

wwPDB X-ray Structure Validation Summary Report (i)

Nov 7, 2023 – 04:17 AM EST

PDB ID : 8DHT

Title : Crystal structure of a typeIII Rubisco

Authors : Qingqiu, H. Deposited on : 2022-06-28

Resolution : 1.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (1)) 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 : 2.36

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

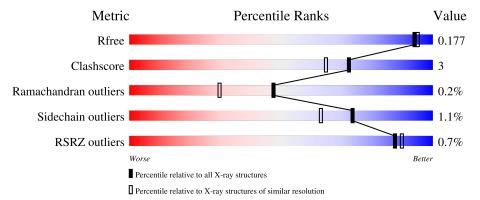
Validation Pipeline (wwPDB-VP) : 2.36

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 1.70 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	Similar resolution
Metric	$(\# ext{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	441	92%	7%
1	В	441	94%	5%
1	С	441	93%	7%
1	D	441	92%	7% •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard



residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	3PG	С	503	-	-	X	-
5	ACT	A	506	-	-	X	-
5	ACT	D	505	-	-	X	-



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 15263 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 Ribulose bisphosphate carboxylase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	440	Total	С	N	О	S	0	3	0
1	A	440	3434	2188	591	643	12	0	3	
1	В	440	Total	С	N	О	S	0	1	0
1	Ъ	440	3425	2182	590	642	11	0		
1	С	440	Total	С	N	О	S	0	2	0
1		440	3432	2186	593	641	12	0		
1	D	440	Total	С	N	О	S	0	1	0
1	ש	440	3417	2178	589	638	12	U	1	U

There are 4 discrepancies between the modelled and reference sequences:

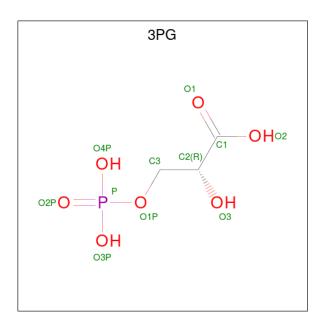
Chain	Residue	Modelled	Actual	Comment	Reference
A	403	ARG	LYS	conflict	UNP O28635
В	403	ARG	LYS	conflict	UNP O28635
С	403	ARG	LYS	conflict	UNP O28635
D	403	ARG	LYS	conflict	UNP O28635

• Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0
2	В	1	Total Mg 1 1	0	0
2	С	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0

• Molecule 3 is 3-PHOSPHOGLYCERIC ACID (three-letter code: 3PG) (formula: C₃H₇O₇P) (labeled as "Ligand of Interest" by depositor).

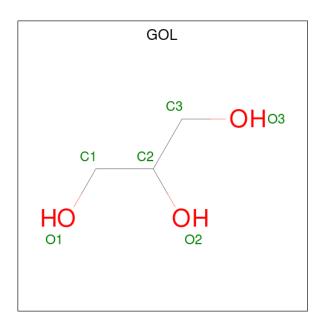




Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O P 11 3 7 1	0	0
3	A	1	Total C O P 11 3 7 1	0	0
3	В	1	Total C O P 11 3 7 1	0	0
3	В	1	Total C O P 11 3 7 1	0	0
3	С	1	Total C O P 11 3 7 1	0	0
3	С	1	Total C O P 11 3 7 1	0	0
3	D	1	Total C O P 11 3 7 1	0	0
3	D	1	Total C O P 11 3 7 1	0	0

• Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$) (labeled as "Ligand of Interest" by depositor).

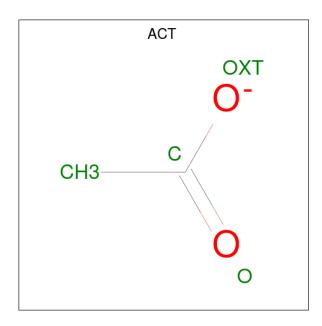




Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	В	1	Total C O 6 3 3	0	0
4	В	1	Total C O 6 3 3	0	0
4	В	1	Total C O 6 3 3	0	0
4	D	1	Total C O 6 3 3	0	0

 \bullet Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2)$ (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	В	1	Total C O 4 2 2	0	0
5	С	1	Total C O 4 2 2	0	0
5	D	1	Total C O 4 2 2	0	0

• Molecule 6 is water.

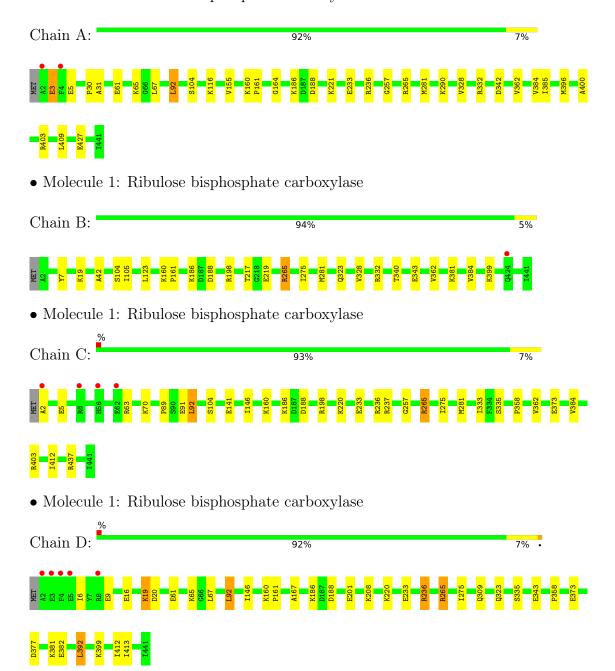
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	353	Total O 353 353	0	0
6	В	372	Total O 372 372	0	0
6	С	312	Total O 312 312	0	0
6	D	370	Total O 370 370	0	0



