



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:05 PM UTC

PDB ID : 6ZNW / pdb_00006znw
Title : Methanosaeta concilii ATP citrate lyase (D541A mutant) in complex with (3S)-citryl-CoA.
Authors : Verschueren, K.H.G.; Verstraete, K.
Deposited on : 2020-07-06
Resolution : 2.12 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

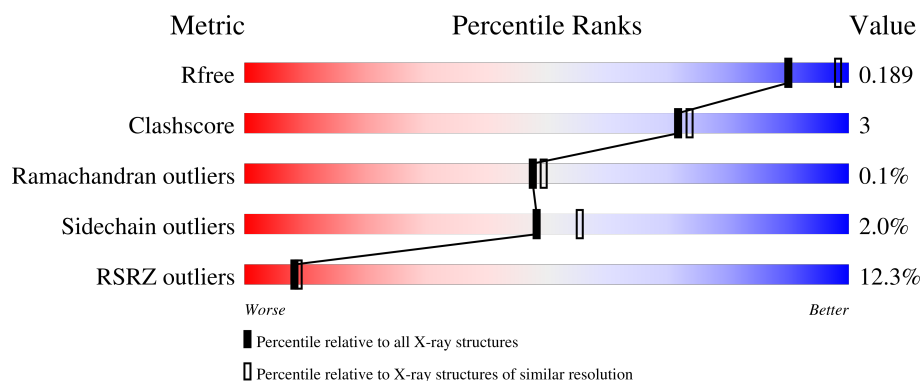
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.12 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	8290 (2.14-2.10)
Clashscore	190562	8817 (2.14-2.10)
Ramachandran outliers	187476	8738 (2.14-2.10)
Sidechain outliers	187428	8739 (2.14-2.10)
RSRZ outliers	180081	8294 (2.14-2.10)

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	421	22% 83% 12% • 5%
2	B	631	5% 91% 6% •

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 8294 atoms, of which 5 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.

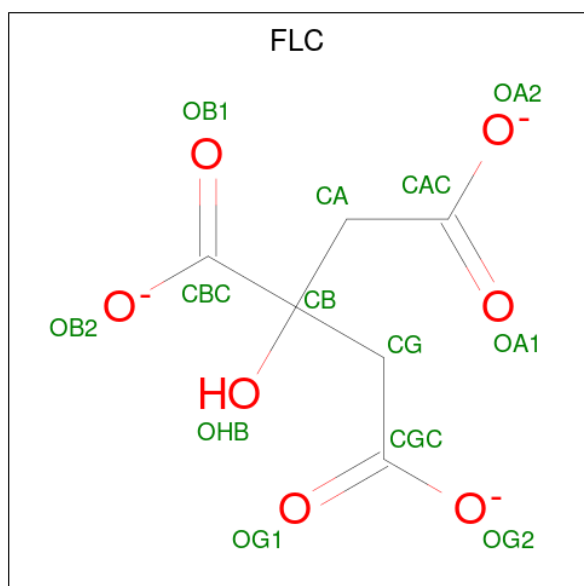
- Molecule 1 is a protein called Citrate lyase, subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	402	Total	C	N	O	S	0	0	0
			3187	2045	516	615	11			

- Molecule 2 is a protein called Methanosaeta concilii ACLY-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	616	Total	C	N	O	S	0	1	0
			4731	3011	811	882	27			

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



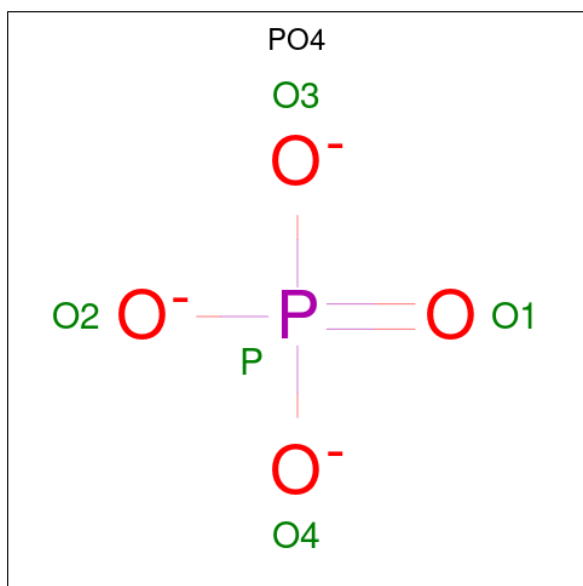
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	5	0
			18	6	5	7		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of

Interest" by depositor).

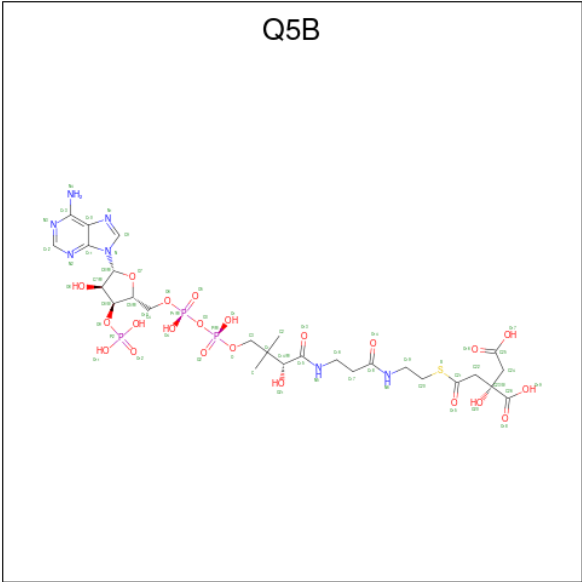
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		

- Molecule 5 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is (3S)-citryl-Coenzyme A (CCD ID: Q5B) (formula: $C_{27}H_{42}N_7O_{22}P_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
6	B	1	60	27	7	22	3	0	0

