2.53	0.43
2:H:551:MET:HE1	2:H:557:VAL:HG22	2.01	0.43
1:A:355:VAL:HB	1:A:381:VAL:HB	2.00	0.43
1:E:336:ILE:HG23	1:E:372:LEU:HD21	2.01	0.43
1:A:300:VAL:HG21	1:A:331:THR:HG22	2.01	0.43
1:C:118:LEU:HB3	1:C:138:ILE:HG23	2.01	0.42
2:D:163:ASN:HB2	2:D:166:ARG:NH2	2.16	0.42
2:F:463:MET:HE1	2:F:478:TRP:CZ3	2.54	0.42
1:C:104:GLU:HB3	1:C:191:PRO:HB3	2.01	0.42
2:F:256:ALA:HB2	2:F:307:LEU:HD13	2.01	0.42
1:G:234:THR:OG1	1:G:237:GLU:HB2	2.19	0.42
1:C:6:GLU:O	1:C:10:MET:HG2	2.19	0.42
2:H:313:LYS:O	2:H:316:GLU:HG2	2.20	0.42
1:C:266:ALA:HB2	1:C:291:TYR:CZ	2.55	0.42
1:A:152:THR:HG22	1:A:166:GLU:HA	2.02	0.42
2:H:256:ALA:HB2	2:H:307:LEU:HD13	2.00	0.42
2:B:370:ALA:HB3	2:B:390:LEU:HD22	2.01	0.42
1:C:6:GLU:CD	1:C:6:GLU:H	2.28	0.42
2:D:170:PHE:O	2:D:194:ILE:HA	2.20	0.42
1:E:276:ASP:CG	2:F:260:THR:H	2.27	0.42
2:H:338:PRO:HG2	2:H:343:VAL:CG2	2.50	0.42
2:B:170:PHE:O	2:B:194:ILE:HA	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:132:TRP:HE1	1:C:137:ARG:HH21	1.67	0.42
2:F:500:ASP:HB3	2:F:503:VAL:HG13	2.00	0.42
2:H:85:TYR:CE1	2:H:110:ILE:HG12	2.54	0.42
2:F:125:LEU:O	2:F:128:LYS:HG2	2.20	0.42
2:D:551:MET:HE1	2:D:557:VAL:HG22	2.01	0.41
2:F:109:MET:HE1	2:F:122:LEU:HD13	2.01	0.41
2:F:128:LYS:HG3	2:F:129:LEU:HG	2.02	0.41
2:F:237:GLU:HB2	2:F:289:LYS:HD3	2.02	0.41
2:F:607:LYS:HE3	2:H:382:TYR:CD1	2.55	0.41
2:D:174:THR:HG22	2:D:229:ILE:HB	2.02	0.41
2:H:314:VAL:O	2:H:318:LEU:HG	2.20	0.41
1:A:184:ALA:HA	1:A:210:VAL:HA	2.03	0.41
2:H:180:SER:O	2:H:184:MET:HG3	2.20	0.41
1:E:162:GLY:O	1:E:166:GLU:HG2	2.21	0.41
2:B:255:ALA:O	2:B:301:PRO:HD2	2.20	0.41
1:A:23:TYR:CD1	1:A:23:TYR:C	2.99	0.41
2:B:491:HIS:HB2	2:B:539:ILE:HD11	2.01	0.41
2:D:510:ILE:HD13	2:D:549:ILE:HD13	2.02	0.41
2:F:84:ILE:HB	2:F:109:MET:HG2	2.03	0.41
1:A:161:GLU:O	1:A:164:ILE:HD12	2.20	0.41
2:B:551:MET:HE1	2:B:557:VAL:HG22	2.03	0.41
1:A:281:ARG:HB3	1:A:396:MET:HG3	2.02	0.41
1:C:176:ILE:O	1:C:180:ASP:HB2	2.20	0.41
1:C:326:THR:O	1:C:360:PRO:HD2	2.21	0.41
1:G:212:TYR:CZ	1:G:215:ARG:HD3	2.56	0.41
1:G:278:VAL:HG11	1:G:285:ILE:HG23	2.02	0.41
2:H:211:VAL:HG12	2:H:240:ALA:HA	2.03	0.41
1:A:120:ILE:HD11	1:A:168:VAL:HG11	2.03	0.41
2:D:163:ASN:HA	2:D:165:TYR:CE1	2.56	0.41
2:D:180:SER:O	2:D:184:MET:HG3	2.21	0.41
2:D:297:GLY:HA2	5:D:1006:PGE:H62	2.02	0.41
2:B:110:ILE:CD1	4:B:1002:COA:H133	2.51	0.40
1:C:281:ARG:HB3	1:C:396:MET:HG3	2.02	0.40
1:C:265:THR:O	1:C:290:GLU:HA	2.21	0.40
1:A:104:GLU:HG2	1:A:193:VAL:HG12	2.02	0.40
1:A:190:ASN:HA	1:A:191:PRO:HA	1.79	0.40
2:B:132:MET:HB2	2:B:132:MET:HE2	1.82	0.40
2:B:85:TYR:CE2	2:B:110:ILE:HG12	2.56	0.40
2:B:167:GLN:OE1	2:B:195:THR:HA	2.22	0.40
2:D:314:VAL:O	2:D:318:LEU:HG	2.20	0.40
1:E:106:TYR:HD1	1:E:190:ASN:HA	1.86	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	328/398 (82%)	311 (95%)	17 (5%)	0	100	100
1	C	320/398 (80%)	304 (95%)	16 (5%)	0	100	100
1	E	316/398 (79%)	297 (94%)	18 (6%)	1 (0%)	36	56
1	G	318/398 (80%)	295 (93%)	22 (7%)	1 (0%)	36	56
2	B	585/617 (95%)	572 (98%)	11 (2%)	2 (0%)	36	56
2	D	587/617 (95%)	573 (98%)	12 (2%)	2 (0%)	36	56
2	F	584/617 (95%)	570 (98%)	12 (2%)	2 (0%)	36	56
2	H	587/617 (95%)	574 (98%)	11 (2%)	2 (0%)	36	56
All	All	3625/4060 (89%)	3496 (96%)	119 (3%)	10 (0%)	36	56

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	329	ASP
2	F	329	ASP
2	D	329	ASP
2	F	451	GLY
2	H	329	ASP
1	G	229	ILE
1	E	191	PRO
2	H	451	GLY
2	B	451	GLY
2	D	451	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	272/319 (85%)	258 (95%)	14 (5%)	21	43
1	C	263/319 (82%)	255 (97%)	8 (3%)	36	62
1	E	260/319 (82%)	248 (95%)	12 (5%)	24	47
1	G	261/319 (82%)	251 (96%)	10 (4%)	29	54
2	B	471/490 (96%)	454 (96%)	17 (4%)	31	56
2	D	472/490 (96%)	454 (96%)	18 (4%)	29	54
2	F	471/490 (96%)	453 (96%)	18 (4%)	29	54
2	H	472/490 (96%)	452 (96%)	20 (4%)	26	50
All	All	2942/3236 (91%)	2825 (96%)	117 (4%)	28	52

All (117) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	VAL
1	A	94	ILE
1	A	126	VAL
1	A	138	ILE
1	A	149	GLU
1	A	164	ILE
1	A	188	GLU
1	A	204	LEU
1	A	228	GLU
1	A	229	ILE
1	A	297	ASP
1	A	314	LYS
1	A	328	VAL
1	A	381	VAL
2	B	54	ILE
2	B	110	ILE
2	B	139	ILE
2	B	236	LEU
2	B	251	ILE

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Mol	Chain	Res	Type
2	B	294	ARG
2	B	346	GLN
2	B	411	ILE
2	B	459	LYS
2	B	463	MET
2	B	483	VAL
2	B	503	VAL
2	B	510	ILE
2	B	527	VAL
2	B	583	ASN
2	B	602	GLN
2	B	604	VAL
1	C	149	GLU
1	C	164	ILE
1	C	188	GLU
1	C	290	GLU
1	C	328	VAL
1	C	370	LYS
1	C	381	VAL
1	C	394	LEU
2	D	54	ILE
2	D	139	ILE
2	D	166	ARG
2	D	231	GLU
2	D	236	LEU
2	D	251	ILE
2	D	294	ARG
2	D	411	ILE
2	D	427	LEU
2	D	459	LYS
2	D	463	MET
2	D	483	VAL
2	D	503	VAL
2	D	510	ILE
2	D	527	VAL
2	D	539	ILE
2	D	583	ASN
2	D	604	VAL
1	E	15	LYS
1	E	110	ILE
1	E	128	ILE
1	E	138	ILE

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Mol	Chain	Res	Type
1	E	168	VAL
1	E	188	GLU
1	E	189	ILE
1	E	204	LEU
1	E	328	VAL
1	E	369	ILE
1	E	370	LYS
1	E	381	VAL
2	F	54	ILE
2	F	110	ILE
2	F	251	ILE
2	F	263	GLU
2	F	287	ARG
2	F	294	ARG
2	F	346	GLN
2	F	393	ASN
2	F	411	ILE
2	F	427	LEU
2	F	459	LYS
2	F	463	MET
2	F	483	VAL
2	F	503	VAL
2	F	510	ILE
2	F	527	VAL
2	F	602	GLN
2	F	604	VAL
1	G	120	ILE
1	G	188	GLU
1	G	197	SER
1	G	204	LEU
1	G	247	ILE
1	G	251	VAL
1	G	285	ILE
1	G	297	ASP
1	G	329	LYS
1	G	381	VAL
2	H	54	ILE
2	H	110	ILE
2	H	139	ILE
2	H	231	GLU
2	H	251	ILE
2	H	253	LEU

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Mol	Chain	Res	Type
2	H	294	ARG
2	H	319	ILE
2	H	346	GLN
2	H	411	ILE
2	H	427	LEU
2	H	459	LYS
2	H	463	MET
2	H	483	VAL
2	H	503	VAL
2	H	510	ILE
2	H	513	GLU
2	H	527	VAL
2	H	539	ILE
2	H	604	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	GLN
1	A	123	HIS
1	A	209	ASN
1	A	239	GLN
1	A	287	ASN
2	B	134	ASN
2	B	235	ASN
2	B	262	GLN
2	B	346	GLN
2	B	595	ASN
2	D	62	ASN
2	D	134	ASN
2	D	163	ASN
2	D	262	GLN
2	D	393	ASN
2	D	512	ASN
2	D	595	ASN
2	F	62	ASN
2	F	127	GLN
2	F	134	ASN
2	F	163	ASN
2	F	346	GLN
2	F	595	ASN
1	G	131	ASN

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Mol	Chain	Res	Type
1	G	150	GLN
2	H	62	ASN
2	H	134	ASN
2	H	163	ASN
2	H	189	GLN
2	H	235	ASN
2	H	346	GLN
2	H	512	ASN
2	H	517	HIS
2	H	537	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	COA	F	1002	-	42,44,50	0.51	0	62,68,75	0.53	0
6	TRS	B	1005	-	7,7,7	0.21	0	9,9,9	0.37	0
3	FLC	E	1001	-	12,12,12	1.08	0	17,17,17	1.27	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	COA	H	1002	-	40,42,50	0.50	1 (2%)	62,66,75	0.59	1 (1%)
7	PG4	C	1002	-	12,12,12	0.19	0	11,11,11	0.28	0
7	PG4	D	1005	-	12,12,12	0.27	0	11,11,11	0.39	0
3	FLC	F	1003	-	12,12,12	1.13	0	17,17,17	1.56	3 (17%)
3	FLC	A	1001	-	12,12,12	1.02	0	17,17,17	1.15	1 (5%)
4	COA	B	1002	-	47,50,50	0.45	1 (2%)	69,75,75	0.89	3 (4%)
4	COA	H	1001	-	32,33,50	0.85	1 (3%)	50,52,75	0.81	0
6	TRS	D	1004	-	7,7,7	0.40	0	9,9,9	0.52	0
5	PGE	F	1004	-	9,9,9	0.33	0	8,8,8	0.24	0
4	COA	F	1001	-	32,33,50	0.70	0	50,52,75	0.72	0
5	PGE	D	1006	-	9,9,9	0.27	0	8,8,8	0.40	0
5	PGE	H	1004	-	9,9,9	0.22	0	8,8,8	0.17	0
3	FLC	C	1001	-	12,12,12	1.10	0	17,17,17	1.05	1 (5%)
4	COA	D	1002	-	41,43,50	0.50	1 (2%)	62,67,75	0.51	0
3	FLC	D	1003	-	12,12,12	1.05	0	17,17,17	1.46	3 (17%)
5	PGE	C	1003	-	9,9,9	0.30	0	8,8,8	0.21	0
3	FLC	H	1003	-	12,12,12	1.28	1 (8%)	17,17,17	1.46	2 (11%)
5	PGE	B	1004	-	9,9,9	0.37	0	8,8,8	0.39	0
4	COA	B	1001	-	39,39,50	0.49	0	57,61,75	0.71	1 (1%)
3	FLC	G	1001	-	12,12,12	1.11	0	17,17,17	1.34	2 (11%)
4	COA	D	1001	-	32,33,50	0.94	2 (6%)	50,52,75	0.79	2 (4%)
3	FLC	B	1003	-	12,12,12	1.02	0	17,17,17	1.69	5 (29%)

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	COA	F	1002	-	-	10/41/57/64	0/3/3/3
6	TRS	B	1005	-	-	4/9/9/9	-
3	FLC	E	1001	-	-	0/16/16/16	-
4	COA	H	1002	-	-	11/37/54/64	0/3/3/3
7	PG4	C	1002	-	-	2/10/10/10	-
7	PG4	D	1005	-	-	5/10/10/10	-
3	FLC	F	1003	-	-	4/16/16/16	-
3	FLC	A	1001	-	-	0/16/16/16	-
4	COA	B	1002	-	-	13/48/64/64	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	COA	H	1001	-	-	9/21/37/64	0/3/3/3
6	TRS	D	1004	-	-	3/9/9/9	-
5	PGE	F	1004	-	-	2/7/7/7	-
4	COA	F	1001	-	-	3/21/37/64	0/3/3/3
5	PGE	D	1006	-	-	4/7/7/7	-
5	PGE	H	1004	-	-	3/7/7/7	-
3	FLC	C	1001	-	-	0/16/16/16	-
4	COA	D	1002	-	-	12/40/56/64	0/3/3/3
3	FLC	D	1003	-	-	2/16/16/16	-
5	PGE	C	1003	-	-	3/7/7/7	-
3	FLC	H	1003	-	-	2/16/16/16	-
5	PGE	B	1004	-	-	6/7/7/7	-
4	COA	B	1001	-	-	12/31/47/64	0/3/3/3
3	FLC	G	1001	-	-	0/16/16/16	-
4	COA	D	1001	-	-	4/21/37/64	0/3/3/3
3	FLC	B	1003	-	-	5/16/16/16	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1001	COA	P2A-O4A	3.69	1.62	1.50
3	H	1003	FLC	OB2-CBC	-2.60	1.21	1.30
4	H	1001	COA	P3B-O3B	2.37	1.63	1.59
4	D	1001	COA	P3B-O3B	2.35	1.63	1.59
4	H	1002	COA	P3B-O3B	2.17	1.63	1.59
4	D	1002	COA	P3B-O3B	2.15	1.63	1.59
4	B	1002	COA	P3B-O3B	2.14	1.63	1.59

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1002	COA	O6A-P2A-O4A	5.09	129.09	108.94
4	B	1001	COA	CCP-CBP-CAP	3.41	115.83	110.08
3	B	1003	FLC	CB-CG-CGC	3.07	122.32	113.92
3	D	1003	FLC	OB1-CBC-CB	-2.76	116.74	122.09
3	B	1003	FLC	CA-CB-CBC	-2.76	103.93	110.03
3	H	1003	FLC	CB-CA-CAC	2.75	121.44	113.92
3	F	1003	FLC	OB1-CBC-CB	-2.62	117.02	122.09
3	A	1001	FLC	OB1-CBC-CB	-2.54	117.17	122.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1003	FLC	OB2-CBC-CB	2.52	117.97	113.14
3	E	1001	FLC	OB1-CBC-CB	-2.50	117.24	122.09
3	F	1003	FLC	OHB-CB-CG	2.50	115.07	109.38
3	G	1001	FLC	OB2-CBC-CB	2.50	117.93	113.14
3	H	1003	FLC	CG-CB-CBC	-2.47	104.56	110.03
3	F	1003	FLC	CB-CG-CGC	2.47	120.68	113.92
4	D	1001	COA	P3B-O3B-C3B	2.45	129.97	123.43
3	E	1001	FLC	OB2-CBC-CB	2.38	117.71	113.14
3	G	1001	FLC	OB1-CBC-CB	-2.38	117.48	122.09
3	D	1003	FLC	CB-CA-CAC	2.38	120.42	113.92
4	B	1002	COA	CDP-CBP-CAP	2.33	112.74	108.77
4	H	1002	COA	CBP-CAP-C9P	2.33	118.13	113.69
4	D	1001	COA	O6A-P2A-O5A	2.32	116.50	107.80
4	B	1002	COA	O5A-P2A-O6A	-2.26	97.31	107.57
3	B	1003	FLC	OA1-CAC-CA	-2.21	116.70	122.95
3	B	1003	FLC	OB1-CBC-CB	-2.20	117.84	122.09
3	C	1001	FLC	OB1-CBC-CB	-2.18	117.87	122.09
3	B	1003	FLC	CG-CB-CBC	2.16	114.81	110.03

There are no chirality outliers.