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: Ribulose bisphosphate carboxylase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	80.33Å 116.21Å 83.28Å	Donositon
a, b, c, α , β , γ	90.00° 96.32° 90.00°	Depositor
Resolution (Å)	49.38 - 1.70	Depositor
rtesolution (A)	49.38 - 1.70	EDS
% Data completeness	99.9 (49.38-1.70)	Depositor
(in resolution range)	99.9 (49.38-1.70)	EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) > 1$	2.06 (at 1.70Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.144 , 0.177	Depositor
it, it free	0.144 , 0.177	DCC
R_{free} test set	1998 reflections (1.20%)	wwPDB-VP
Wilson B-factor (Å ²)	17.9	Xtriage
Anisotropy	0.193	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.39, 50.4	EDS
L-test for twinning ²	$< L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	0.016 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	15263	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 22.00 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.2433e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

²Theoretical 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.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, KCX, MG, 3PG, ACT

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	Bo	nd lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z >5	
1	A	0.38	1/3499~(0.0%)	0.56	1/4733 (0.0%)	
1	В	0.36	0/3490	0.54	0/4720	
1	С	0.34	0/3497	0.52	1/4729 (0.0%)	
1	D	0.39	0/3482	0.58	3/4710 (0.1%)	
All	All	0.37	$1/13968 \; (0.0\%)$	0.55	5/18892 (0.0%)	

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(ext{\AA})$
1	A	5	GLU	CD-OE1	-5.69	1.19	1.25

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\mathrm{Ideal}(^{o})$
1	D	92	LEU	CA-CB-CG	6.28	129.74	115.30
1	D	392	LEU	CA-CB-CG	-6.06	101.37	115.30
1	A	92	LEU	CA-CB-CG	5.76	128.56	115.30
1	С	92	LEU	CA-CB-CG	5.44	127.81	115.30
1	D	236	ARG	CD-NE-CZ	5.25	130.94	123.60

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	3434	0	3399	27	0
1	В	3425	0	3393	18	0
1	С	3432	0	3399	23	0
1	D	3417	0	3383	24	0
2	A	1	0	0	0	0
2	В	1	0	0	0	0
2	С	1	0	0	0	0
2	D	1	0	0	0	0
3	A	22	0	7	3	0
3	В	22	0	7	3	0
3	С	22	0	7	4	0
3	D	22	0	7	2	0
4	A	12	0	16	1	0
4	В	18	0	24	0	0
4	D	6	0	8	0	0
5	A	8	0	6	2	0
5	В	4	0	3	0	0
5	С	4	0	3	0	0
5	D	4	0	3	2	0
6	A	353	0	0	8	8
6	В	372	0	0	6	4
6	С	312	0	0	6	6
6	D	370	0	0	9	1
All	All	15263	0	13665	93	10

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.

The worst 5 of 93 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} ext{Interatomic} \ ext{distance} & (ext{Å}) \end{aligned}$	Clash overlap (Å)	
1:B:219:GLU:OE2	6:B:601:HOH:O	1.81	0.97	
1:A:155[A]:VAL:HG21	1:A:409:LEU:HD11	1.62	0.82	
1:D:343:GLU:O	6:D:601:HOH:O	1.97	0.80	
1:A:160:LYS:NZ	3:A:503:3PG:H2	1.98	0.79	
1:A:342:ASP:OD1	6:A:601:HOH:O	2.02	0.78	

The worst 5 of 10 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.



Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ (\rm \mathring{A}) \end{array}$	Clash overlap (Å)
6:A:723:HOH:O	6:C:614:HOH:O[2_555]	1.87	0.33
6:A:601:HOH:O	6:C:779:HOH:O[2_555]	1.92	0.28
6:A:821:HOH:O	6:C:807:HOH:O[2_555]	1.94	0.26
6:A:935:HOH:O	6:B:912:HOH:O[2_656]	1.96	0.24
6:B:943:HOH:O	6:D:890:HOH:O[2_646]	1.98	0.22

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	Perce	ntiles
1	A	440/441 (100%)	427 (97%)	12 (3%)	1 (0%)	47	30
1	В	438/441 (99%)	425 (97%)	12 (3%)	1 (0%)	47	30
1	\mathbf{C}	439/441 (100%)	425 (97%)	13 (3%)	1 (0%)	47	30
1	D	438/441 (99%)	425 (97%)	13 (3%)	0	100	100
All	All	1755/1764 (100%)	1702 (97%)	50 (3%)	3 (0%)	47	30

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	281	MET
1	В	281	MET
1	С	281	MET

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	$353/353 \; (100\%)$	349 (99%)	4 (1%)	73	63	
1	В	$352/353\ (100\%)$	348 (99%)	4 (1%)	73	63	
1	С	$352/353\ (100\%)$	348 (99%)	4 (1%)	73	63	
1	D	350/353~(99%)	346 (99%)	4 (1%)	73	63	
All	All	1407/1412 (100%)	1391 (99%)	16 (1%)	73	63	

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	265	ARG
1	D	188	ASP
1	С	70	LYS
1	D	19	LYS
1	В	265	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	С	56	HIS
1	D	323	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)

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	\mathbf{B}_{0}	ond leng	gths	В	ond ang	gles
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	KCX	A	186	1,2	9,11,12	0.98	0	5,12,14	2.22	1 (20%)



Mol	Tuno	Chain	Dec	Link	Bond lengths			Bond angles		
MIOI	Type		nes	Lilik	Counts	RMSZ # Z > 2 Counts	RMSZ	# Z > 2		
1	KCX	С	186	1,2	9,11,12	1.01	1 (11%)	5,12,14	2.04	1 (20%)
1	KCX	D	186	1,2	9,11,12	0.79	0	5,12,14	1.75	1 (20%)
1	KCX	В	186	1,2	9,11,12	0.93	0	5,12,14	1.52	1 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	KCX	A	186	1,2	-	0/9/10/12	-
1	KCX	С	186	1,2	-	0/9/10/12	-
1	KCX	D	186	1,2	-	0/9/10/12	-
1	KCX	В	186	1,2	-	0/9/10/12	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$\operatorname{Ideal}(ext{\AA})$
1	С	186	KCX	OQ1-CX	2.25	1.25	1.21

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$Ideal(^{o})$
1	A	186	KCX	OQ1-CX-NZ	-4.45	118.06	124.96
1	С	186	KCX	OQ1-CX-NZ	-4.05	118.68	124.96
1	D	186	KCX	OQ1-CX-NZ	-3.42	119.66	124.96
1	В	186	KCX	OQ1-CX-NZ	-3.09	120.17	124.96

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.