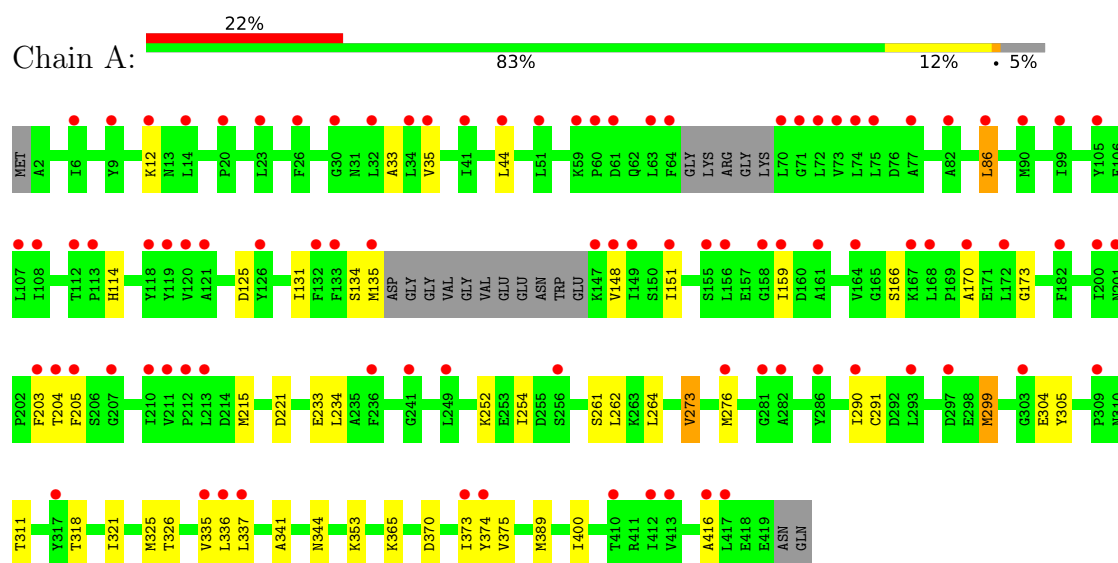
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	30	Total	O	0	0
			30	30		
7	B	262	Total	O	0	0
			262	262		

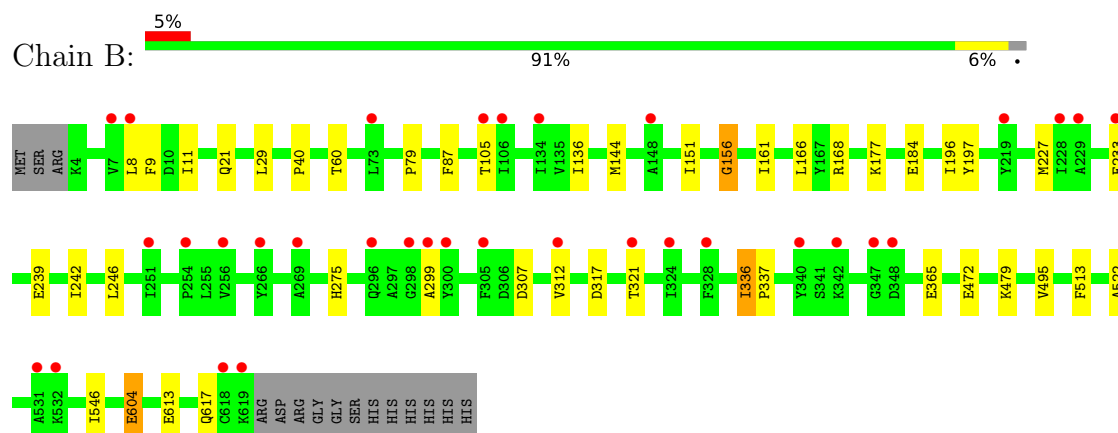
3 Residue-property plots [i](#)

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: Citrate lyase, subunit 1



- Molecule 2: Methanosaeta concilii ACLY-B



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	73.53Å 154.37Å 276.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	79.04 – 2.12 79.04 – 2.12	Depositor EDS
% Data completeness (in resolution range)	99.2 (79.04-2.12) 99.2 (79.04-2.12)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.25 (at 2.12Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.186 , 0.203 (Not available) , 0.189	Depositor DCC
R_{free} test set	4490 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	45.4	Xtriage
Anisotropy	0.392	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 92.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8294	wwPDB-VP
Average B, all atoms (Å ²)	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.70% 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: PO4, Q5B, FLC, MG

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	0.67	1/3257 (0.0%)	1.09	5/4412 (0.1%)
2	B	0.82	0/4819	1.08	5/6507 (0.1%)
All	All	0.76	1/8076 (0.0%)	1.09	10/10919 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	299	MET	SD-CE	-5.08	1.66	1.79

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	513	PHE	CA-CB-CG	6.89	120.69	113.80
1	A	221	ASP	CA-CB-CG	6.24	118.84	112.60
2	B	156	GLY	N-CA-C	6.01	122.28	111.34
1	A	203	PHE	CA-CB-CG	5.81	119.61	113.80
2	B	197	TYR	N-CA-C	-5.55	104.05	112.04
1	A	166	SER	CA-C-N	5.51	129.44	122.16
1	A	166	SER	C-N-CA	5.51	129.44	122.16
1	A	125	ASP	CA-CB-CG	5.22	117.82	112.60
2	B	495	VAL	CA-C-N	5.03	127.43	120.29
2	B	495	VAL	C-N-CA	5.03	127.43	120.29

There are no chirality outliers.

There are no planarity outliers.