All (119) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1003	FLC	CG-CB-CBC-OB1
4	B	1001	COA	C5B-O5B-P1A-O1A
4	B	1001	COA	C5B-O5B-P1A-O3A
4	B	1001	COA	CCP-O6A-P2A-O3A
4	B	1002	COA	C5B-O5B-P1A-O1A
4	B	1002	COA	N8P-C9P-CAP-CBP
4	B	1002	COA	N8P-C9P-CAP-OAP
4	D	1002	COA	C5B-O5B-P1A-O2A
4	D	1002	COA	CCP-O6A-P2A-O3A
4	D	1002	COA	CCP-O6A-P2A-O4A
4	D	1002	COA	CCP-O6A-P2A-O5A
4	D	1002	COA	CDP-CBP-CCP-O6A
4	D	1002	COA	CEP-CBP-CCP-O6A
4	D	1002	COA	CAP-CBP-CCP-O6A
4	F	1001	COA	P1A-O3A-P2A-O6A
4	F	1002	COA	C5B-O5B-P1A-O2A
4	F	1002	COA	CCP-O6A-P2A-O3A
4	F	1002	COA	CCP-O6A-P2A-O4A
4	F	1002	COA	CCP-O6A-P2A-O5A

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Mol	Chain	Res	Type	Atoms
4	F	1002	COA	CDP-CBP-CCP-O6A
4	F	1002	COA	CEP-CBP-CCP-O6A
4	F	1002	COA	CAP-CBP-CCP-O6A
4	H	1001	COA	C5B-O5B-P1A-O1A
4	H	1001	COA	C5B-O5B-P1A-O2A
4	H	1001	COA	C5B-O5B-P1A-O3A
4	H	1001	COA	P1A-O3A-P2A-O6A
4	H	1002	COA	C5B-O5B-P1A-O2A
4	H	1002	COA	CCP-O6A-P2A-O3A
4	H	1002	COA	CCP-O6A-P2A-O4A
4	H	1002	COA	CCP-O6A-P2A-O5A
4	H	1002	COA	CDP-CBP-CCP-O6A
4	H	1002	COA	CEP-CBP-CCP-O6A
4	H	1002	COA	CAP-CBP-CCP-O6A
4	H	1002	COA	N8P-C9P-CAP-OAP
6	B	1005	TRS	C1-C-C3-O3
6	B	1005	TRS	C2-C-C3-O3
6	B	1005	TRS	N-C-C3-O3
4	H	1001	COA	C3B-C4B-C5B-O5B
4	H	1001	COA	O4B-C4B-C5B-O5B
5	H	1004	PGE	O1-C1-C2-O2
7	C	1002	PG4	O4-C7-C8-O5
5	B	1004	PGE	O2-C3-C4-O3
6	D	1004	TRS	C1-C-C2-O2
5	B	1004	PGE	O3-C5-C6-O4
7	D	1005	PG4	O2-C3-C4-O3
4	B	1002	COA	O9P-C9P-CAP-OAP
4	H	1001	COA	C3B-O3B-P3B-O7A
5	D	1006	PGE	O3-C5-C6-O4
3	B	1003	FLC	OHB-CB-CBC-OB1
3	B	1003	FLC	CG-CB-CBC-OB2
3	F	1003	FLC	CG-CB-CBC-OB1
4	B	1002	COA	O9P-C9P-CAP-CBP
6	D	1004	TRS	N-C-C2-O2
4	B	1001	COA	P2A-O3A-P1A-O5B
4	B	1001	COA	P1A-O3A-P2A-O6A
4	D	1001	COA	P2A-O3A-P1A-O5B
4	D	1002	COA	P2A-O3A-P1A-O5B
4	F	1002	COA	P2A-O3A-P1A-O5B
4	H	1002	COA	P2A-O3A-P1A-O5B
5	F	1004	PGE	C3-C4-O3-C5
7	D	1005	PG4	C6-C5-O3-C4

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Mol	Chain	Res	Type	Atoms
5	D	1006	PGE	C1-C2-O2-C3
4	H	1001	COA	P1A-O3A-P2A-O5A
5	B	1004	PGE	C3-C4-O3-C5
5	H	1004	PGE	C6-C5-O3-C4
5	F	1004	PGE	C1-C2-O2-C3
5	H	1004	PGE	C3-C4-O3-C5
5	D	1006	PGE	C6-C5-O3-C4
5	C	1003	PGE	C6-C5-O3-C4
5	D	1006	PGE	C3-C4-O3-C5
3	B	1003	FLC	CA-CB-CBC-OB2
3	D	1003	FLC	CA-CB-CBC-OB2
3	D	1003	FLC	CG-CB-CBC-OB2
7	C	1002	PG4	C4-C3-O2-C2
4	B	1002	COA	CEP-CBP-CCP-O6A
7	D	1005	PG4	C1-C2-O2-C3
5	B	1004	PGE	C1-C2-O2-C3
5	C	1003	PGE	C4-C3-O2-C2
6	D	1004	TRS	C3-C-C2-O2
4	B	1002	COA	CAP-CBP-CCP-O6A
4	B	1001	COA	C5B-O5B-P1A-O2A
4	B	1001	COA	CCP-O6A-P2A-O4A
4	B	1002	COA	C5B-O5B-P1A-O2A
4	B	1002	COA	C5B-O5B-P1A-O3A
4	D	1002	COA	C5B-O5B-P1A-O1A
4	D	1002	COA	C5B-O5B-P1A-O3A
4	F	1002	COA	C5B-O5B-P1A-O1A
4	F	1002	COA	C5B-O5B-P1A-O3A
4	H	1002	COA	C5B-O5B-P1A-O1A
4	B	1001	COA	C4B-C5B-O5B-P1A
5	B	1004	PGE	C6-C5-O3-C4
4	D	1001	COA	C4B-C5B-O5B-P1A
4	D	1002	COA	O9P-C9P-N8P-C7P
3	F	1003	FLC	CB-CG-CGC-OG2
3	B	1003	FLC	CA-CB-CBC-OB1
3	F	1003	FLC	CA-CB-CBC-OB1
3	F	1003	FLC	CB-CG-CGC-OG1
4	D	1001	COA	P1A-O3A-P2A-O4A
4	B	1001	COA	OAP-CAP-CBP-CEP
7	D	1005	PG4	O3-C5-C6-O4
4	F	1001	COA	C4B-C5B-O5B-P1A
4	B	1002	COA	P2A-O3A-P1A-O1A
4	B	1002	COA	P2A-O3A-P1A-O5B

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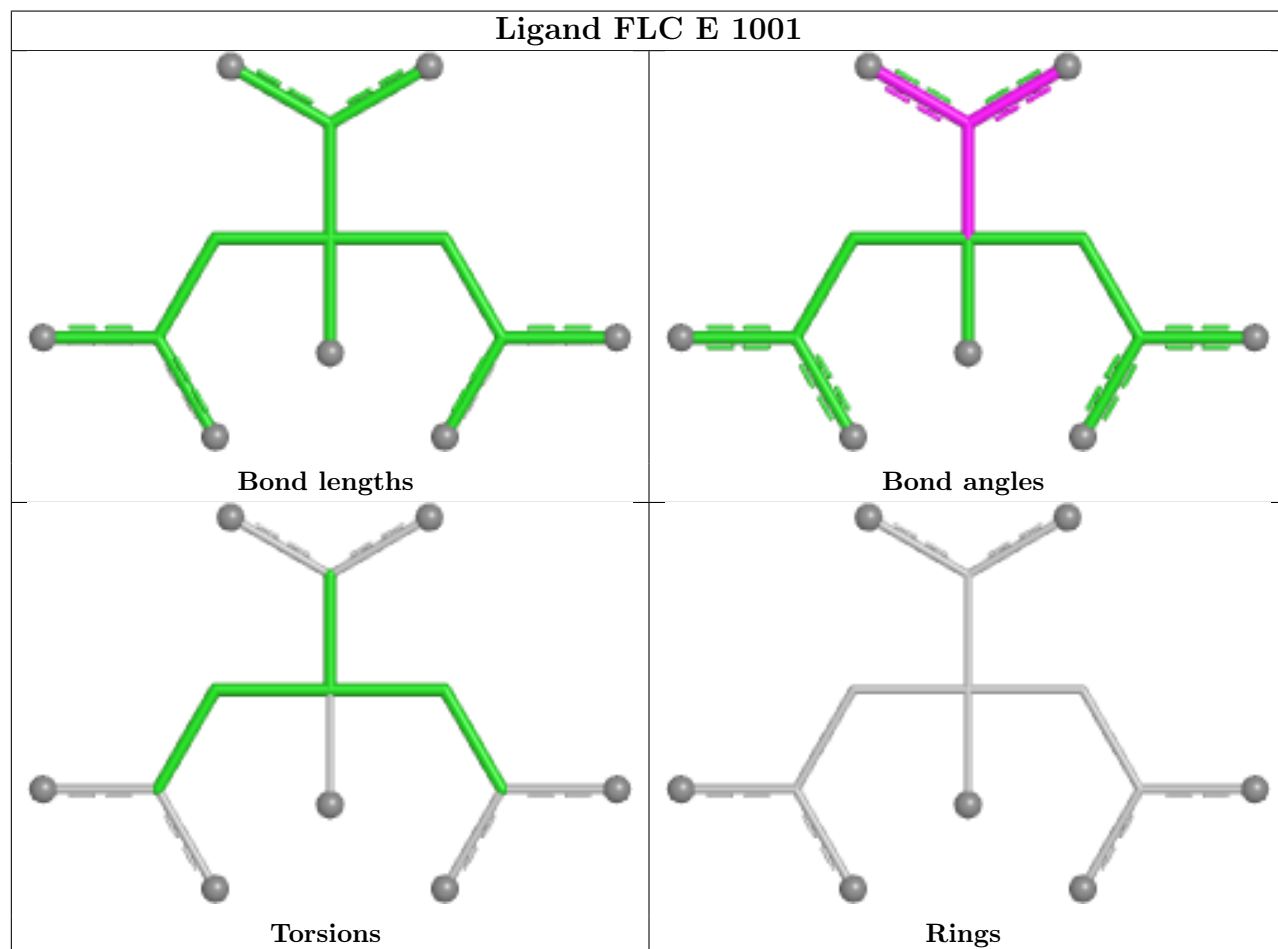
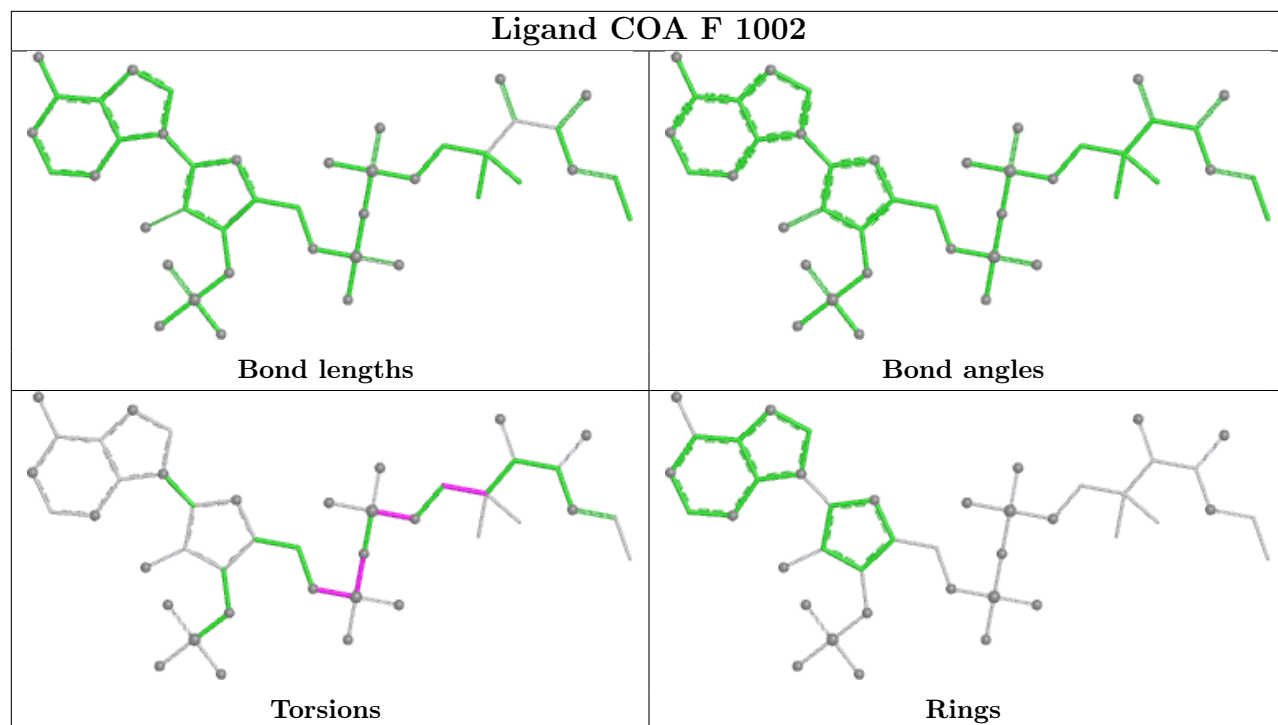
Mol	Chain	Res	Type	Atoms
4	H	1001	COA	C4B-C5B-O5B-P1A
6	B	1005	TRS	C3-C-C2-O2
5	C	1003	PGE	O3-C5-C6-O4
7	D	1005	PG4	C8-C7-O4-C6
4	D	1001	COA	C3B-O3B-P3B-O8A
5	B	1004	PGE	C4-C3-O2-C2
3	H	1003	FLC	CB-CA-CAC-OA1
3	H	1003	FLC	CB-CA-CAC-OA2
4	F	1001	COA	P1A-O3A-P2A-O4A
4	B	1002	COA	CDP-CBP-CCP-O6A
4	B	1001	COA	C3B-O3B-P3B-O7A
4	B	1001	COA	OAP-CAP-CBP-CCP
4	D	1002	COA	N8P-C9P-CAP-OAP
4	B	1002	COA	C4B-C5B-O5B-P1A
4	B	1001	COA	P1A-O3A-P2A-O4A
4	H	1002	COA	P2A-O3A-P1A-O2A