5.6 Ligand geometry (i)

Of 23 ligands modelled in this entry, 4 are monoatomic - leaving 19 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	В	ond leng	gths	В	ond ang	les
IVIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GOL	A	505	-	5,5,5	0.95	0	5, 5, 5	1.07	0
3	3PG	D	503	2	9,10,10	1.17	0	12,14,14	2.04	3 (25%)
3	3PG	A	503	2	9,10,10	1.07	0	12,14,14	2.04	3 (25%)
4	GOL	В	505	-	5,5,5	0.74	0	5,5,5	1.24	1 (20%)
3	3PG	В	502	2	9,10,10	1.10	0	12,14,14	1.17	1 (8%)
5	ACT	A	507	-	3,3,3	1.35	0	3,3,3	1.19	0
4	GOL	В	506	-	5,5,5	0.87	0	5,5,5	1.17	1 (20%)
3	3PG	С	503	2	9,10,10	1.11	0	12,14,14	1.97	4 (33%)
5	ACT	В	507	-	3,3,3	1.42	0	3,3,3	1.53	0
3	3PG	С	502	2	9,10,10	1.06	0	12,14,14	1.16	1 (8%)
4	GOL	A	504	-	5,5,5	0.87	0	5,5,5	1.07	0
5	ACT	С	504	_	3,3,3	1.51	1 (33%)	3,3,3	1.30	0
4	GOL	В	504	-	5,5,5	0.99	0	5,5,5	0.78	0
3	3PG	D	502	2	9,10,10	1.12	0	12,14,14	1.12	1 (8%)
5	ACT	A	506	-	3,3,3	1.34	0	3,3,3	1.29	0
3	3PG	A	502	2	9,10,10	1.03	0	12,14,14	1.27	2 (16%)
3	3PG	В	503	2	9,10,10	1.00	0	12,14,14	2.06	4 (33%)
5	ACT	D	505	-	3,3,3	0.79	0	3,3,3	1.95	2 (66%)
4	GOL	D	504	-	5,5,5	1.05	0	5,5,5	0.64	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
3	3PG	В	502	2	-	2/10/10/10	-
3	3PG	A	503	2	-	5/10/10/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	3PG	A	502	2	-	0/10/10/10	-
3	3PG	В	503	2	-	5/10/10/10	-
4	GOL	A	505	-	-	0/4/4/4	-
4	GOL	В	506	-	-	2/4/4/4	-
4	GOL	В	504	-	-	0/4/4/4	-
3	3PG	С	503	2	-	4/10/10/10	-
3	3PG	D	503	2	-	4/10/10/10	-
4	GOL	D	504	_	-	0/4/4/4	_
3	3PG	С	502	2	-	0/10/10/10	-
4	GOL	A	504	-	-	2/4/4/4	-
3	3PG	D	502	2	-	3/10/10/10	_
4	GOL	В	505	_	-	2/4/4/4	_

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$\operatorname{Ideal}(ext{\AA})$
5	С	504	ACT	СН3-С	2.19	1.58	1.49

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
3	D	503	3PG	O1P-C3-C2	-5.66	91.61	107.94
3	В	503	3PG	O1P-C3-C2	-5.58	91.85	107.94
3	A	503	3PG	O1P-C3-C2	-5.51	92.06	107.94
3	С	503	3PG	O1P-C3-C2	-5.21	92.91	107.94
3	A	502	3PG	O2-C1-C2	3.19	119.73	112.72

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

Mol	Chain	Res	Type	${f Atoms}$
3	A	503	3PG	C1-C2-C3-O1P
3	A	503	3PG	O3-C2-C3-O1P
3	В	503	3PG	C1-C2-C3-O1P
3	В	503	3PG	O3-C2-C3-O1P
3	С	503	3PG	C1-C2-C3-O1P

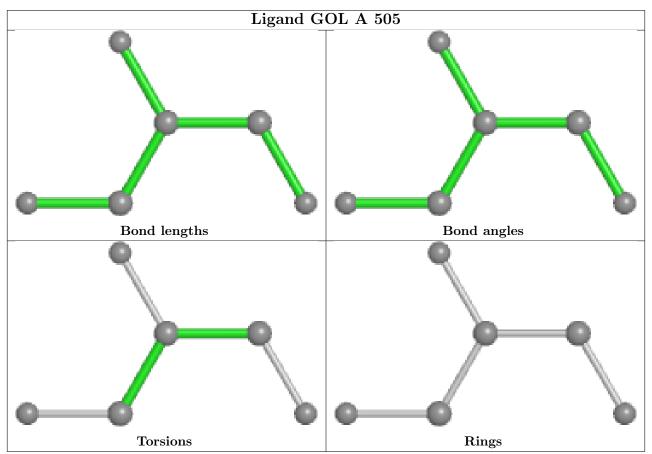
There are no ring outliers.