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	3187	0	3131	34	0
2	B	4731	0	4802	21	0
3	A	13	5	5	0	0
4	A	1	0	0	0	0
5	A	5	0	0	1	0
6	B	60	0	0	0	0
7	A	30	0	0	0	0
7	B	262	0	0	0	0
All	All	8289	5	7938	53	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (53) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:HIS:HB2	1:A:204:THR:HG21	1.59	0.84
1:A:204:THR:HG22	1:A:205:PHE:H	1.51	0.75
2:B:613:GLU:O	2:B:617:GLN:HG2	1.90	0.71
1:A:375:VAL:HG21	1:A:389:MET:HE2	1.76	0.65
1:A:131:ILE:HB	1:A:151:ILE:CG1	2.28	0.64
5:A:503:PO4:O4	2:B:275:HIS:NE2	2.28	0.63
2:B:8:LEU:HD21	2:B:136:ILE:HD11	1.81	0.62
1:A:276:MET:HE1	1:A:318:THR:HG23	1.84	0.60
1:A:204:THR:HG22	1:A:205:PHE:N	2.17	0.59
1:A:273:VAL:HG22	1:A:299:MET:HA	1.84	0.57
1:A:12:LYS:HZ3	1:A:215:MET:HB2	1.69	0.57
2:B:60:THR:CG2	2:B:337:PRO:HG3	2.37	0.55
1:A:276:MET:HE2	1:A:321:ILE:HD12	1.89	0.55
1:A:131:ILE:HB	1:A:151:ILE:HG12	1.91	0.52
1:A:33:ALA:HB1	1:A:44:LEU:HD21	1.92	0.51
1:A:311:THR:HG21	1:A:353:LYS:HE3	1.93	0.51
2:B:21:GLN:HG3	2:B:87:PHE:CG	2.47	0.50
1:A:35:VAL:HG21	1:A:86:LEU:HD11	1.94	0.49
1:A:114:HIS:CB	1:A:204:THR:HG21	2.38	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:335:VAL:HG11	1:A:416:ALA:HB1	1.95	0.49
1:A:135:MET:HE1	1:A:170:ALA:HB3	1.93	0.48
1:A:373:ILE:HB	1:A:400:ILE:HG12	1.94	0.48
1:A:131:ILE:HB	1:A:151:ILE:HG13	1.95	0.48
1:A:35:VAL:HG11	1:A:86:LEU:HD11	1.95	0.47
1:A:341:ALA:HB1	2:B:184:GLU:HB2	1.96	0.47
2:B:79:PRO:O	2:B:105:THR:OG1	2.29	0.47
2:B:239:GLU:HA	2:B:242:ILE:HD12	1.97	0.46
2:B:227:MET:HE1	2:B:312:VAL:HG13	1.96	0.46
1:A:12:LYS:NZ	1:A:215:MET:HB2	2.31	0.46
2:B:317:ASP:O	2:B:321:THR:HG23	2.15	0.46
1:A:290:ILE:HB	1:A:299:MET:HE2	1.98	0.45
1:A:326:THR:HG21	1:A:365:LYS:HD3	1.99	0.45
2:B:60:THR:HG23	2:B:337:PRO:HG3	1.97	0.45
2:B:9:PHE:CZ	2:B:151:ILE:HD11	2.51	0.45
1:A:344:ASN:O	2:B:156:GLY:HA2	2.17	0.45
2:B:60:THR:HG22	2:B:337:PRO:HG3	1.99	0.45
1:A:291:CYS:SG	1:A:299:MET:HE1	2.57	0.45
2:B:29:LEU:CD2	2:B:40:PRO:HB3	2.45	0.44
1:A:134:SER:HB2	1:A:148:VAL:HG22	1.99	0.44
1:A:35:VAL:HG11	1:A:86:LEU:HD21	1.98	0.43
2:B:336:ILE:HG12	2:B:337:PRO:HD2	1.99	0.43
1:A:337:LEU:HD23	1:A:374:TYR:HB2	2.00	0.43
1:A:261:SER:O	1:A:305:TYR:HA	2.18	0.43
1:A:204:THR:CG2	1:A:205:PHE:H	2.24	0.42
1:A:252:LYS:NZ	1:A:264:LEU:H	2.17	0.42
2:B:177:LYS:HD3	2:B:233:GLU:HG2	2.02	0.42
2:B:246:LEU:HD21	2:B:299:ALA:HB2	2.01	0.42
1:A:325:MET:HE1	1:A:336:LEU:HB2	2.01	0.42
2:B:144:MET:HE1	2:B:166:LEU:HB3	2.02	0.41
2:B:522:ALA:CB	2:B:546:ILE:HD13	2.51	0.41
1:A:326:THR:OG1	1:A:365:LYS:HB3	2.21	0.41
2:B:604[A]:GLU:H	2:B:604[A]:GLU:CD	2.29	0.40
1:A:254:ILE:HG22	1:A:262:LEU:HD13	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	396/421 (94%)	376 (95%)	19 (5%)	1 (0%)	36	36
2	B	615/631 (98%)	604 (98%)	11 (2%)	0	100	100
All	All	1011/1052 (96%)	980 (97%)	30 (3%)	1 (0%)	48	49

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	173	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	339/353 (96%)	332 (98%)	7 (2%)	47	54
2	B	498/510 (98%)	487 (98%)	11 (2%)	45	52
All	All	837/863 (97%)	819 (98%)	18 (2%)	48	52

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	LEU
1	A	159	ILE
1	A	233	GLU
1	A	234	LEU
1	A	273	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	304	GLU
1	A	370	ASP
2	B	11	ILE
2	B	161	ILE
2	B	168	ARG
2	B	196	ILE
2	B	307	ASP
2	B	336	ILE
2	B	365	GLU
2	B	472	GLU
2	B	479	LYS
2	B	604[A]	GLU
2	B	604[B]	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	ASN
1	A	227	GLN
1	A	316	HIS
2	B	187	ASN
2	B	281	ASN
2	B	512	ASN
2	B	524	GLN

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

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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
5	PO4	A	503	4	4,4,4	2.68	3 (75%)	6,6,6	0.56	0
3	FLC	A	501	4	12,12,12	1.08	0	17,17,17	1.13	1 (5%)
6	Q5B	B	701	-	60,62,62	0.55	0	87,93,93	0.90	5 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FLC	A	501	4	-	3/16/16/16	-
6	Q5B	B	701	-	-	17/66/83/83	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	503	PO4	P-O1	4.52	1.61	1.50
5	A	503	PO4	P-O4	2.05	1.60	1.54
5	A	503	PO4	P-O3	2.04	1.60	1.54

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	701	Q5B	O4-P1-O3	2.91	115.14	107.27
6	B	701	Q5B	C23-C24-C25	2.58	120.97	113.92
6	B	701	Q5B	O9-P2-O12	-2.29	101.16	109.33
3	A	501	FLC	OB1-CBC-CB	-2.20	117.83	122.09
6	B	701	Q5B	O8-C7-C6	2.15	117.19	111.19
6	B	701	Q5B	O9-C6-C5	-2.01	102.93	110.03

There are no chirality outliers.