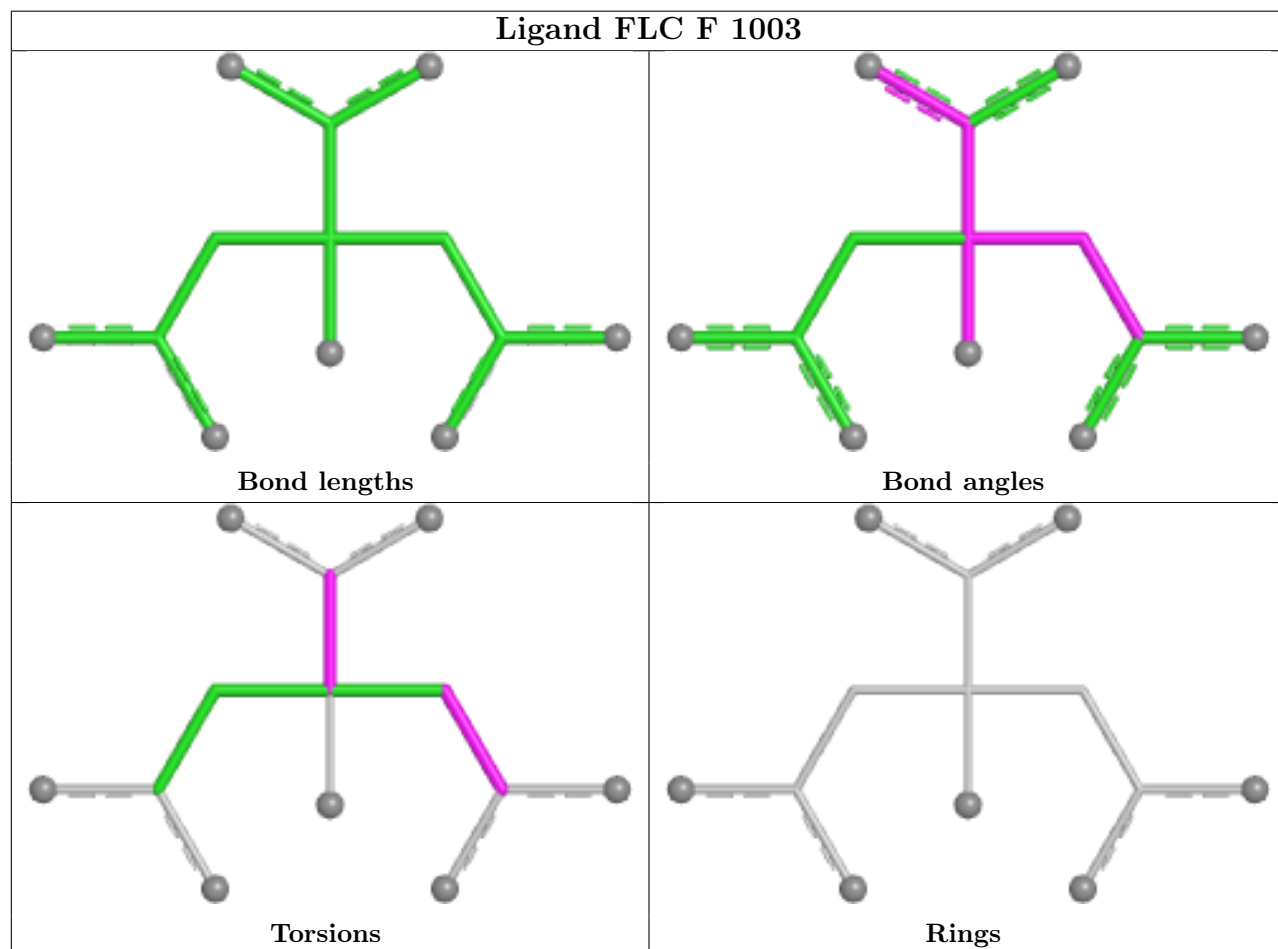
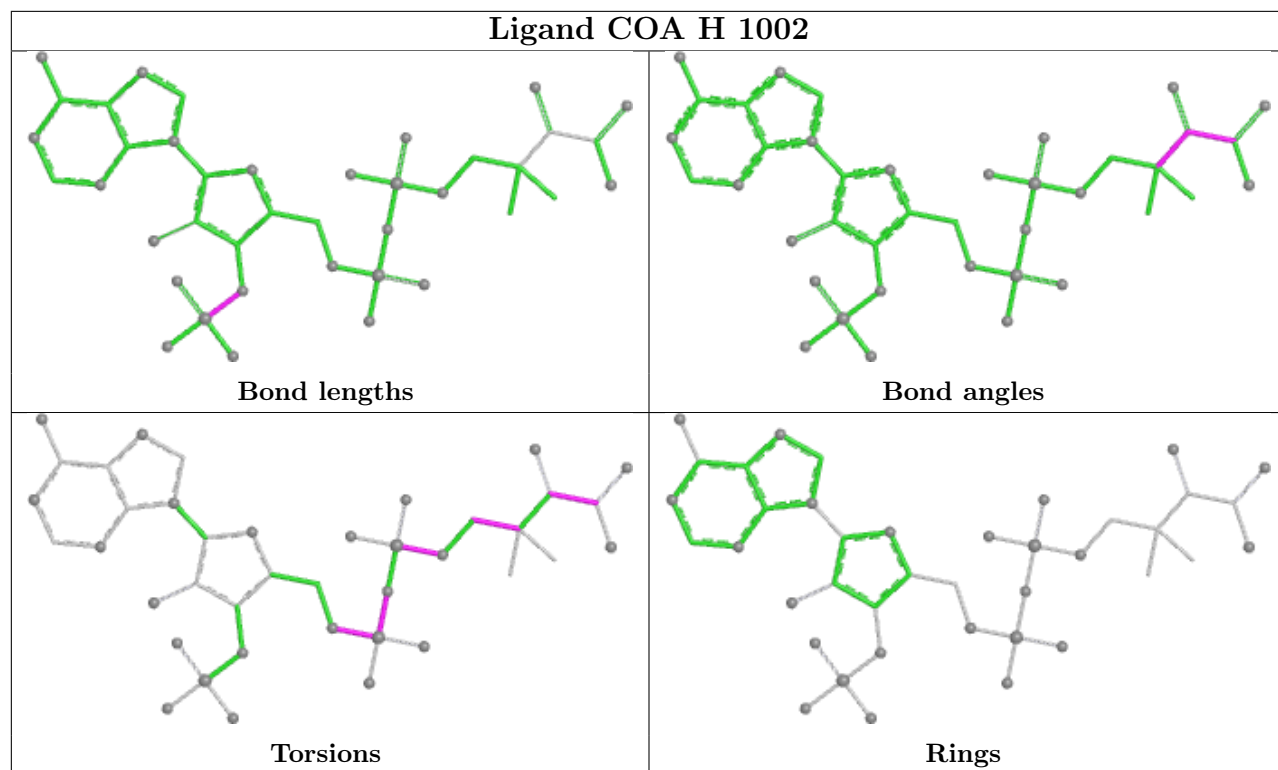
There are no ring outliers.

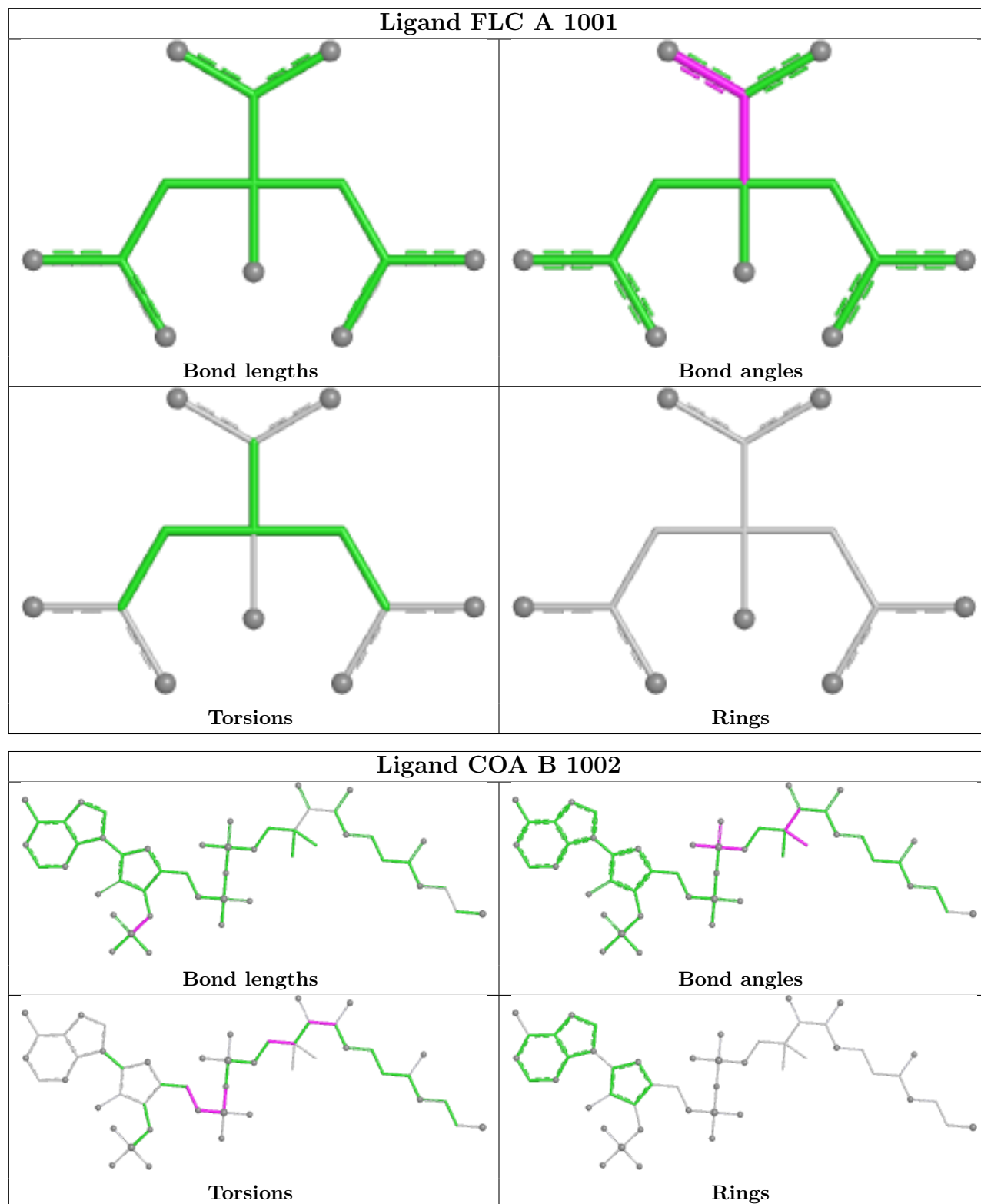
6 monomers are involved in 9 short contacts:

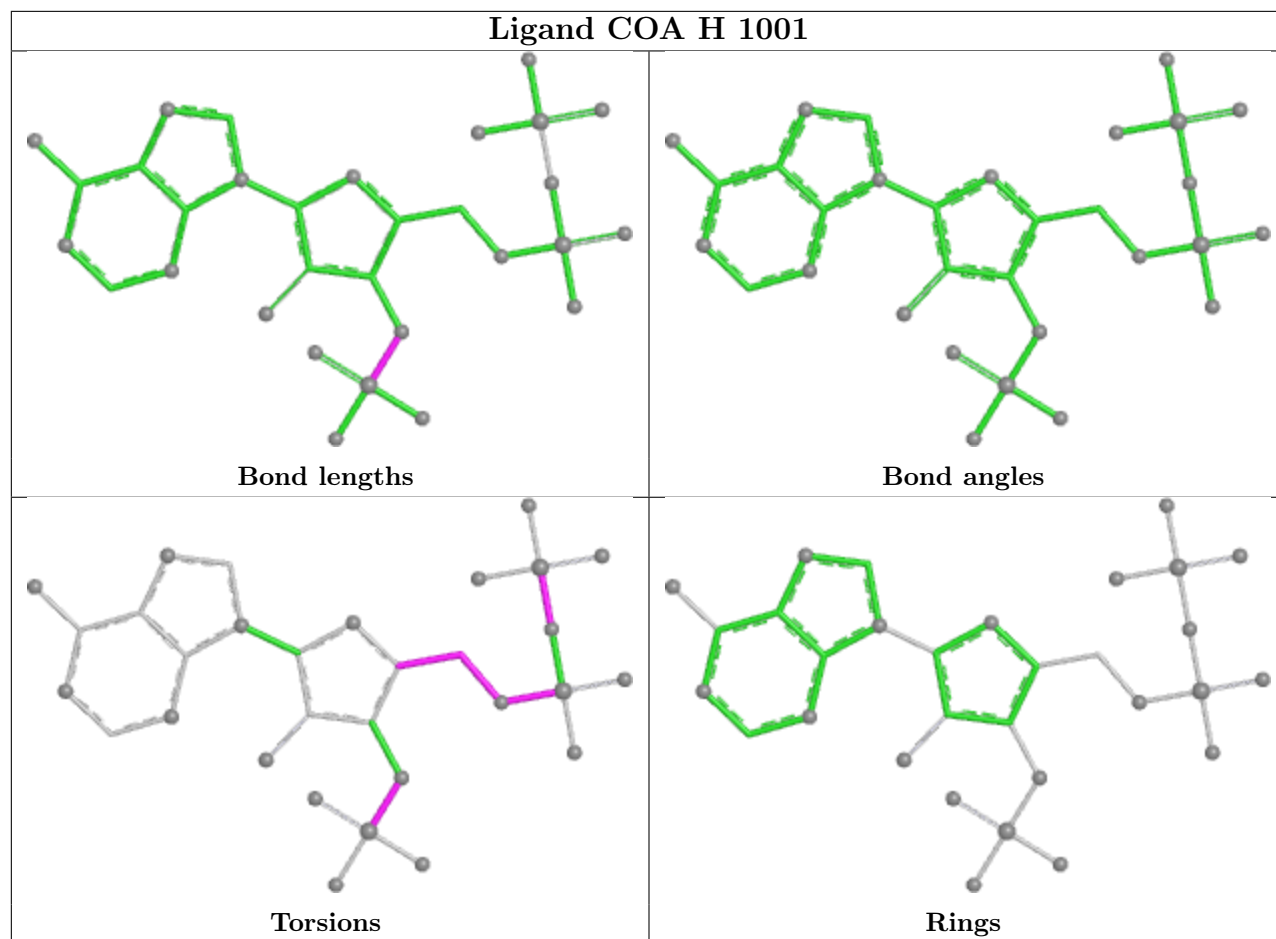
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	1002	PG4	1	0
7	D	1005	PG4	1	0
4	B	1002	COA	2	0
5	D	1006	PGE	1	0
5	H	1004	PGE	2	0
5	B	1004	PGE	2	0