7 monomers are involved in 17 short contacts:

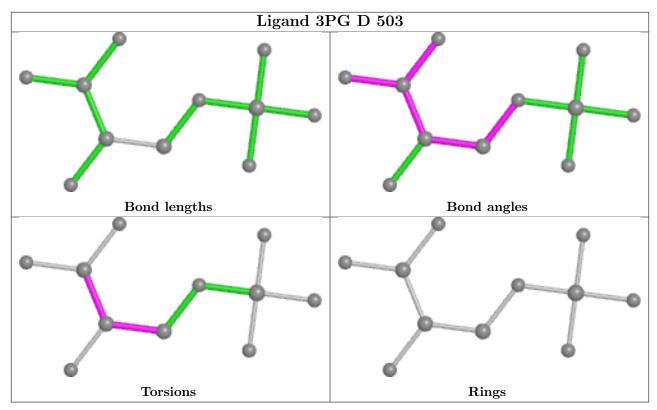


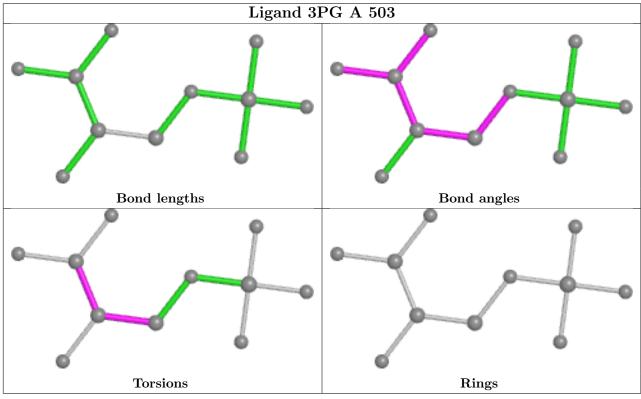
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	505	GOL	1	0
3	D	503	3PG	2	0
3	A	503	3PG	3	0
3	С	503	3PG	4	0
5	A	506	ACT	2	0
3	В	503	3PG	3	0
5	D	505	ACT	2	0

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 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.