All (20) torsion outliers are listed below:

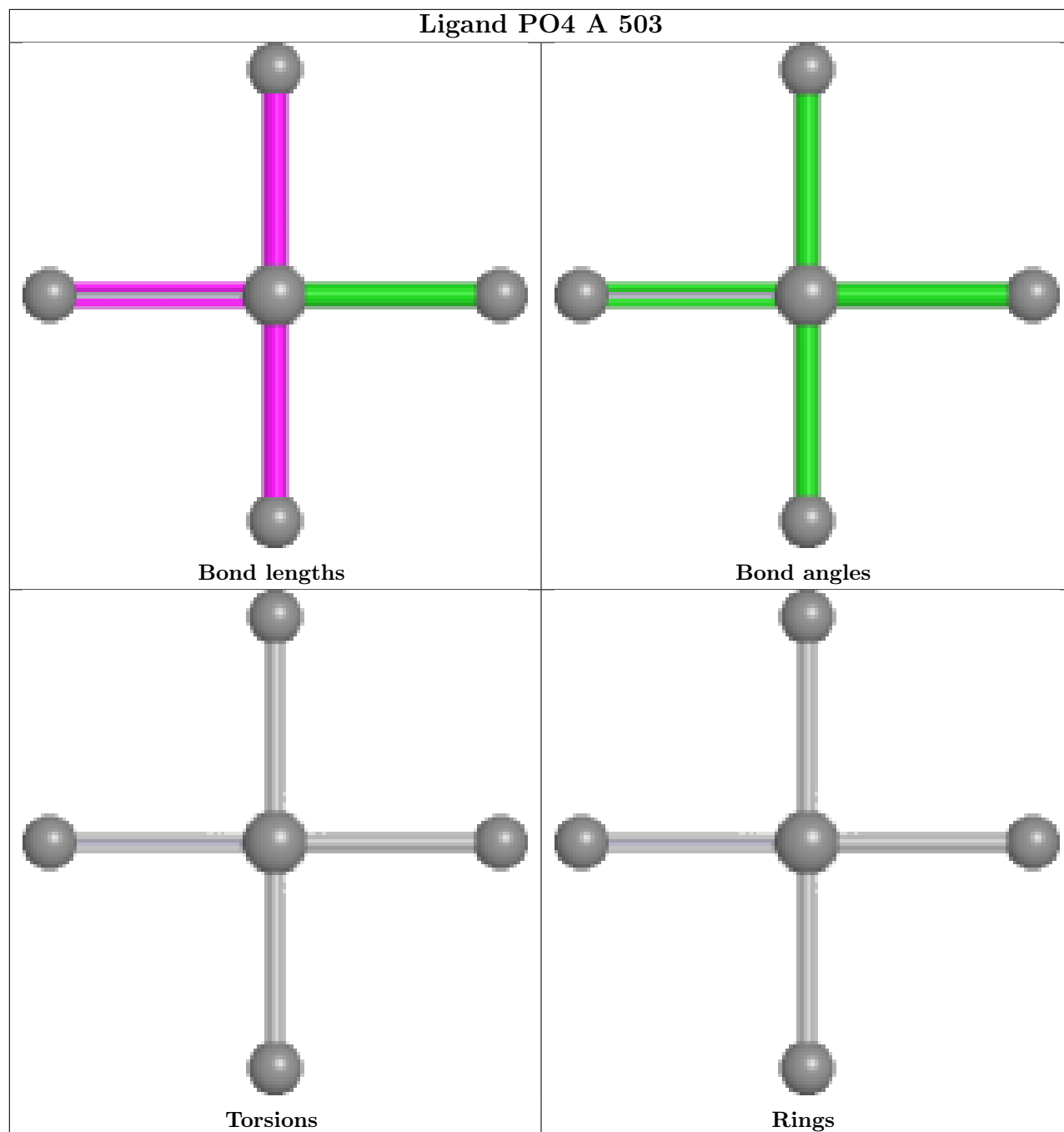
Mol	Chain	Res	Type	Atoms
6	B	701	Q5B	C3-O-P-O1
6	B	701	Q5B	C3-O-P-O2
6	B	701	Q5B	C3-O-P-O3
6	B	701	Q5B	C24-C23-C26-O18
6	B	701	Q5B	C24-C23-C26-O19
6	B	701	Q5B	O20-C23-C26-O18
6	B	701	Q5B	O20-C23-C26-O19
3	A	501	FLC	CA-CB-CG-CGC
6	B	701	Q5B	C21-C22-C23-C24
3	A	501	FLC	CBC-CB-CG-CGC
6	B	701	Q5B	O6-C4-C5-O7
6	B	701	Q5B	O6-C4-C5-C6
6	B	701	Q5B	C21-C22-C23-C26
6	B	701	Q5B	C4-O6-P1-O3
6	B	701	Q5B	C4-O6-P1-O4
6	B	701	Q5B	C4-O6-P1-O5
3	A	501	FLC	OHB-CB-CG-CGC
6	B	701	Q5B	C21-C22-C23-O20
6	B	701	Q5B	C23-C24-C25-O17
6	B	701	Q5B	C23-C24-C25-O16