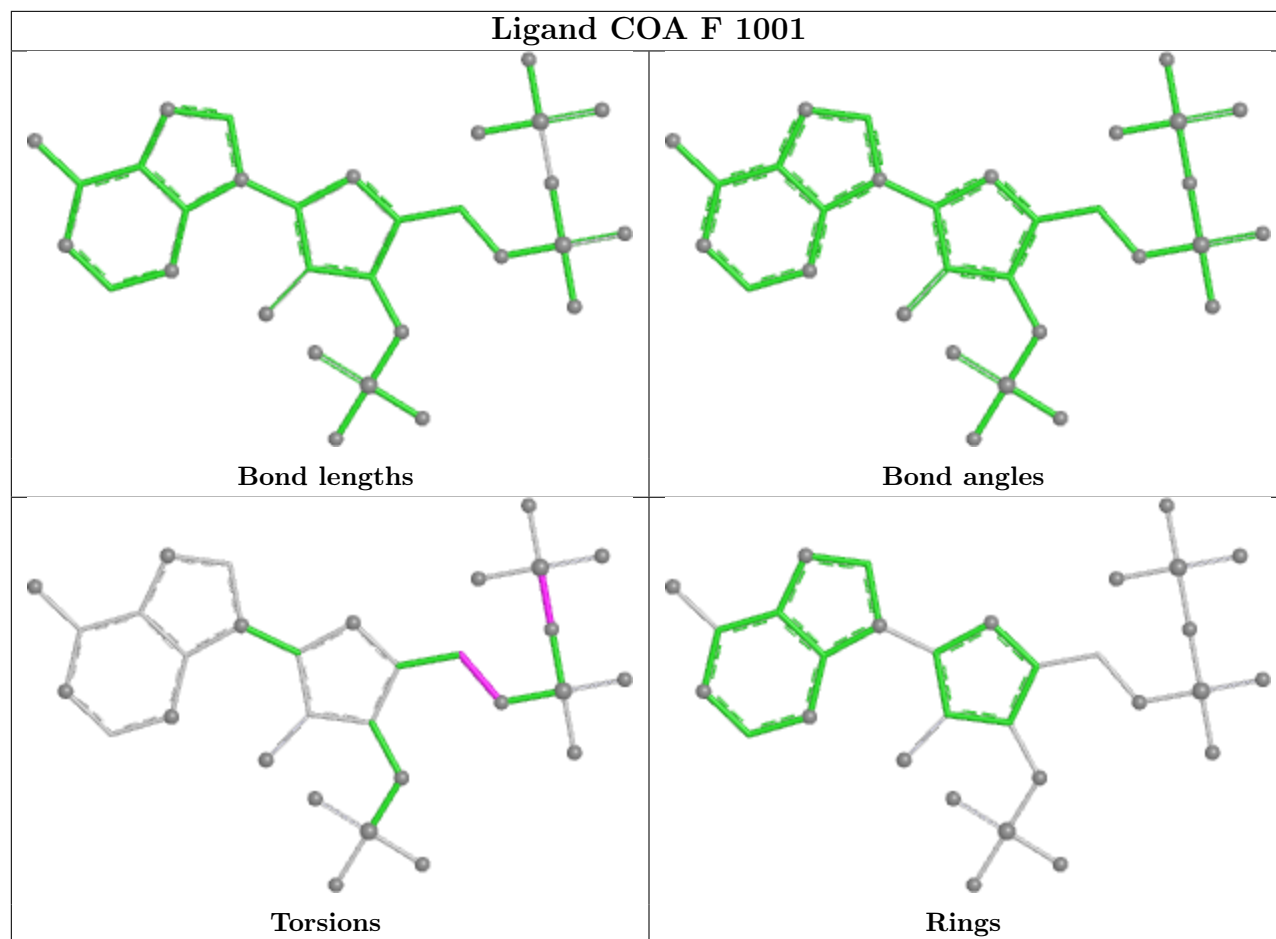
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

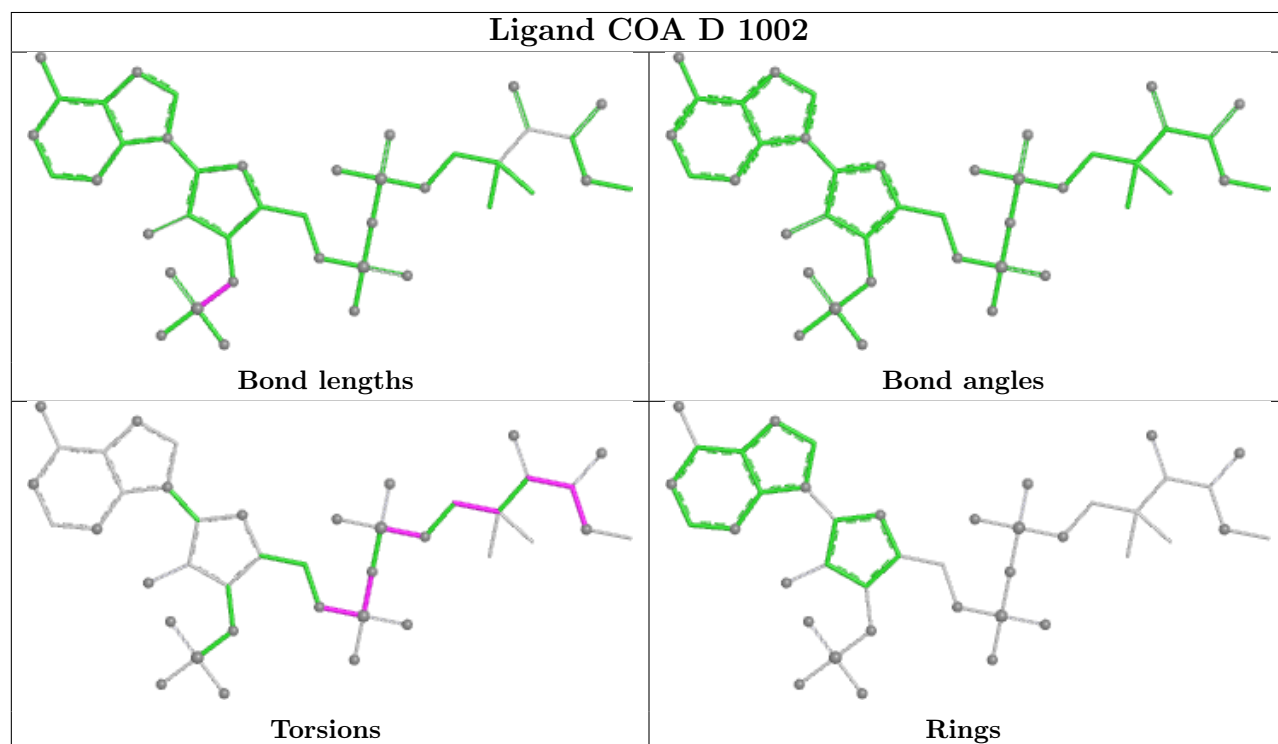
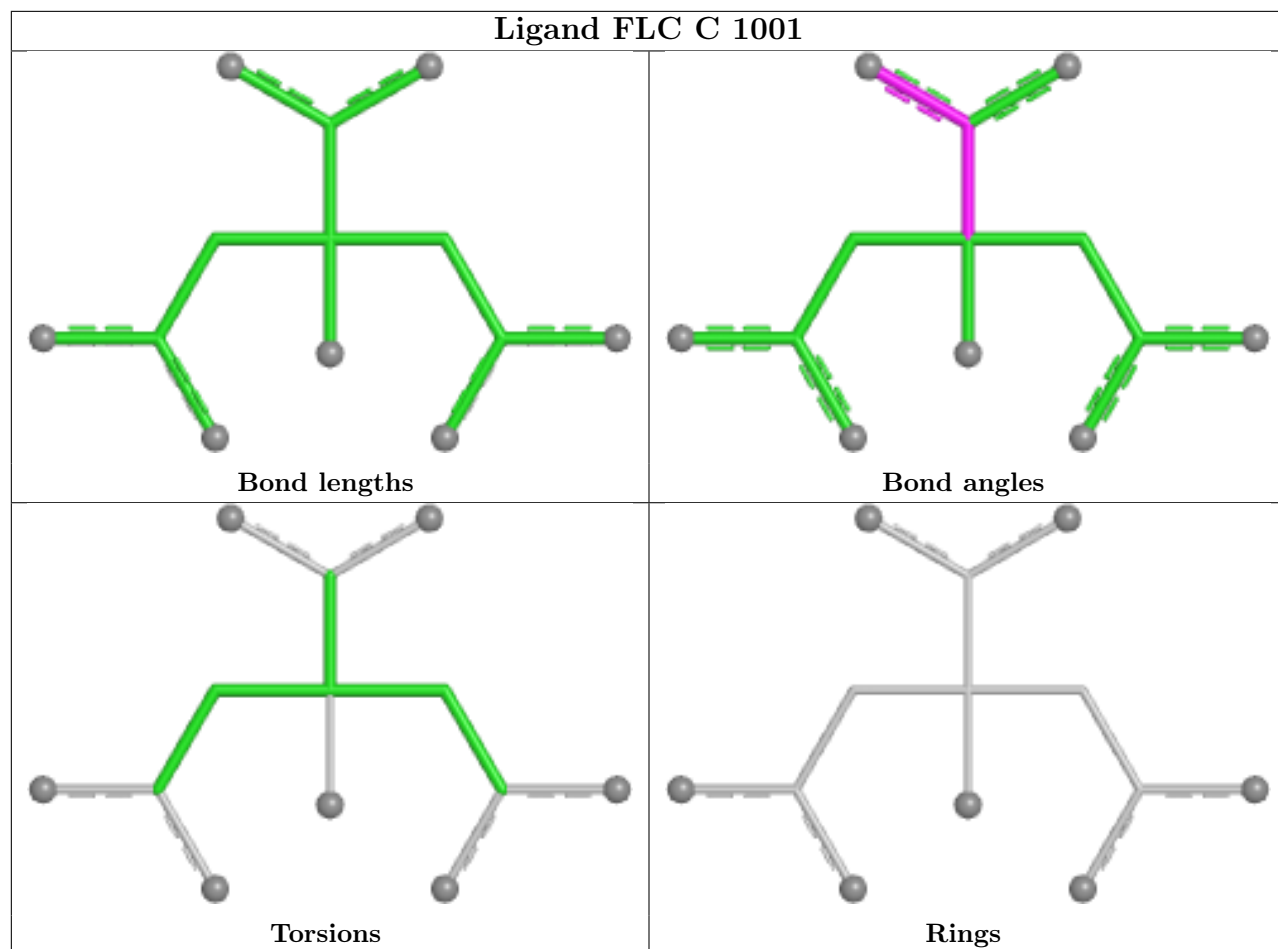