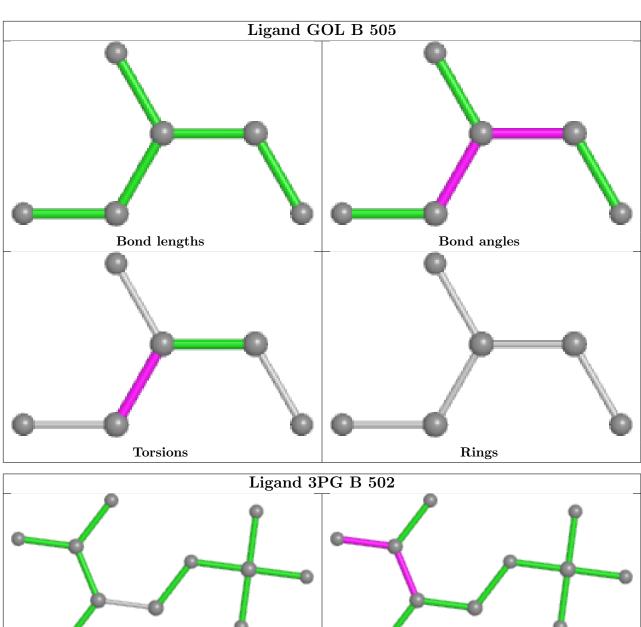


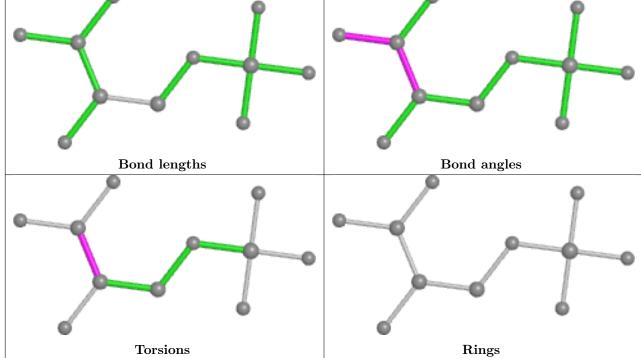




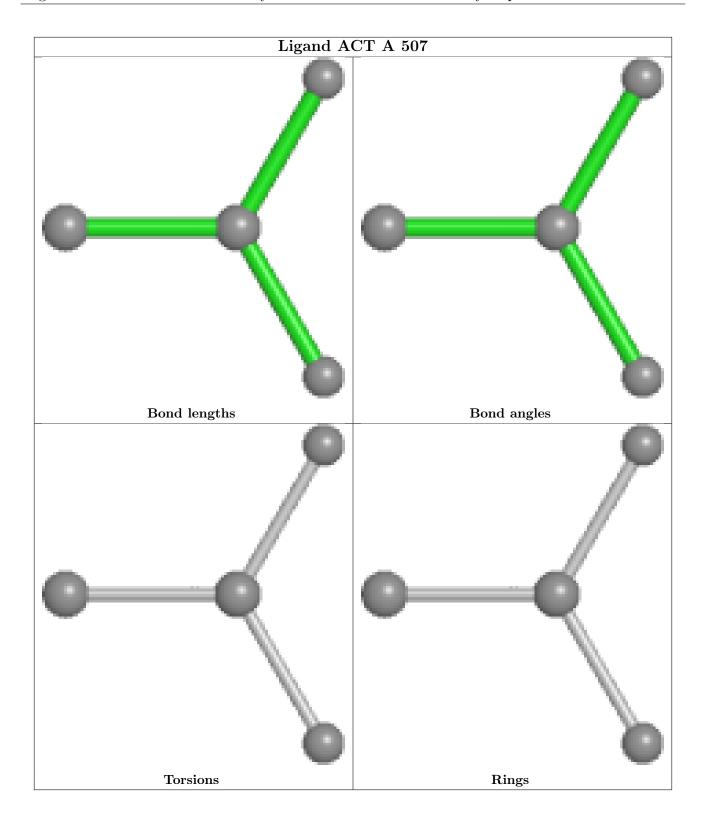




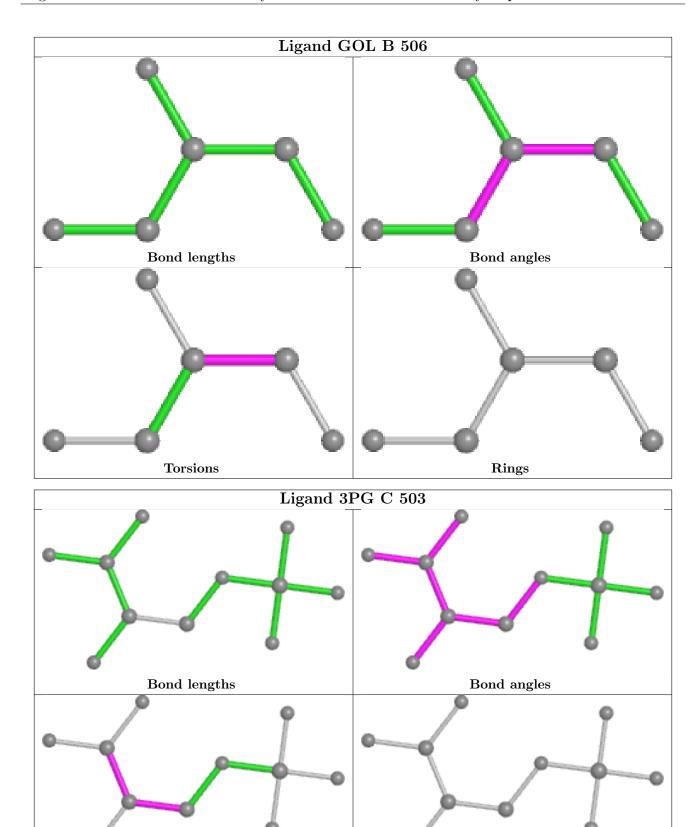








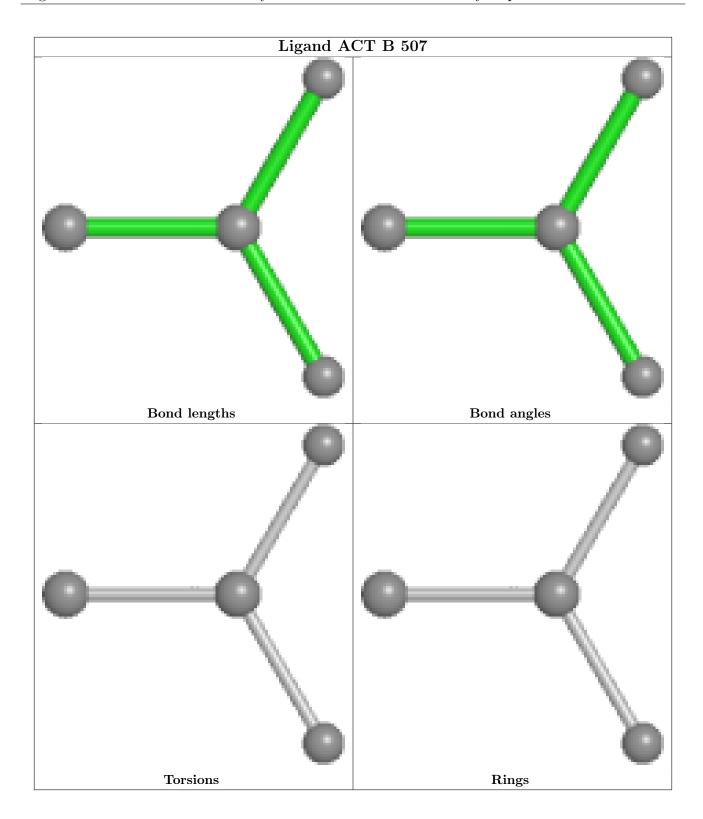




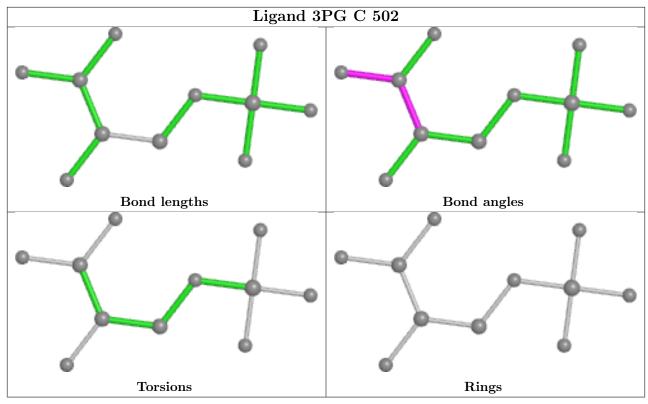


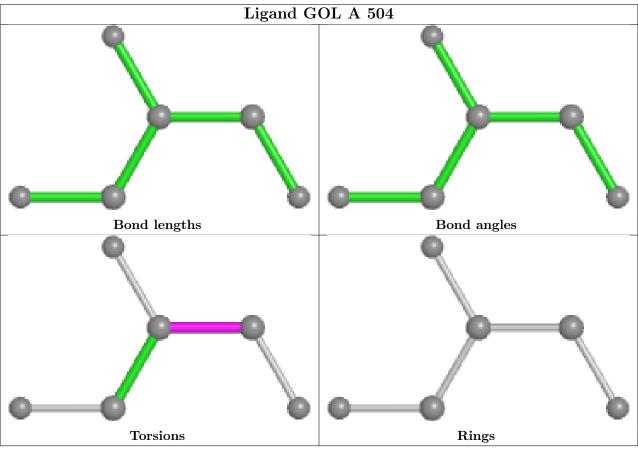
Rings

Torsions

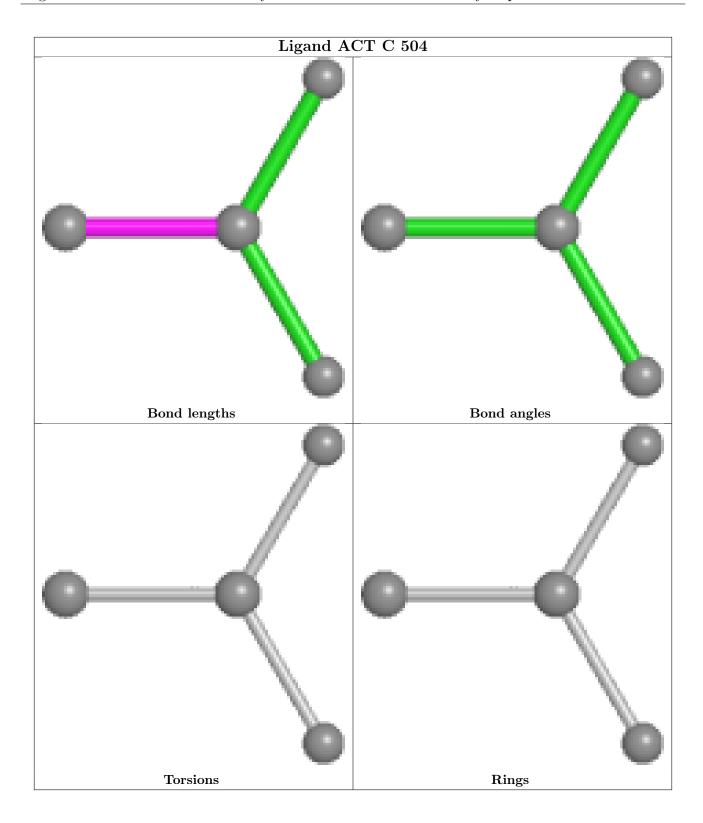




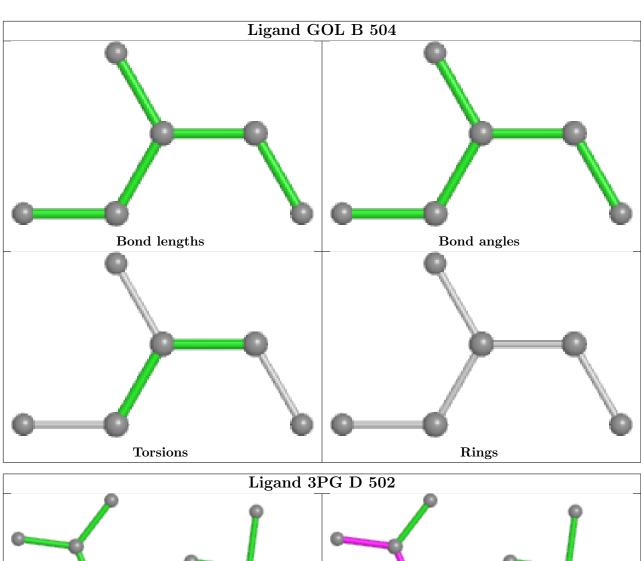