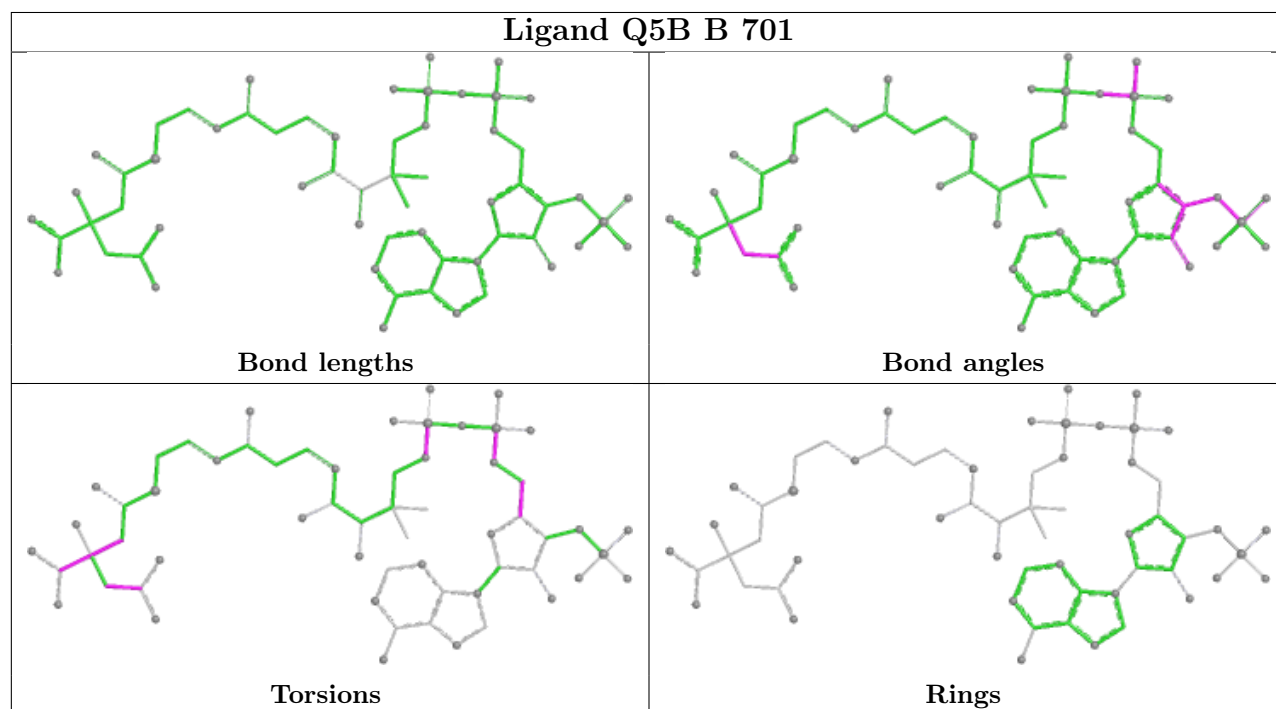
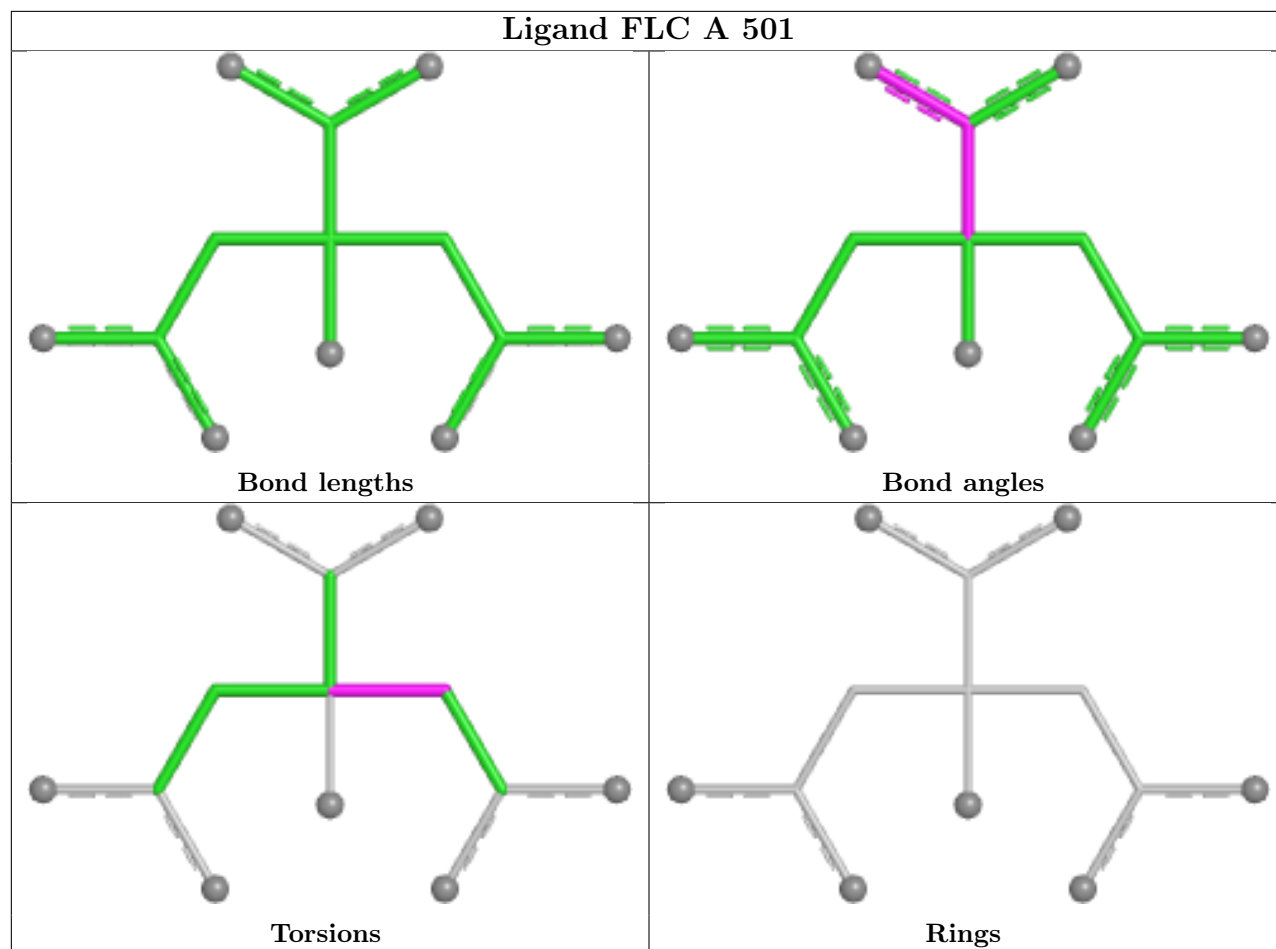
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	503	PO4	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	402/421 (95%)	1.28	92 (22%) 2 2	71, 143, 199, 211	0
2	B	616/631 (97%)	0.41	33 (5%) 31 34	27, 78, 127, 150	1 (0%)
All	All	1018/1052 (96%)	0.76	125 (12%) 8 9	27, 99, 188, 211	1 (0%)