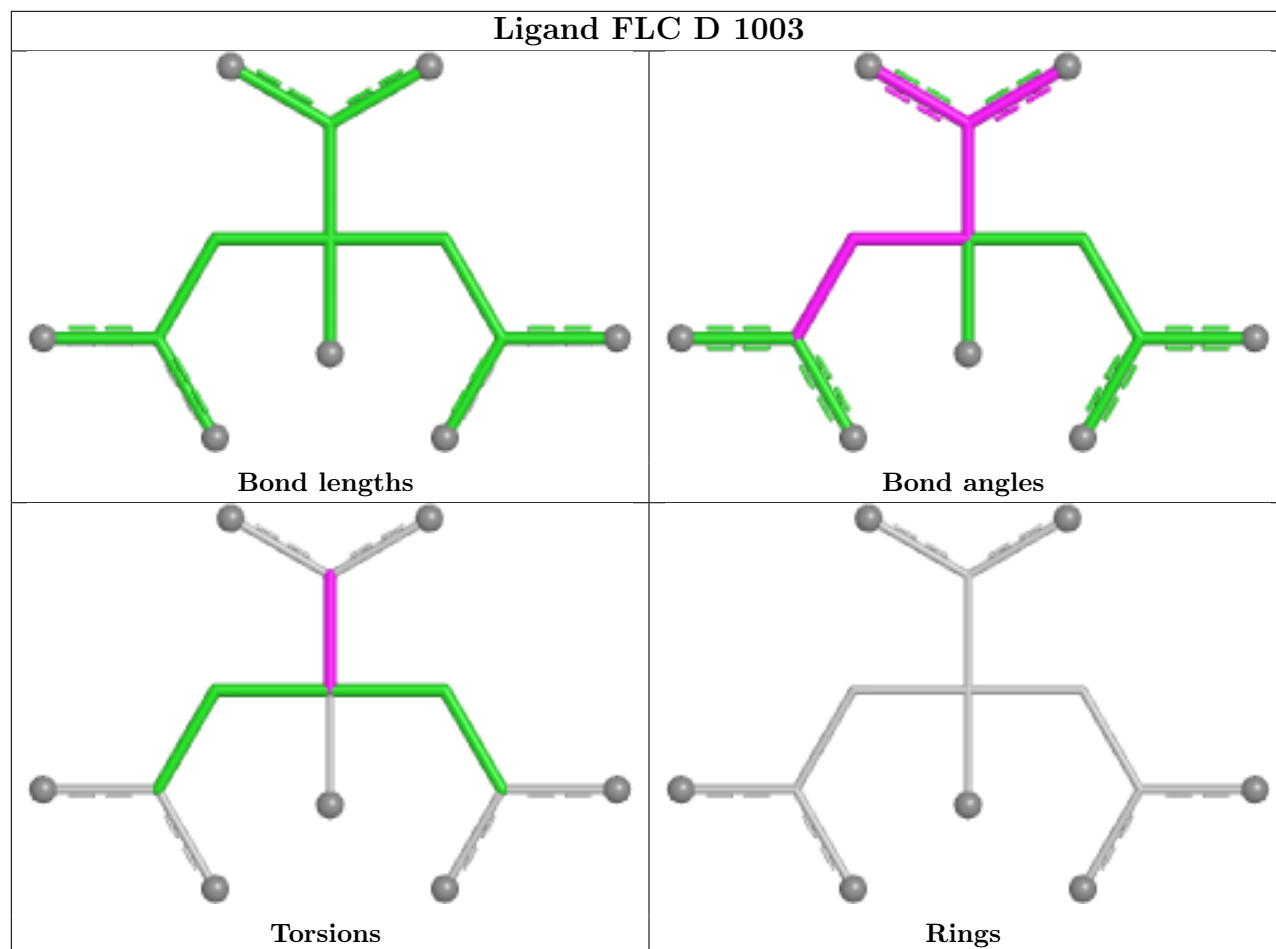


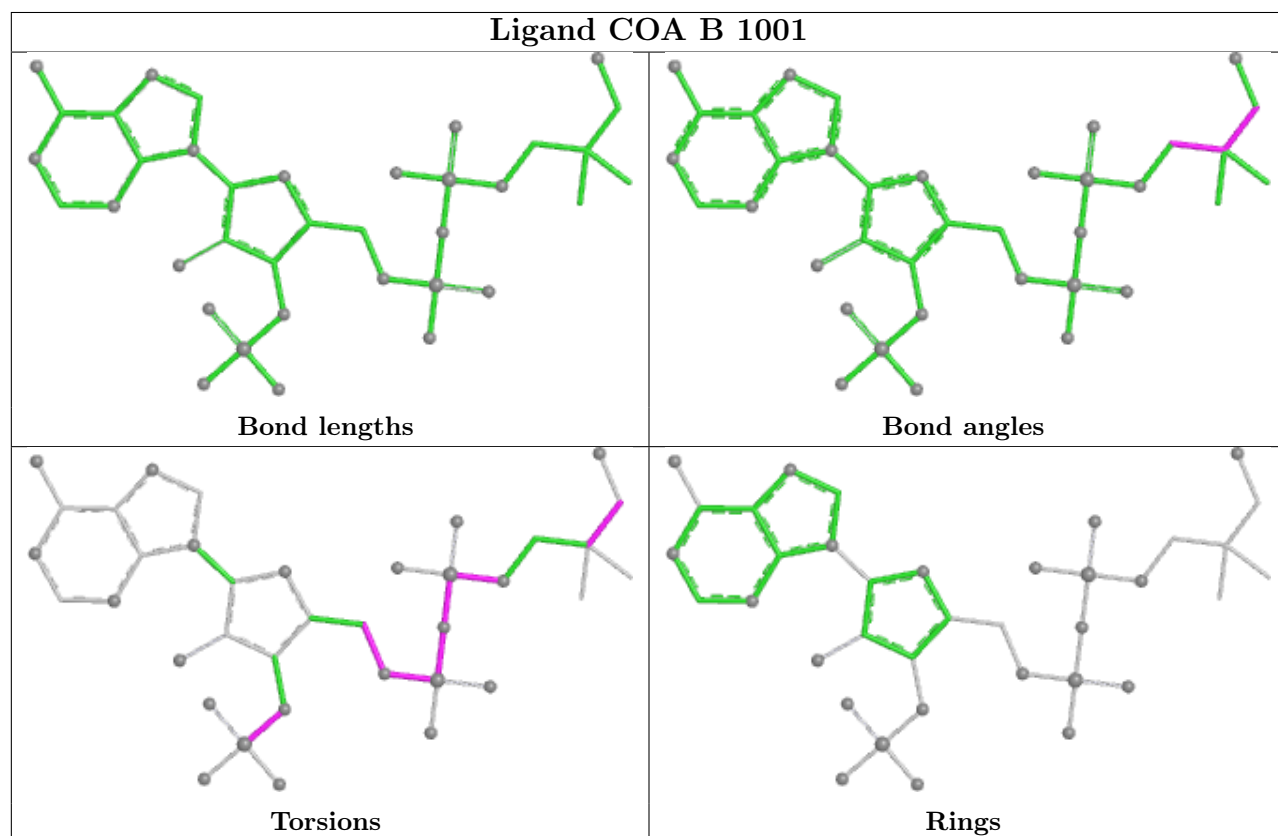
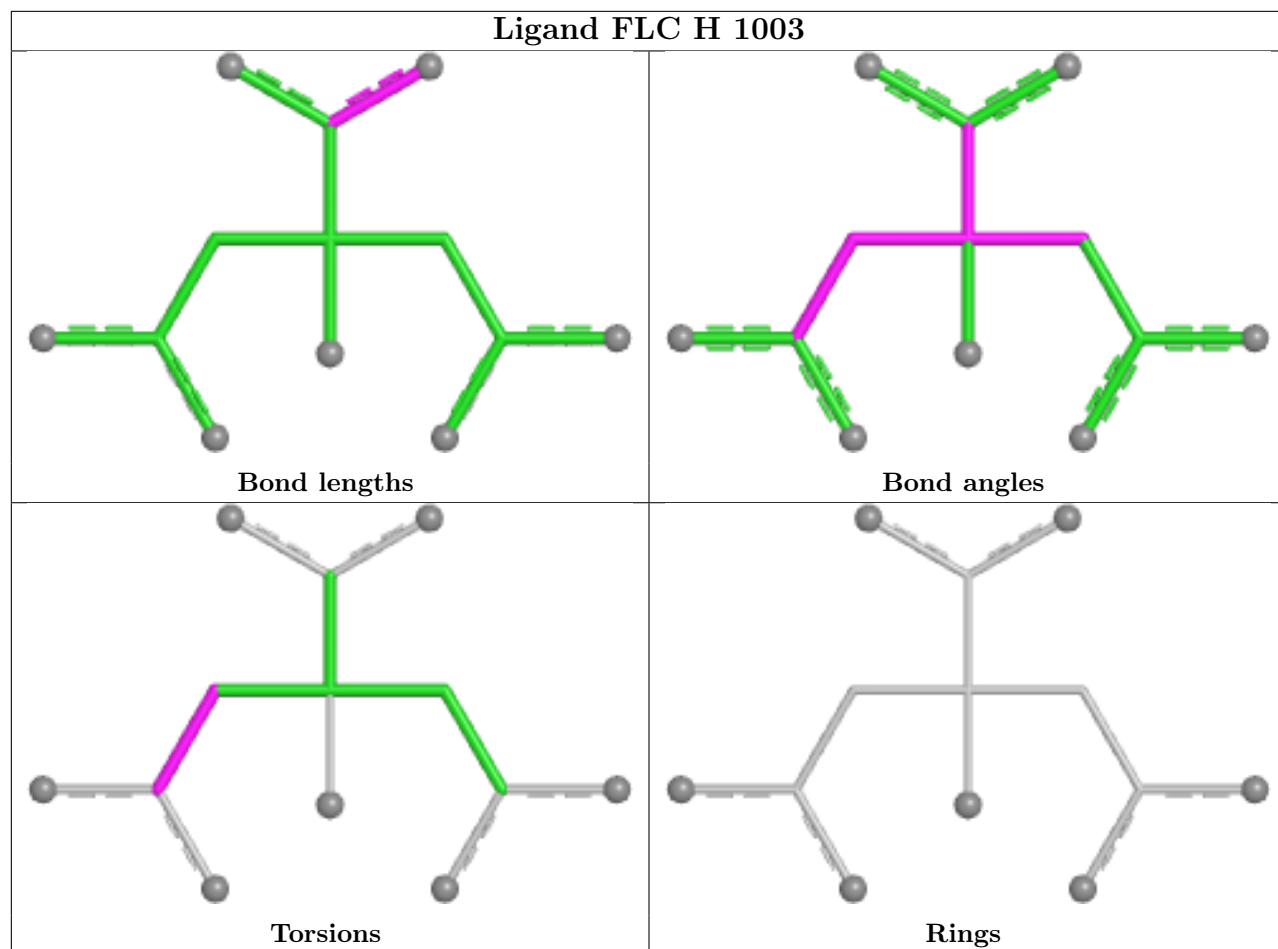