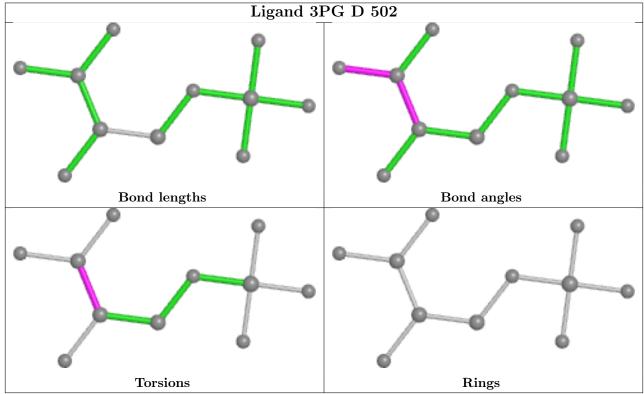




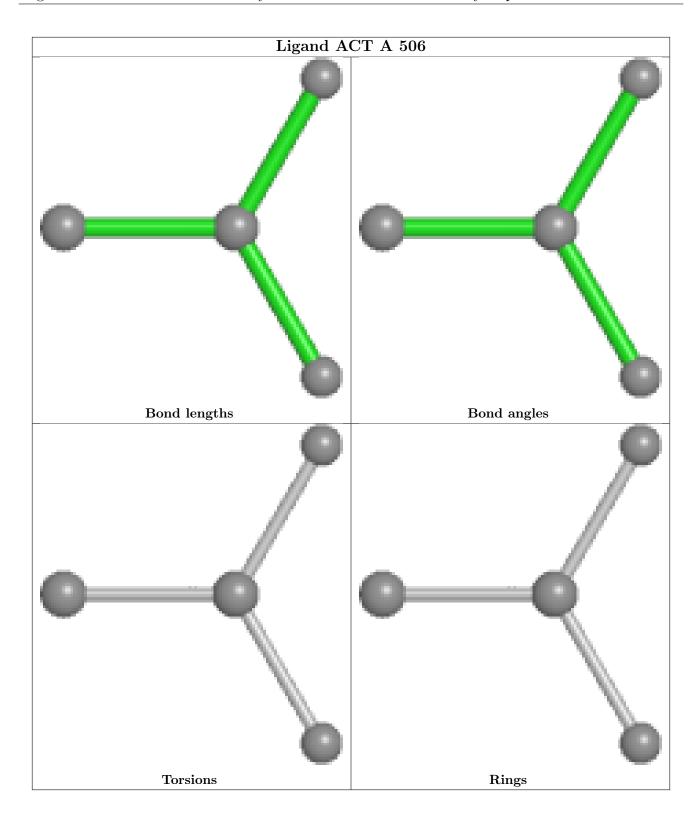




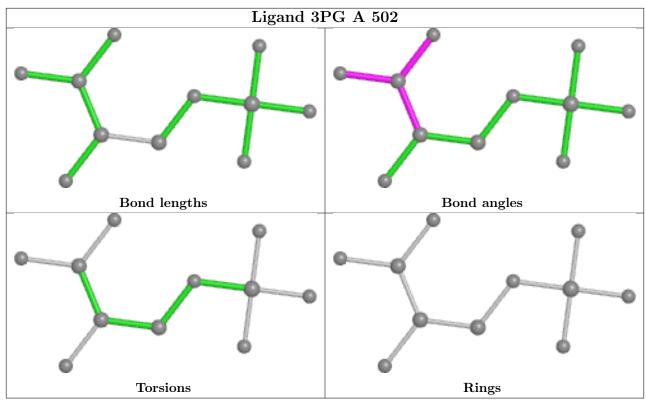


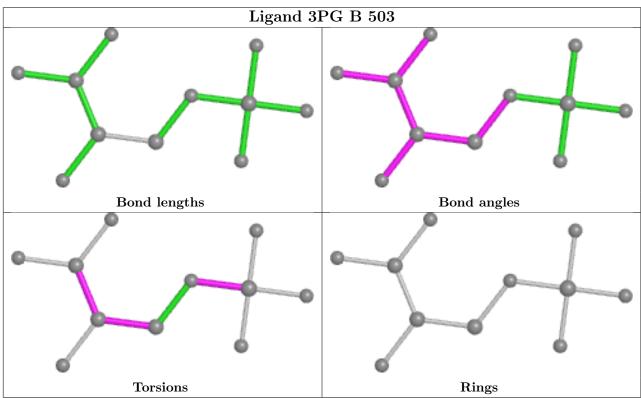




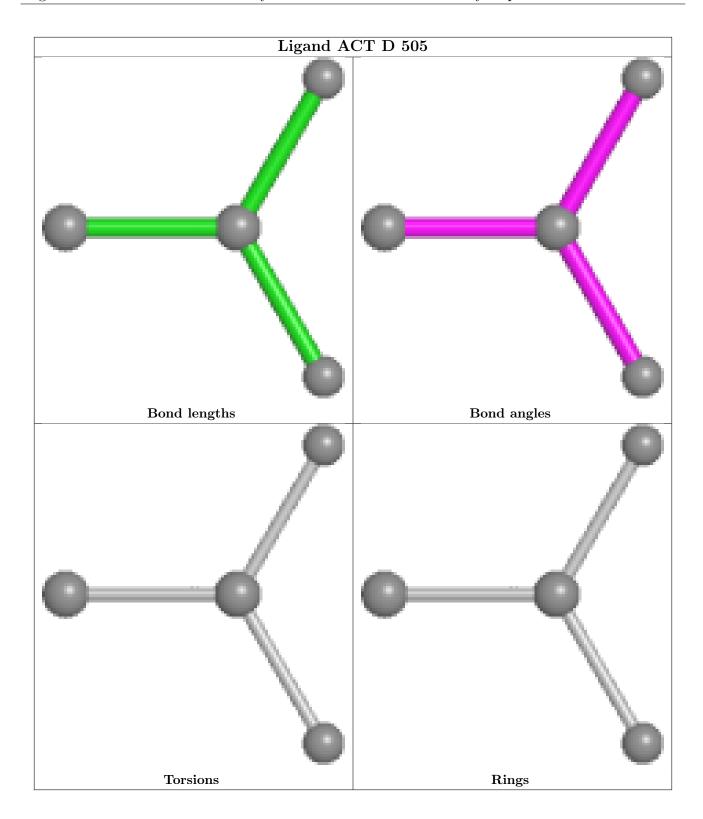




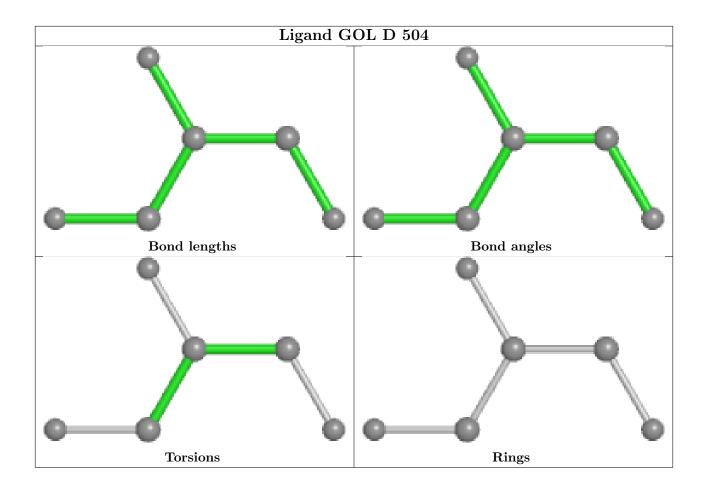












5.7 Other polymers (i)

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, 95^{th} 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>	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	439/441 (99%)	-0.48	2 (0%) 91 92	12, 18, 31, 57	0
1	В	439/441 (99%)	-0.53	1 (0%) 95 95	12, 18, 30, 44	0
1	С	439/441 (99%)	-0.40	4 (0%) 84 87	14, 20, 34, 47	0
1	D	439/441 (99%)	-0.42	5 (1%) 80 83	12, 17, 31, 54	0
All	All	1756/1764 (99%)	-0.46	12 (0%) 87 90	12, 18, 32, 57	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	3	GLU	3.7
1	D	4	PHE	3.5
1	D	2	ALA	3.5
1	D	8	ARG	3.0
1	С	8	ARG	2.6