All (125) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	70	LEU	8.3
1	A	44	LEU	5.6
1	A	182	PHE	5.6
1	A	41	ILE	4.9
1	A	286	TYR	4.8
1	A	60	PRO	4.6
1	A	241	GLY	4.3
1	A	303	GLY	4.3
2	B	105	THR	4.3
1	A	86	LEU	4.0
1	A	64	PHE	4.0
1	A	161	ALA	3.8
1	A	156	LEU	3.7
1	A	337	LEU	3.7
1	A	71	GLY	3.7
1	A	256	SER	3.7
2	B	134	ILE	3.6
1	A	210	ILE	3.6
1	A	170	ALA	3.6
1	A	168	LEU	3.5
1	A	34	LEU	3.5
1	A	336	LEU	3.5
2	B	618	CYS	3.4
1	A	281	GLY	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	324	ILE	3.3
1	A	118	TYR	3.3
1	A	75	LEU	3.3
1	A	203	PHE	3.3
1	A	200	ILE	3.3
2	B	8	LEU	3.3
1	A	374	TYR	3.2
1	A	213	LEU	3.2
1	A	135	MET	3.1
1	A	73	VAL	3.1
1	A	172	LEU	3.0
1	A	133	PHE	3.0
1	A	410	THR	3.0
1	A	201	ASN	2.9
1	A	249	LEU	2.9
1	A	108	ILE	2.9
1	A	276	MET	2.9
2	B	328	PHE	2.9
1	A	149	ILE	2.9
1	A	151	ILE	2.8
1	A	59	LYS	2.8
1	A	416	ALA	2.8
1	A	212	PRO	2.8
1	A	6	ILE	2.8
1	A	26	PHE	2.8
1	A	282	ALA	2.8
2	B	299	ALA	2.8
1	A	12	LYS	2.7
2	B	269	ALA	2.7
1	A	72	LEU	2.7
1	A	159	ILE	2.7
1	A	51	LEU	2.7
1	A	9	TYR	2.7
1	A	211	VAL	2.7
1	A	413	VAL	2.7
2	B	106	ILE	2.6
1	A	207	GLY	2.6
1	A	335	VAL	2.6
1	A	412	ILE	2.5
2	B	229	ALA	2.5
1	A	23	LEU	2.5
1	A	297	ASP	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	348	ASP	2.5
2	B	321	THR	2.5
1	A	63	LEU	2.5
1	A	90	MET	2.5
1	A	205	PHE	2.5
1	A	99	ILE	2.5
1	A	105	TYR	2.4
2	B	305	PHE	2.4
2	B	254	PRO	2.4
1	A	147	LYS	2.4
1	A	164	VAL	2.4
1	A	112	THR	2.4
2	B	300	TYR	2.4
2	B	256	VAL	2.4
2	B	347	GLY	2.3
1	A	290	ILE	2.3
1	A	120	VAL	2.3
1	A	167	LYS	2.3
1	A	293	LEU	2.3
2	B	73	LEU	2.3
1	A	204	THR	2.2
1	A	155	SER	2.2
1	A	132	PHE	2.2
1	A	113	PRO	2.2
1	A	373	ILE	2.2
1	A	148	VAL	2.2
1	A	107	LEU	2.2
2	B	228	ILE	2.2
1	A	417	LEU	2.2
1	A	119	TYR	2.2
2	B	340	TYR	2.2
2	B	7	VAL	2.1
1	A	158	GLY	2.1
2	B	298	GLY	2.1
1	A	77	ALA	2.1
1	A	121	ALA	2.1
2	B	531	ALA	2.1
1	A	32	LEU	2.1
1	A	317	TYR	2.1
1	A	309	PRO	2.1
1	A	236	PHE	2.1
1	A	35	VAL	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	342	LYS	2.1
1	A	82	ALA	2.1
1	A	14	LEU	2.1
1	A	61	ASP	2.1
1	A	30	GLY	2.1
2	B	532	LYS	2.1
2	B	312	VAL	2.1
2	B	148	ALA	2.1
2	B	296	GLN	2.0
1	A	126	TYR	2.0
2	B	266	TYR	2.0
2	B	251	ILE	2.0
2	B	233	GLU	2.0
1	A	74	LEU	2.0
2	B	619	LYS	2.0
1	A	20	PRO	2.0
2	B	219	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