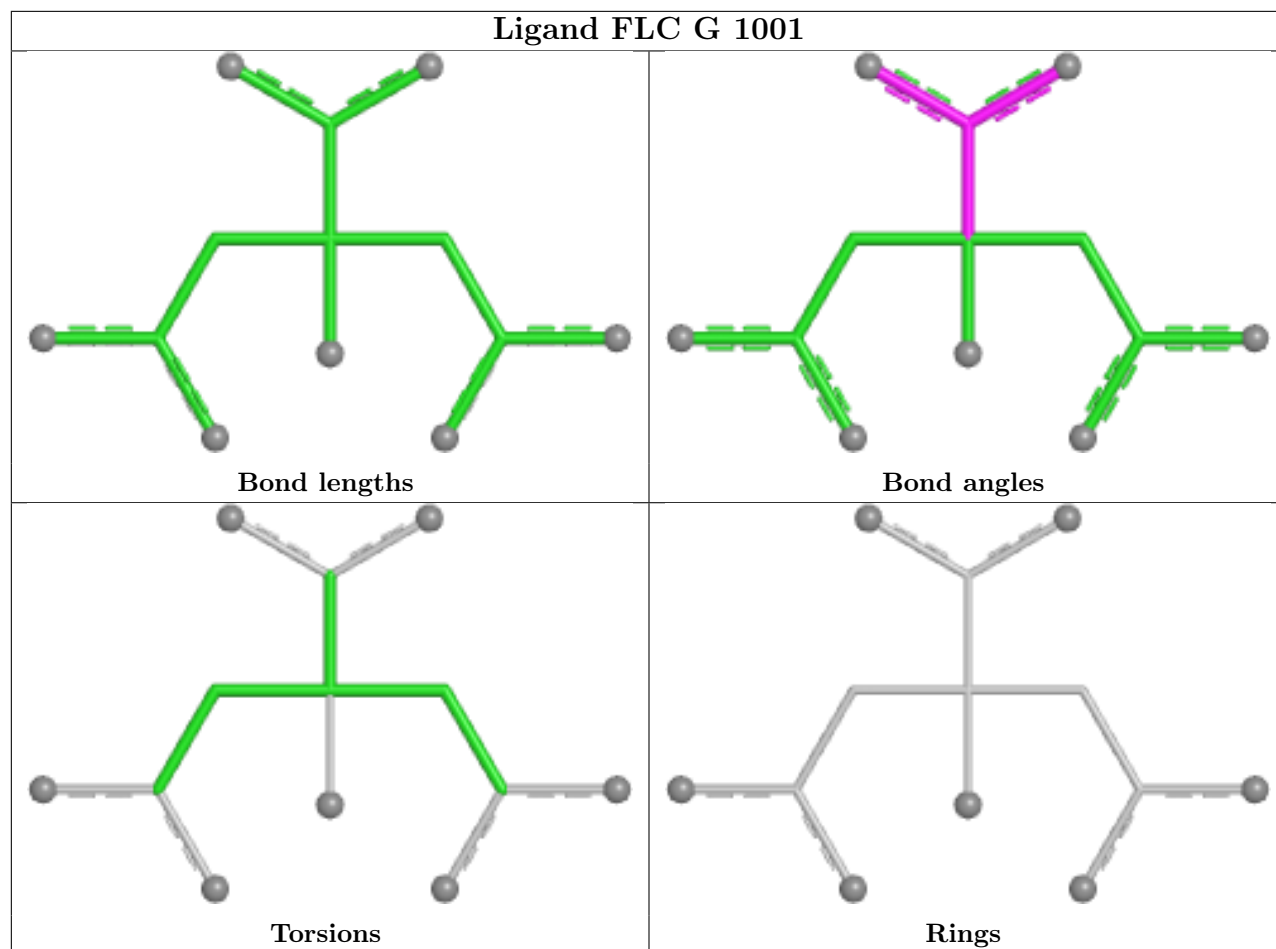


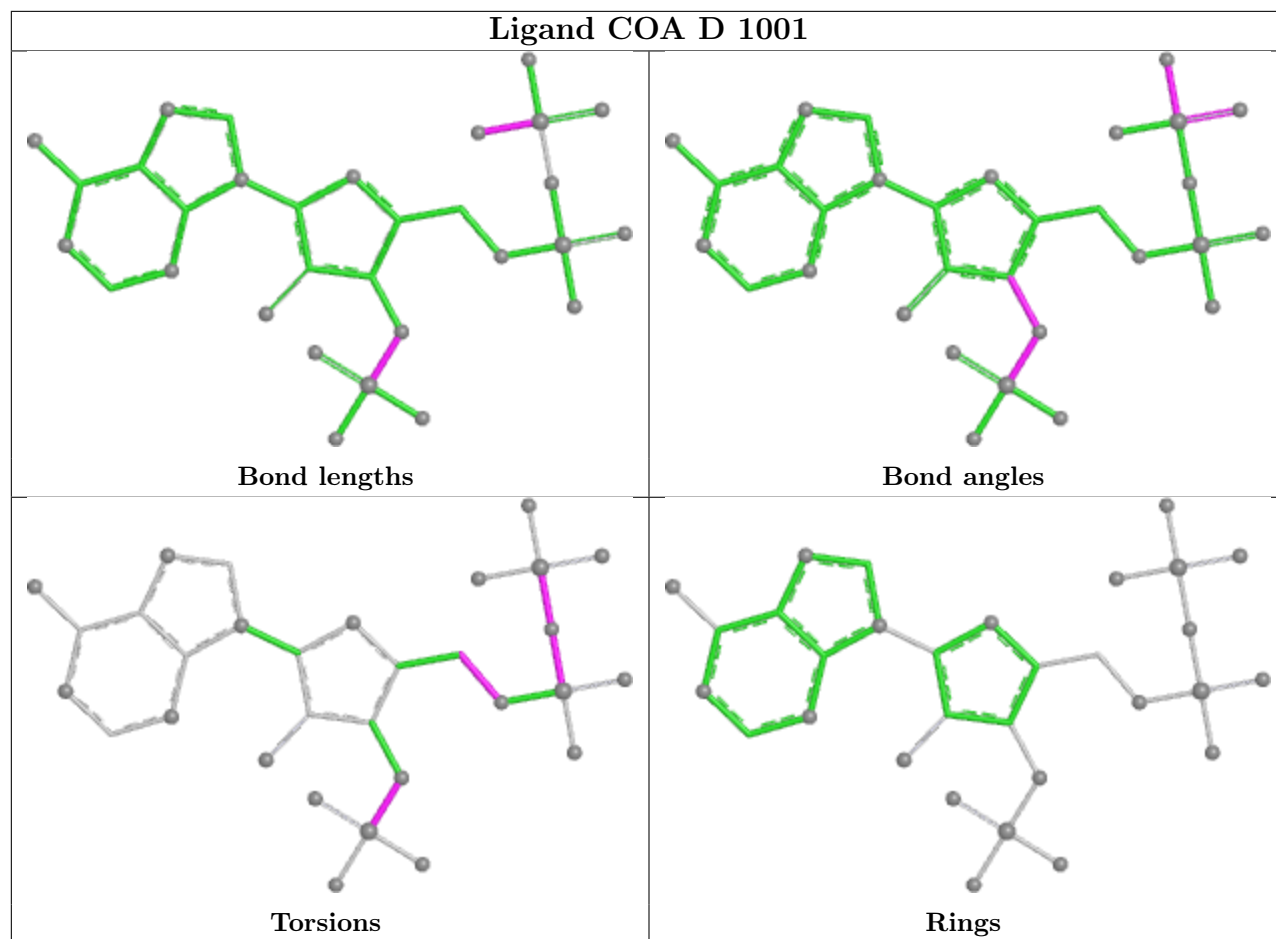


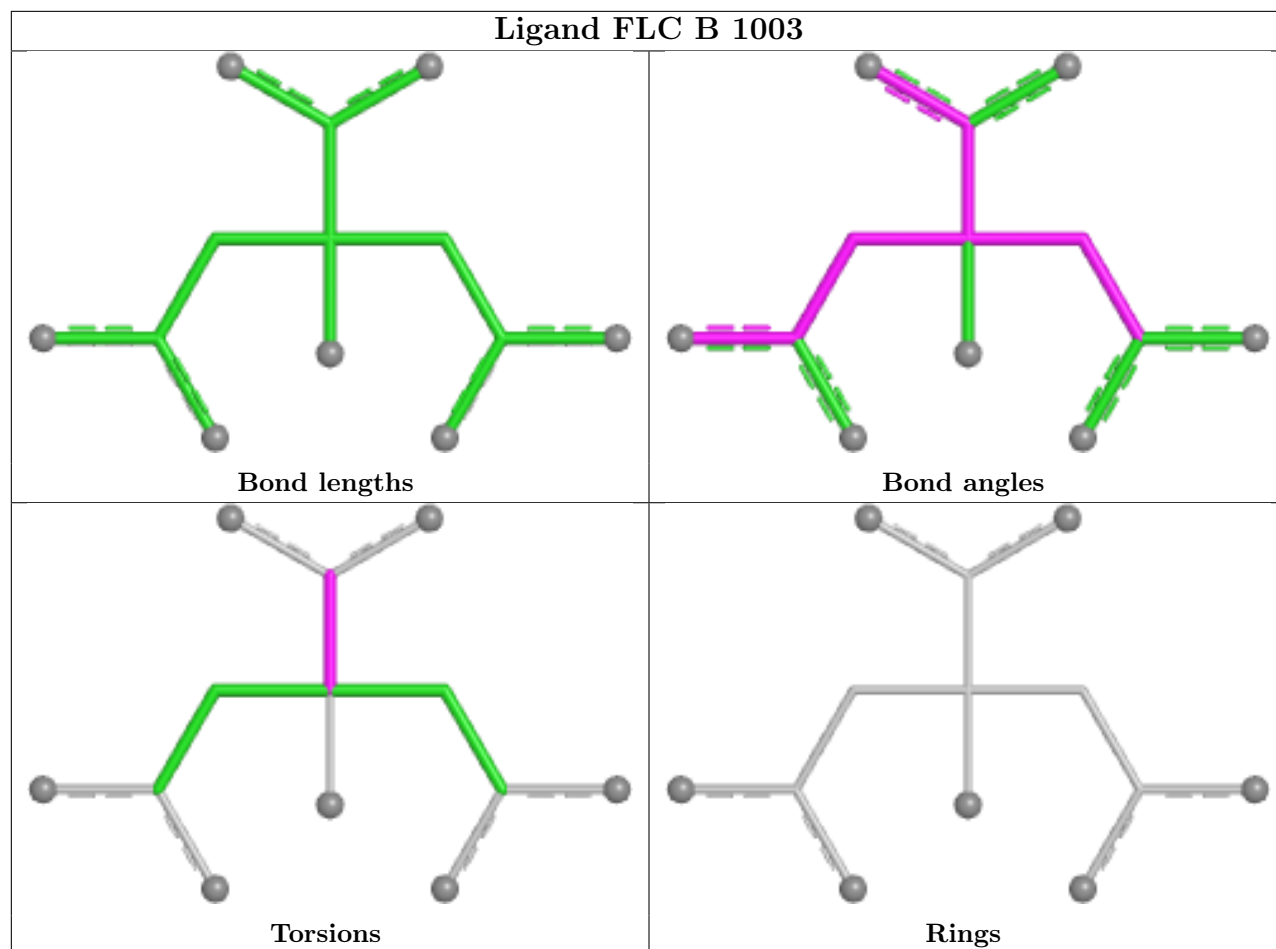












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	336/398 (84%)	0.61	17 (5%) 33 29	76, 112, 155, 183	0
1	C	324/398 (81%)	0.31	5 (1%) 72 69	65, 96, 129, 155	0
1	E	320/398 (80%)	0.69	21 (6%) 24 20	73, 120, 157, 182	0
1	G	322/398 (80%)	0.67	23 (7%) 22 18	80, 120, 158, 177	0
2	B	589/617 (95%)	0.02	9 (1%) 72 69	43, 74, 120, 184	0
2	D	591/617 (95%)	0.06	6 (1%) 79 77	45, 76, 116, 189	0
2	F	588/617 (95%)	0.03	5 (0%) 81 79	44, 75, 119, 172	0
2	H	591/617 (95%)	0.15	15 (2%) 58 54	41, 77, 147, 212	0
All	All	3661/4060 (90%)	0.24	101 (2%) 55 50	41, 87, 146, 212	0

All (101) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	172	CYS	4.8
2	B	265	LEU	4.8
2	F	265	LEU	4.8
2	D	265	LEU	4.6
1	E	128	ILE	4.3
2	H	304	PHE	3.9
1	G	229	ILE	3.9
2	H	265	LEU	3.7
2	B	264	VAL	3.7
1	G	164	ILE	3.6
2	H	326	THR	3.4
1	A	229	ILE	3.4
1	A	26	ILE	3.3
1	E	26	ILE	3.2
1	E	229	ILE	3.2
1	E	164	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
1	G	99	LEU	3.1
2	H	236	LEU	3.1
1	A	154	LEU	3.1
1	E	199	MET	3.1
2	H	451	GLY	3.1
2	F	328	ILE	3.1
1	E	126	VAL	3.0
1	G	236	ALA	3.0
2	B	261	CYS	2.9
2	B	324	ILE	2.9
2	B	304	PHE	2.9
1	G	313	ILE	2.8
1	G	296	ALA	2.8
1	G	302	ALA	2.8
1	A	98	MET	2.8
1	G	252	LYS	2.8
1	G	23	TYR	2.8
1	G	251	VAL	2.8
2	B	328	ILE	2.8
1	E	206	ALA	2.8
1	G	369	ILE	2.7
1	E	110	ILE	2.7
1	A	47	LEU	2.7
2	D	283	ALA	2.7
1	E	140	ILE	2.7
1	C	26	ILE	2.6
1	E	148	ILE	2.6
2	H	260	THR	2.6
1	A	207	VAL	2.6
2	H	264	VAL	2.6
1	G	247	ILE	2.6
1	G	285	ILE	2.6
1	A	233	PHE	2.6
1	A	348	LEU	2.6
1	E	107	VAL	2.6
2	D	100	GLU	2.5
1	G	253	PHE	2.5
1	E	18	ILE	2.5
1	G	372	LEU	2.5
1	A	49	VAL	2.5
1	C	229	ILE	2.4
1	G	298	TRP	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	47	GLU	2.4
2	F	306	GLY	2.4
2	H	305	GLY	2.4
1	E	176	ILE	2.4
2	B	283	ALA	2.4
1	A	394	LEU	2.3
2	F	92	ALA	2.3
1	G	226	VAL	2.3
1	E	197	SER	2.2
1	E	21	PRO	2.2
1	A	243	ILE	2.2
1	A	344	SER	2.2
1	G	279	VAL	2.2
2	D	331	ALA	2.2
2	D	97	GLU	2.2
1	C	23	TYR	2.1
1	E	19	PRO	2.1
1	E	20	VAL	2.1
1	G	277	ALA	2.1
2	F	326	THR	2.1
2	B	323	GLU	2.1
2	H	542	VAL	2.1
1	E	132	TRP	2.1
1	E	258	GLY	2.1
2	H	324	ILE	2.1
1	A	232	PRO	2.1
1	A	201	PHE	2.1
1	A	103	ALA	2.1
2	H	222	ALA	2.1
2	H	283	ALA	2.1
2	H	185	TRP	2.1
1	G	314	LYS	2.1
1	C	378	ASP	2.1
2	D	343	VAL	2.0
1	G	289	ALA	2.0
2	H	320	ALA	2.0
1	A	175	LEU	2.0
1	A	204	LEU	2.0
2	H	129	LEU	2.0
1	G	284	THR	2.0
1	G	316	ILE	2.0
1	C	25	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
1	E	192	LEU	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(Å ²)	Q<0.9
4	COA	B	1001	37/48	0.77	0.12	92,131,159,160	0
4	COA	F	1002	42/48	0.82	0.12	95,107,146,149	0
5	PGE	C	1003	10/10	0.82	0.14	94,106,111,111	0
6	TRS	B	1005	8/8	0.85	0.13	83,92,96,97	0
3	FLC	E	1001	13/13	0.86	0.11	114,116,131,131	0
4	COA	H	1002	40/48	0.86	0.10	111,123,163,164	0
6	TRS	D	1004	8/8	0.86	0.12	100,109,112,114	0
3	FLC	C	1001	13/13	0.87	0.12	91,105,111,111	0
3	FLC	G	1001	13/13	0.87	0.11	98,109,121,123	0
5	PGE	H	1004	10/10	0.88	0.15	89,94,97,99	0
4	COA	D	1002	41/48	0.88	0.09	96,104,149,151	0
5	PGE	D	1006	10/10	0.88	0.11	98,110,115,116	0
5	PGE	B	1004	10/10	0.89	0.12	106,112,116,117	0
3	FLC	B	1003	13/13	0.89	0.11	70,75,91,94	0
3	FLC	H	1003	13/13	0.90	0.10	67,76,89,89	0
4	COA	D	1001	31/48	0.90	0.08	91,122,166,168	0
5	PGE	F	1004	10/10	0.90	0.12	99,100,104,104	0
7	PG4	D	1005	13/13	0.90	0.13	83,90,96,98	0
3	FLC	A	1001	13/13	0.91	0.10	97,104,108,111	0
4	COA	F	1001	31/48	0.91	0.08	92,113,163,165	0
4	COA	B	1002	48/48	0.92	0.09	74,85,111,114	0
4	COA	H	1001	31/48	0.93	0.07	63,86,140,141	0

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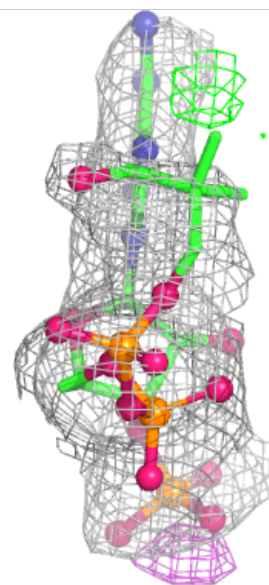
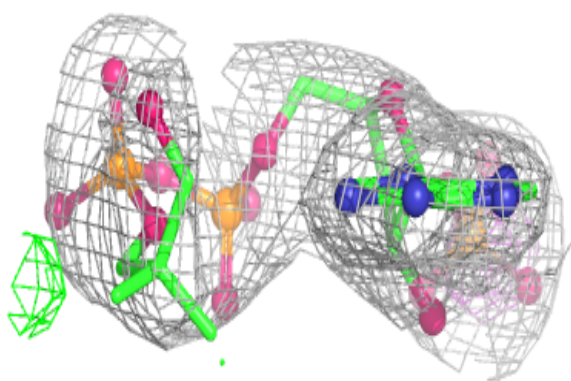
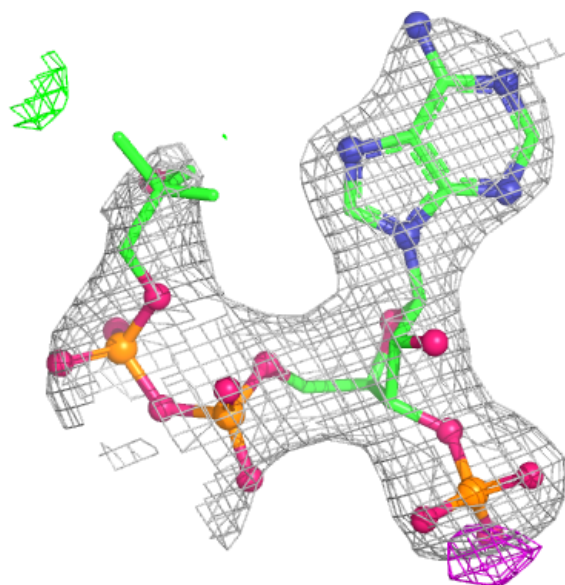
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	FLC	F	1003	13/13	0.93	0.10	75,78,84,86	0
3	FLC	D	1003	13/13	0.95	0.09	69,83,98,100	0
7	PG4	C	1002	13/13	0.96	0.09	80,83,91,92	0

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

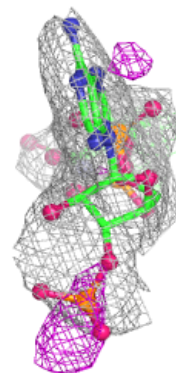
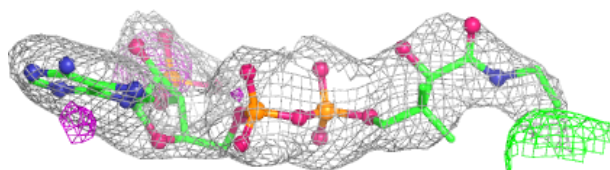
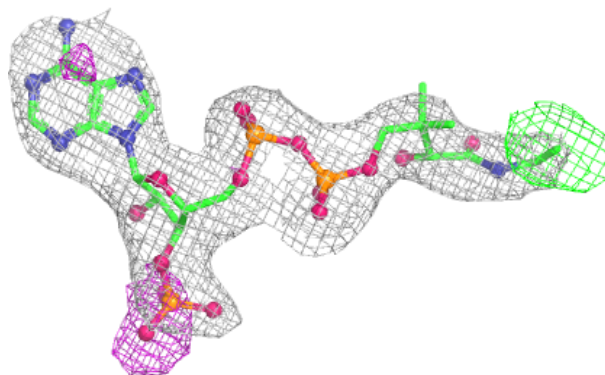
Electron density around COA B 1001:

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

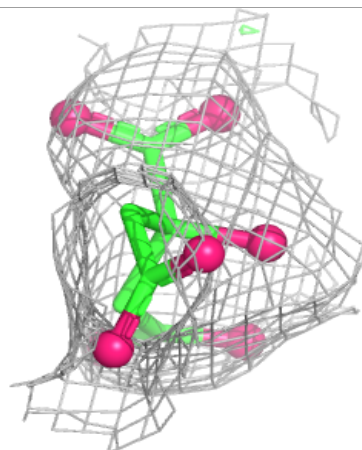
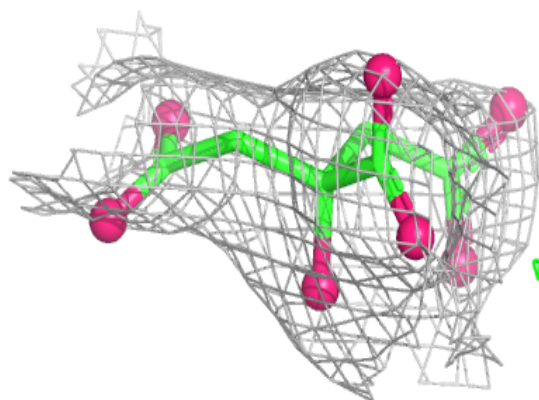


Electron density around COA F 1002:

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

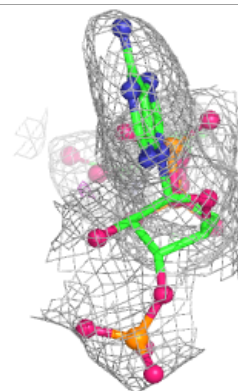
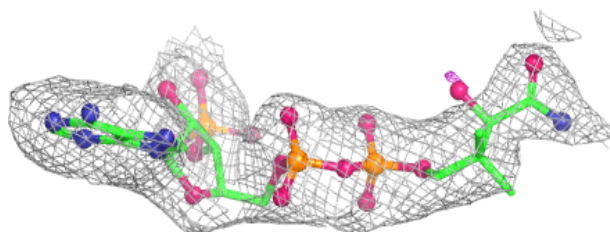
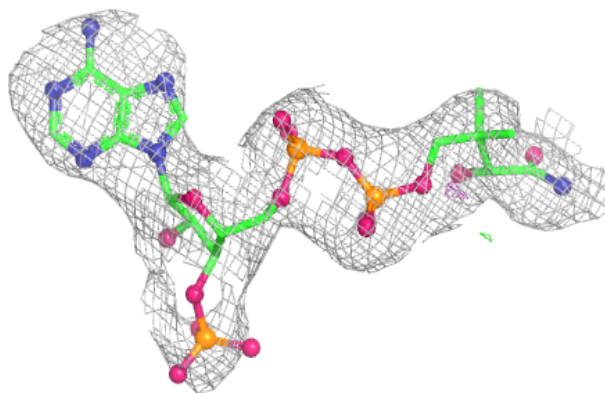
**Electron density around FLC E 1001:**

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



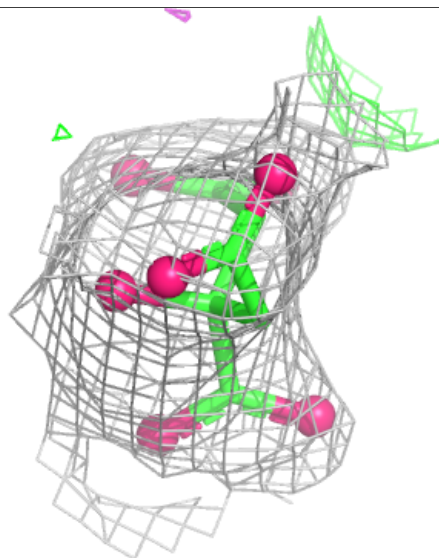
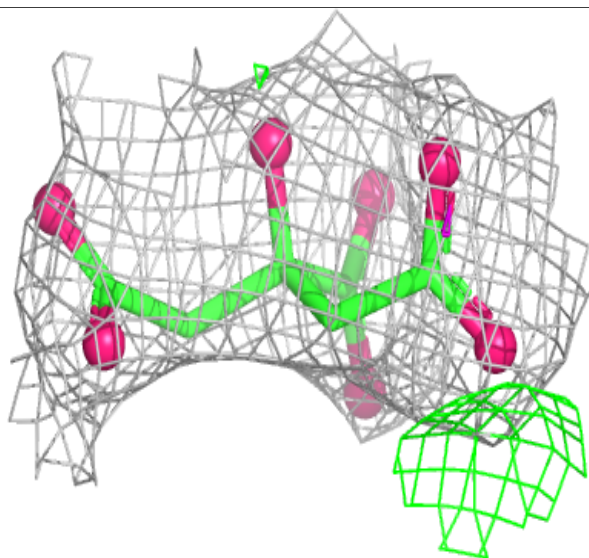
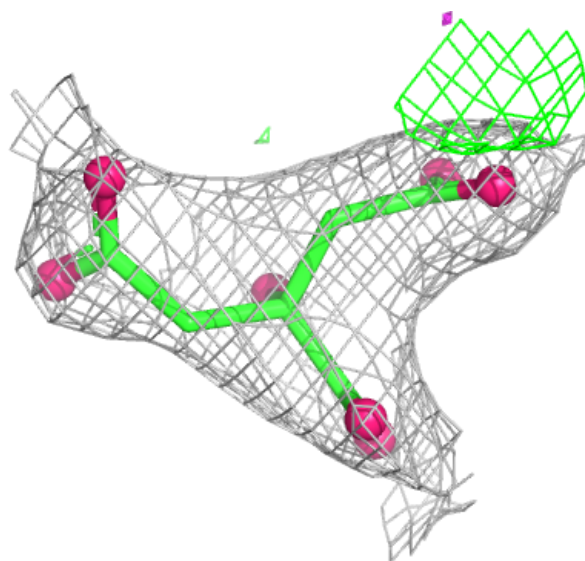
Electron density around COA H 1002:

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



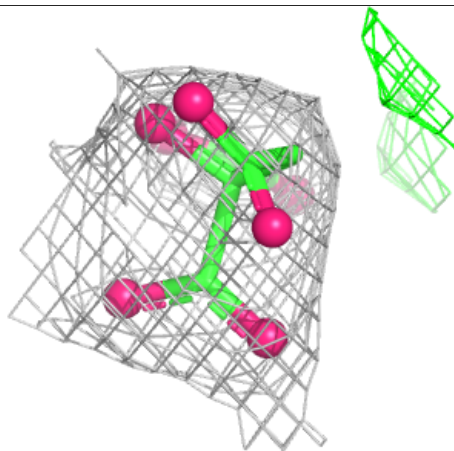
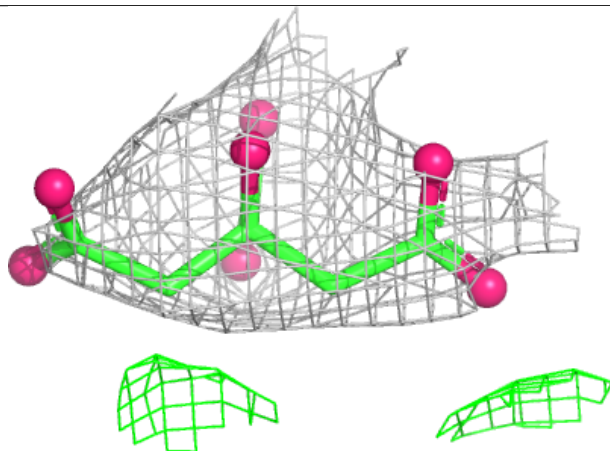
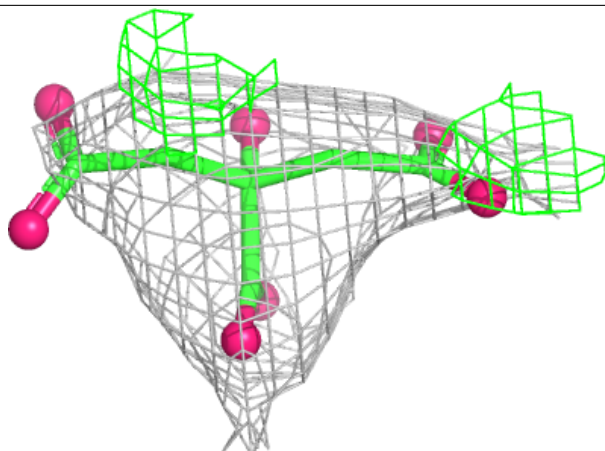
Electron density around FLC C 1001:

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

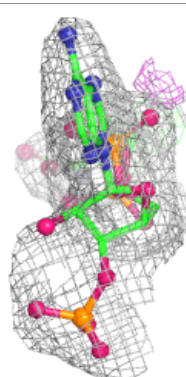
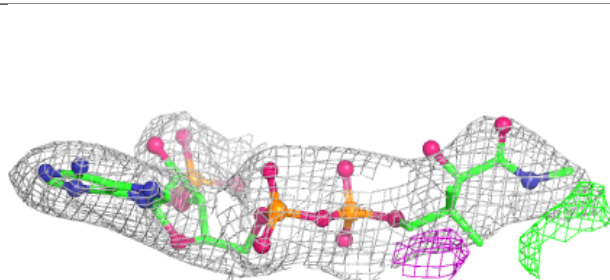
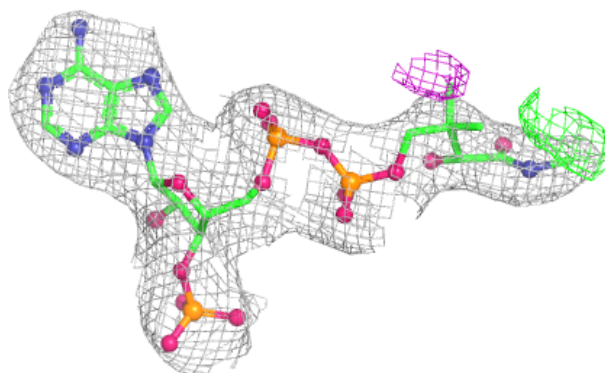


Electron density around FLC G 1001:

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

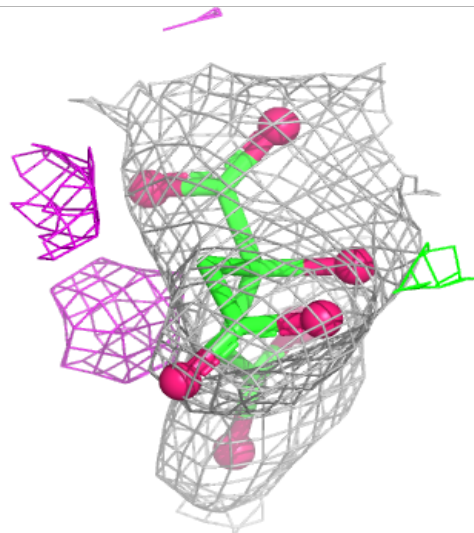
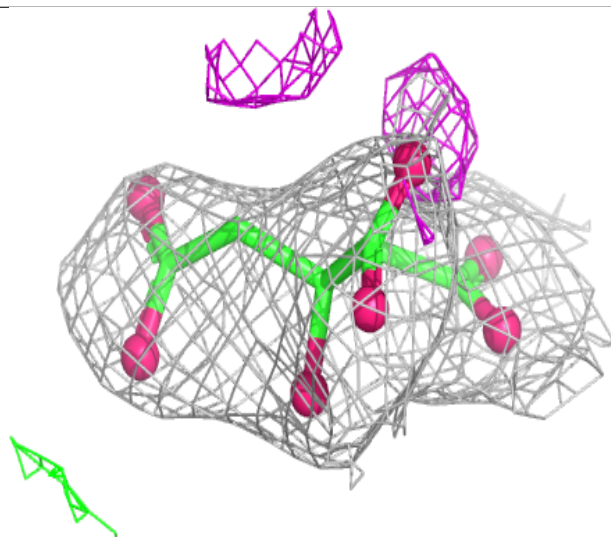
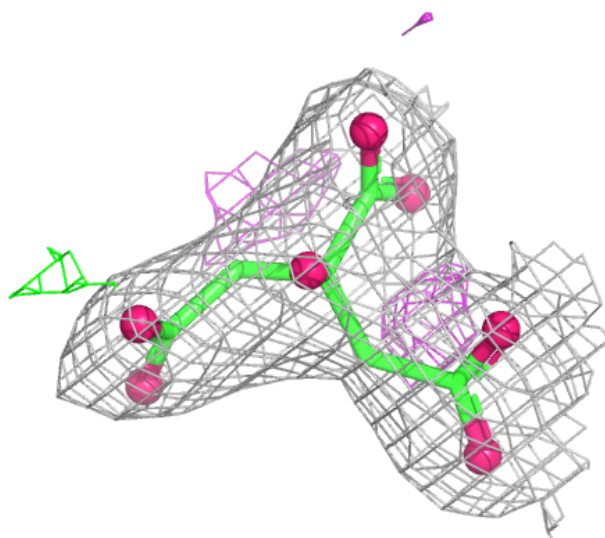
**Electron density around COA D 1002:**

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



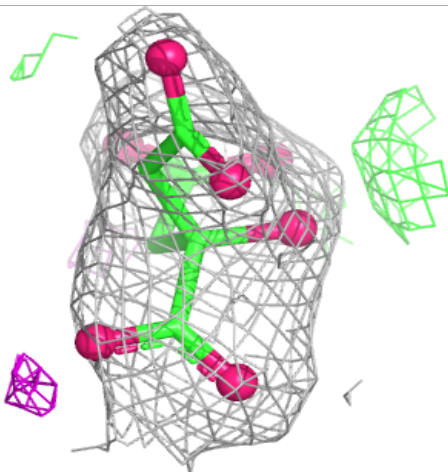
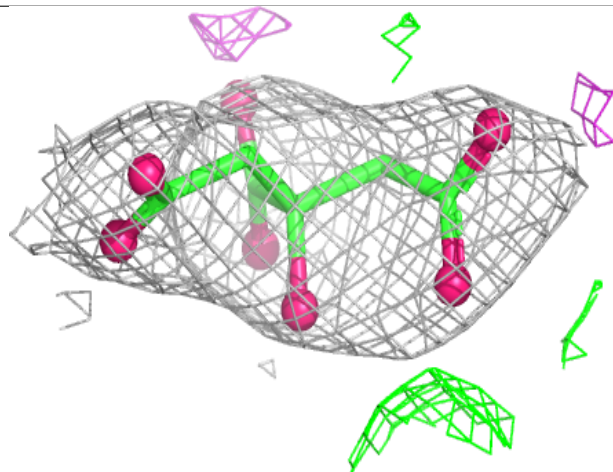
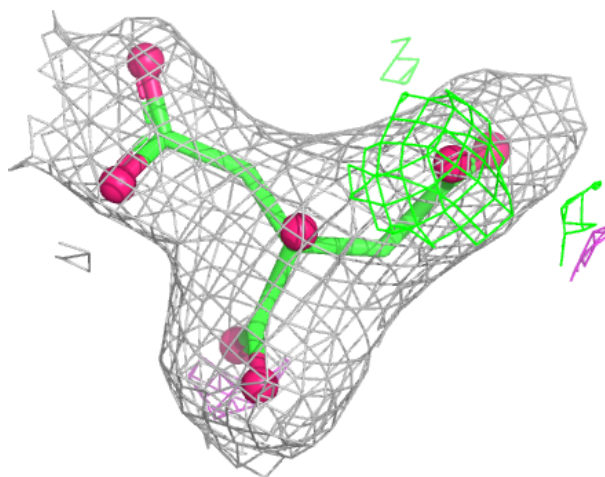
Electron density around FLC B 1003:

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



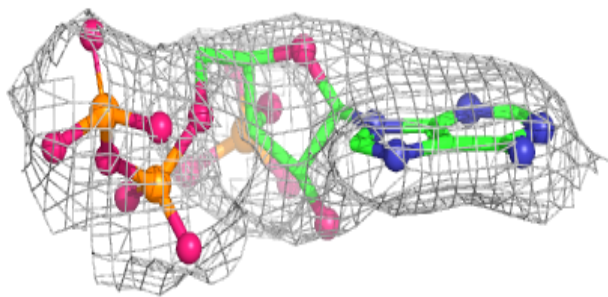
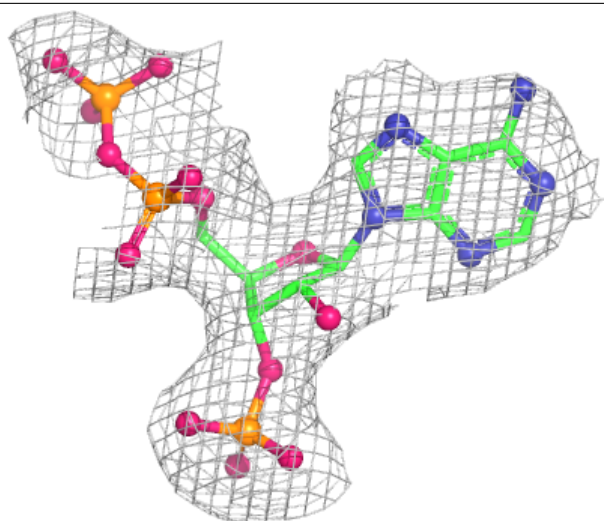
Electron density around FLC H 1003:

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



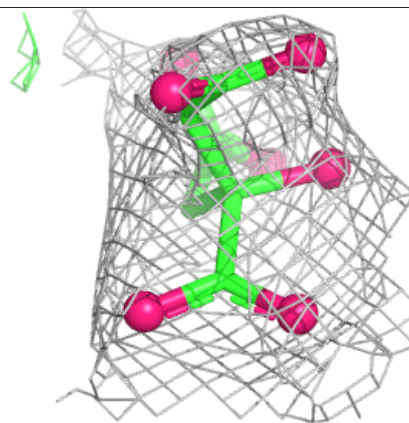
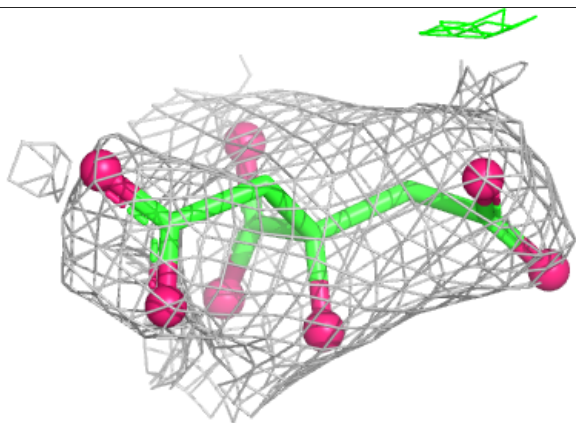
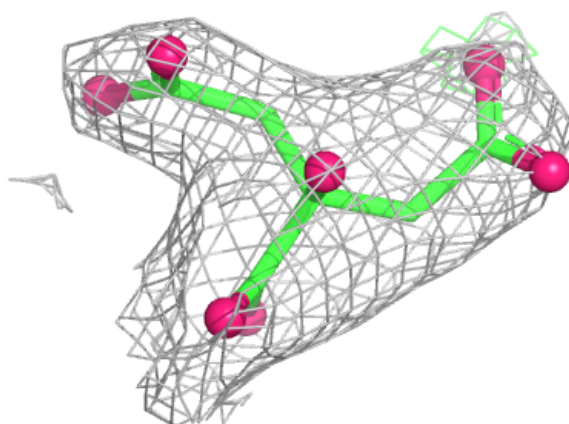
Electron density around COA D 1001:

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and green (positive)



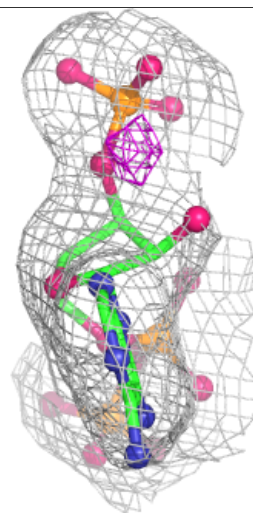
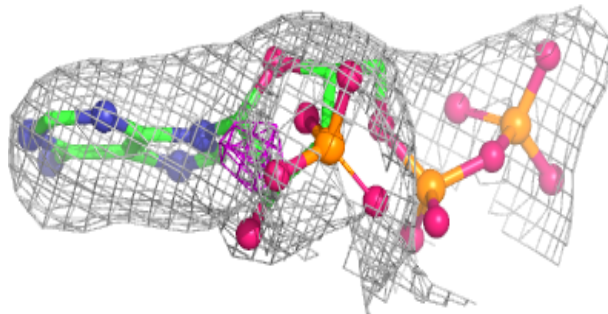
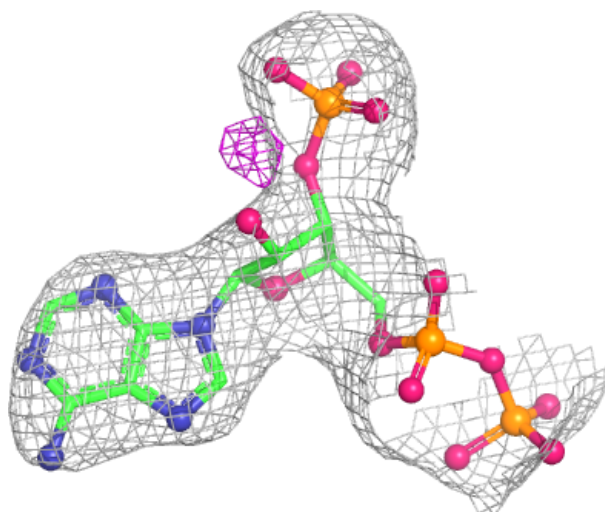
Electron density around FLC A 1001:

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



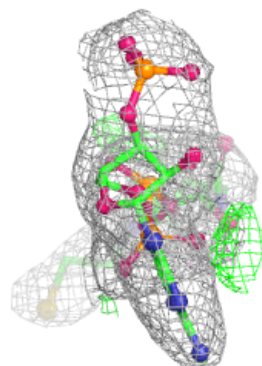
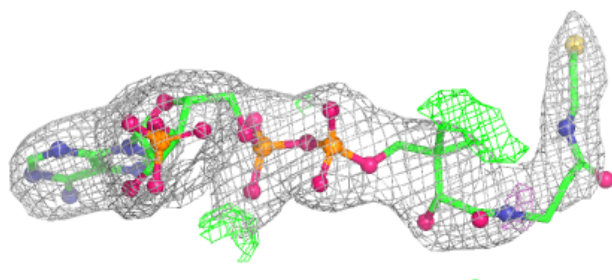
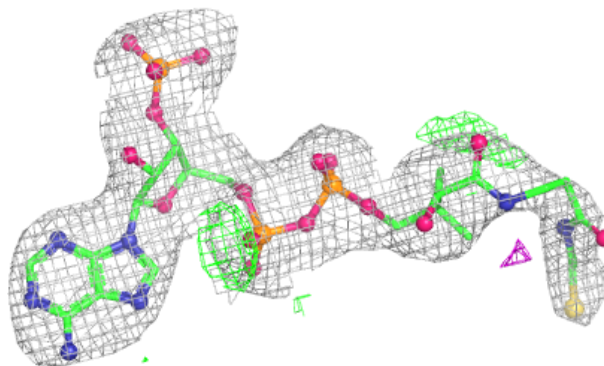
Electron density around COA F 1001:

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



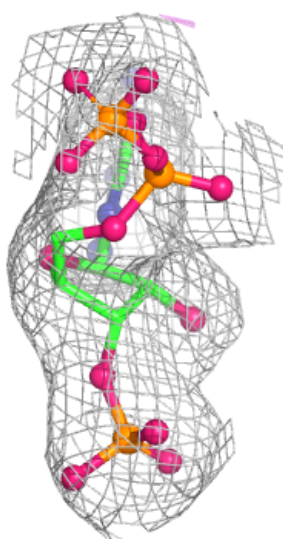
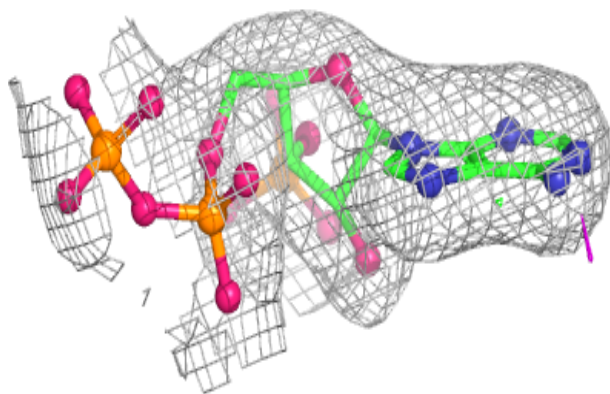
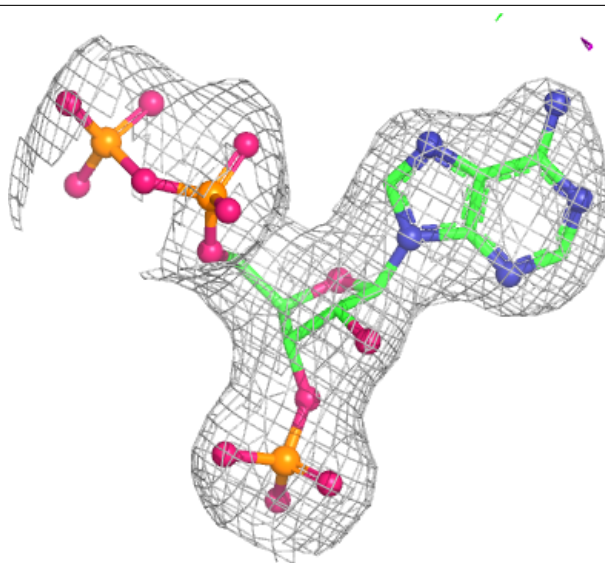
Electron density around COA B 1002:

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



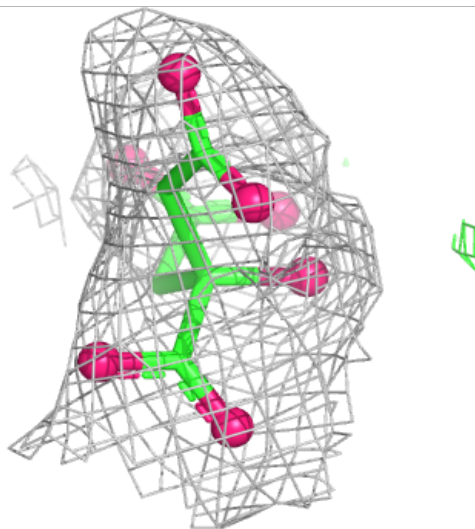
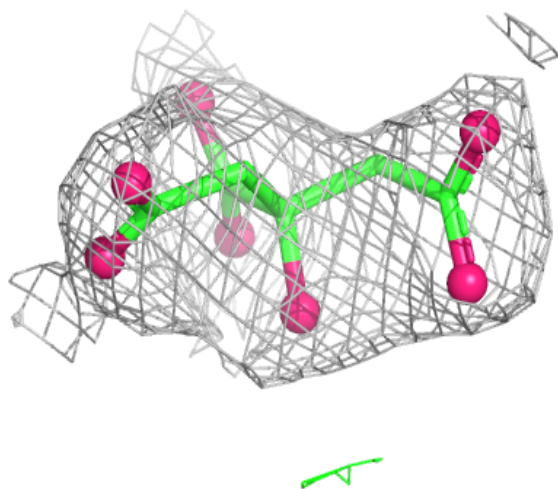
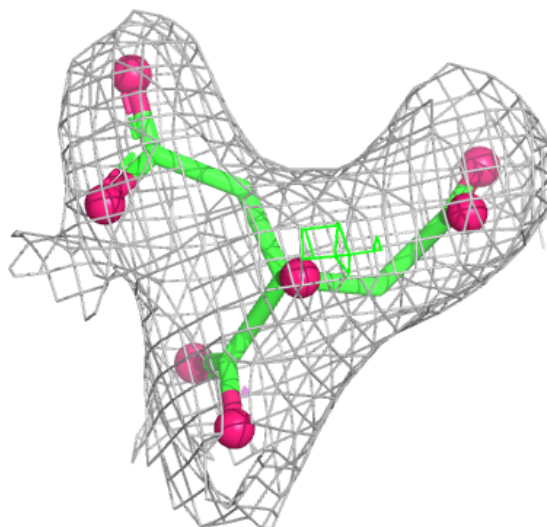
Electron density around COA H 1001:

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



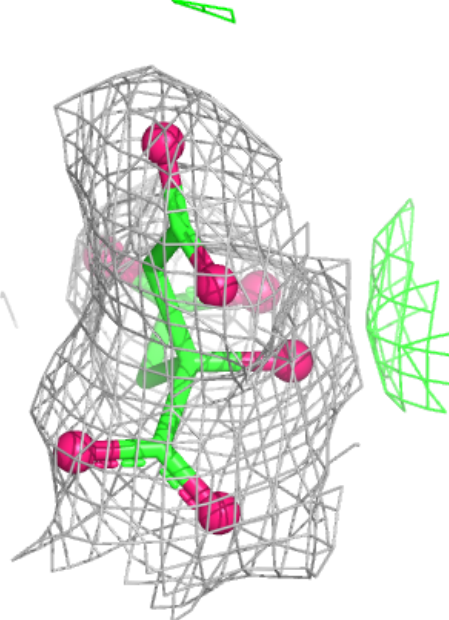
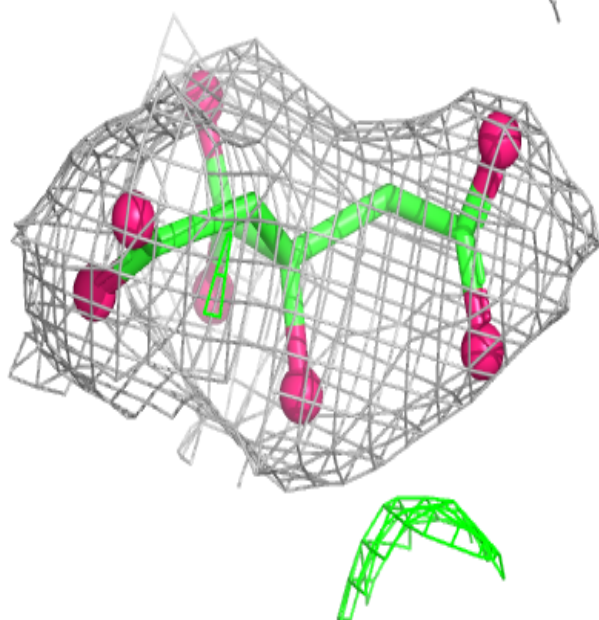
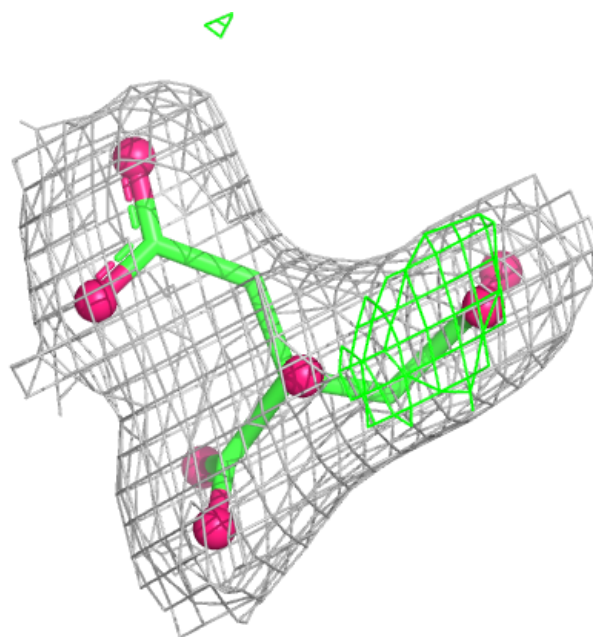
Electron density around FLC F 1003:

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



Electron density around FLC D 1003:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.