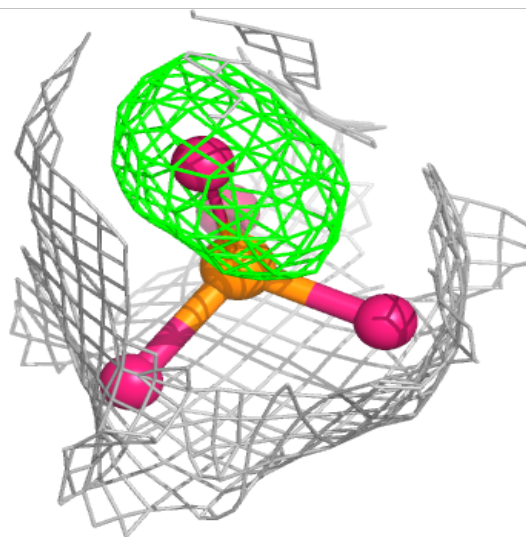
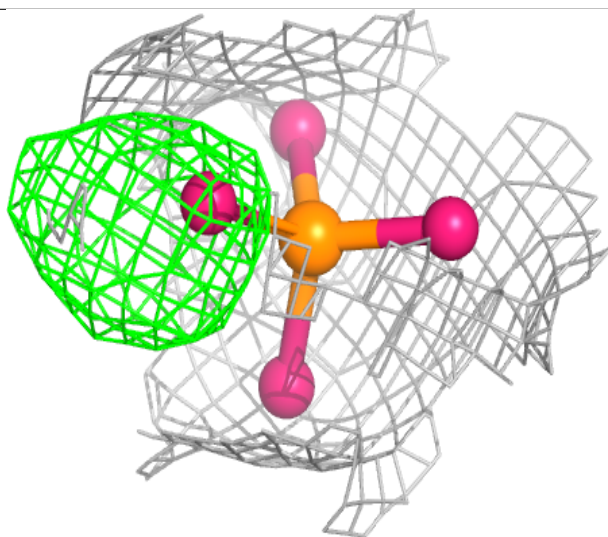
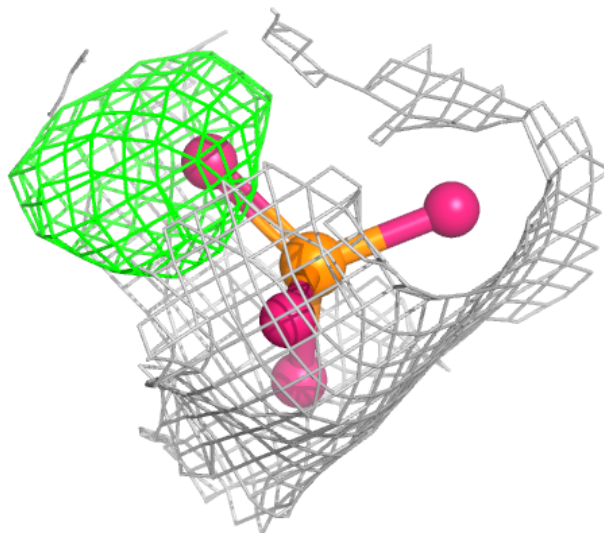
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	PO4	A	503	5/5	0.86	0.12	106,107,107,107	0
4	MG	A	502	1/1	0.92	0.07	113,113,113,113	0
6	Q5B	B	701	60/60	0.95	0.09	43,65,85,86	0
3	FLC	A	501	13/13	0.96	0.08	75,77,92,92	5

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.

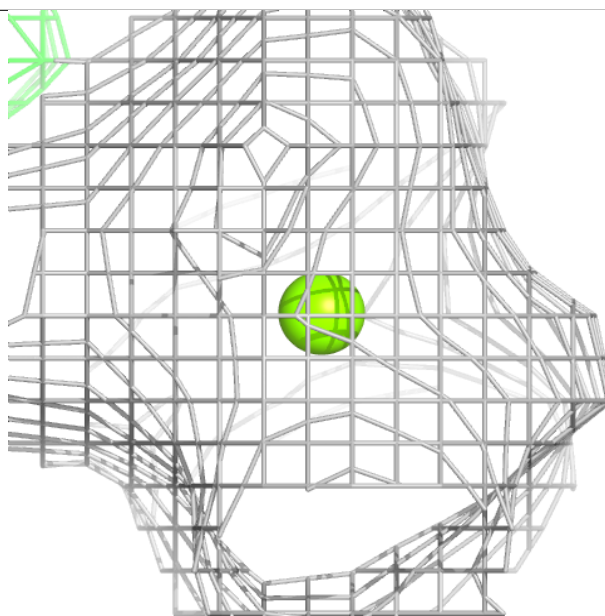
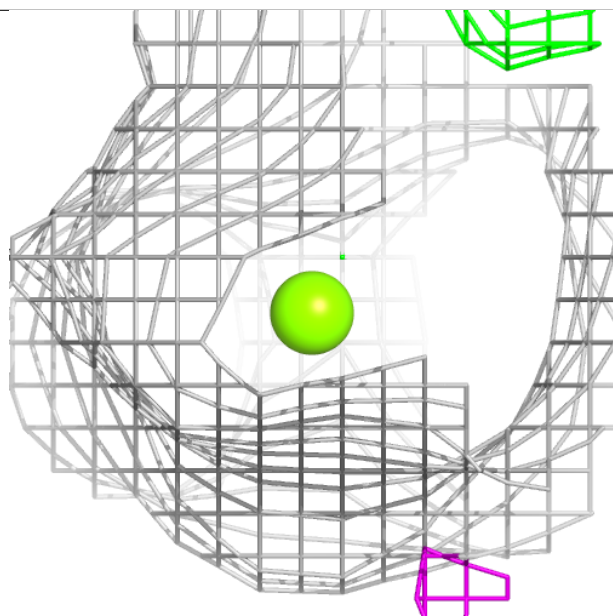
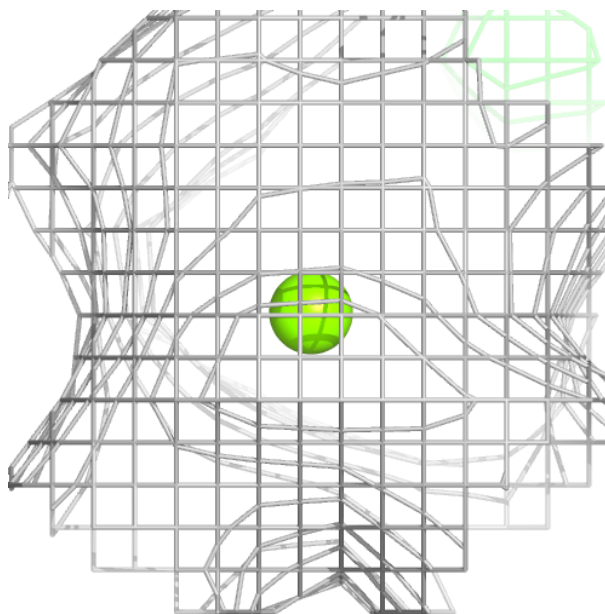
Electron density around PO4 A 503:

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



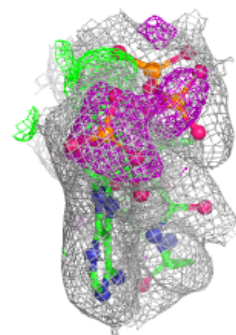
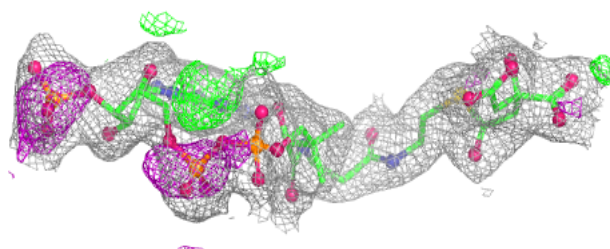
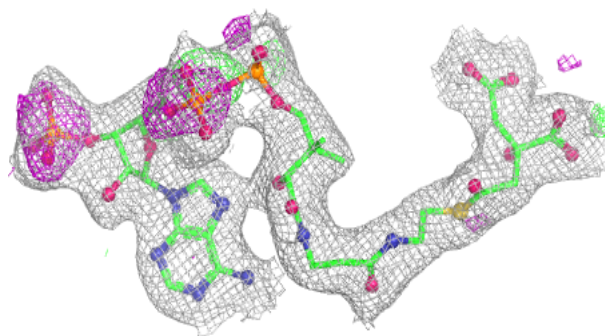
Electron density around MG A 502:

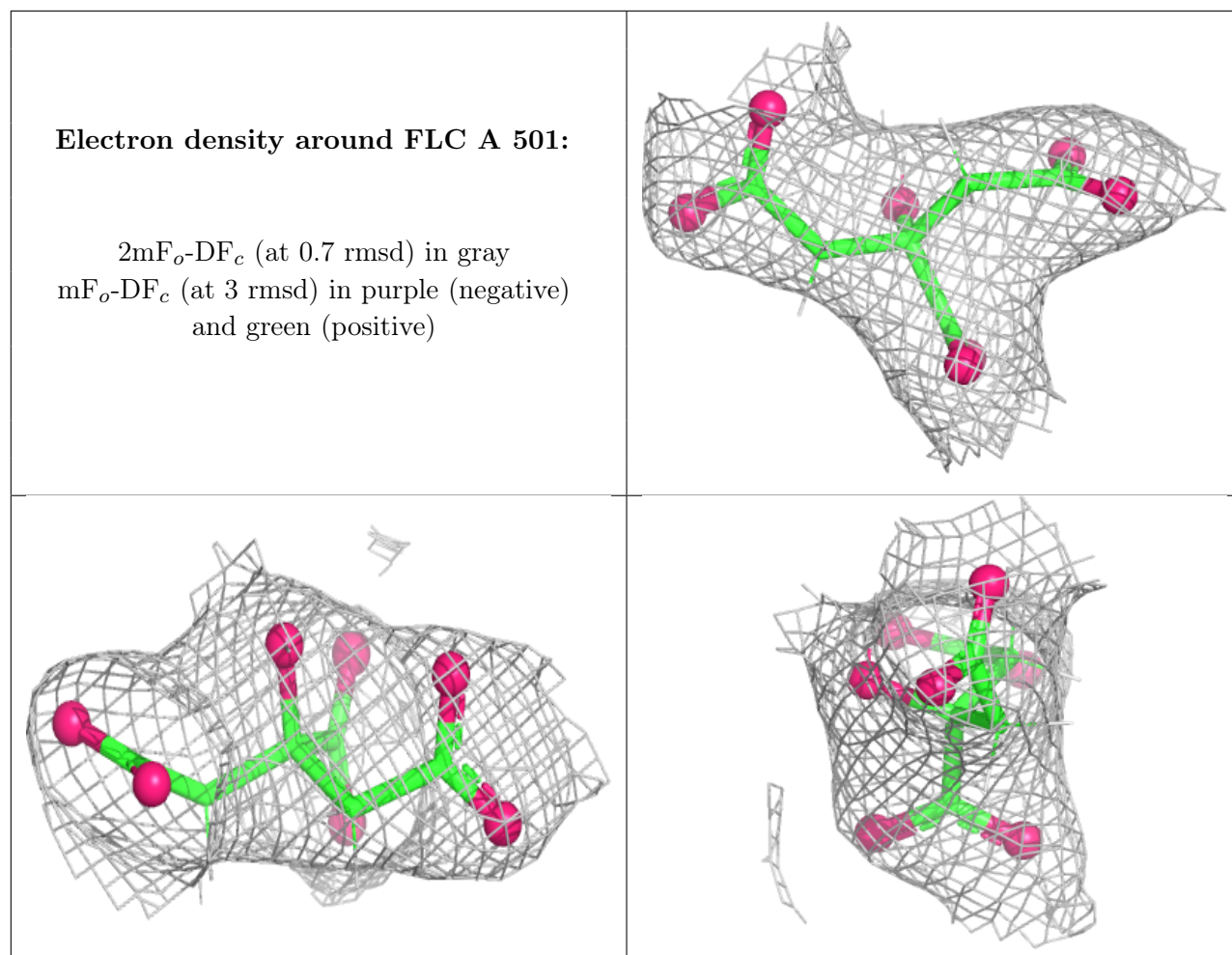
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Q5B B 701:

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





6.5 Other polymers [i](#)

There are no such residues in this entry.