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
1	KCX	D	186	12/13	0.96	0.07	11,12,14,16	0
1	KCX	С	186	12/13	0.97	0.06	12,14,18,18	0
1	KCX	A	186	12/13	0.98	0.06	11,13,14,17	0
1	KCX	В	186	12/13	0.98	0.05	12,14,16,16	0



6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

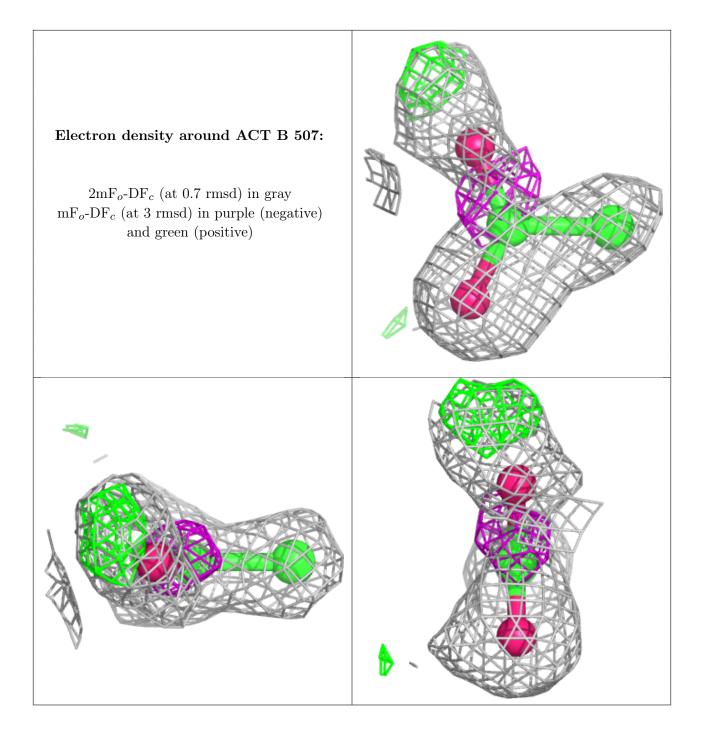
6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} 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.

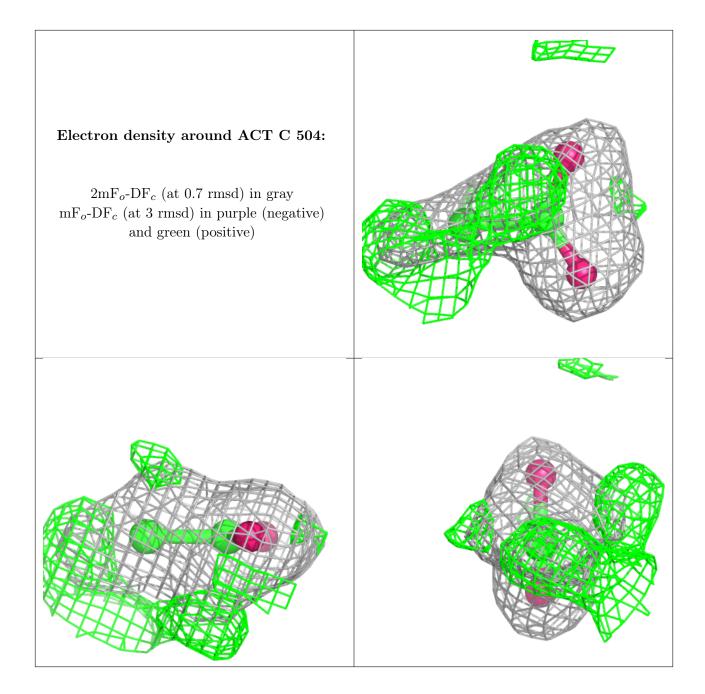
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\operatorname{B-factors}(\mathring{\mathbf{A}}^2)$	Q<0.9
5	ACT	В	507	4/4	0.67	0.23	36,40,48,48	0
5	ACT	С	504	4/4	0.84	0.14	29,36,44,44	0
4	GOL	В	505	6/6	0.85	0.11	24,32,35,36	0
5	ACT	A	507	4/4	0.88	0.10	31,35,39,39	0
4	GOL	A	505	6/6	0.90	0.11	26,34,40,42	0
5	ACT	D	505	4/4	0.90	0.10	29,30,39,45	0
5	ACT	A	506	4/4	0.93	0.12	26,33,33,36	0
4	GOL	В	506	6/6	0.94	0.16	31,35,43,45	0
4	GOL	В	504	6/6	0.94	0.08	19,27,30,30	0
4	GOL	A	504	6/6	0.94	0.09	23,25,36,36	0
4	GOL	D	504	6/6	0.98	0.08	14,16,16,17	0
3	3PG	В	502	11/11	0.98	0.09	16,19,20,20	0
3	3PG	В	503	11/11	0.98	0.06	16,18,23,23	0
3	3PG	С	502	11/11	0.98	0.08	20,21,22,23	0
3	3PG	С	503	11/11	0.98	0.08	17,19,22,23	0
3	3PG	D	503	11/11	0.98	0.06	13,14,16,18	0
3	3PG	A	502	11/11	0.99	0.05	15,17,18,20	0
3	3PG	A	503	11/11	0.99	0.06	14,15,19,19	0
3	3PG	D	502	11/11	0.99	0.04	15,16,17,20	0
2	MG	A	501	1/1	0.99	0.03	14,14,14,14	0
2	MG	В	501	1/1	0.99	0.04	15,15,15,15	0
2	MG	D	501	1/1	1.00	0.03	15,15,15,15	0
2	MG	С	501	1/1	1.00	0.03	16,16,16,16	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.





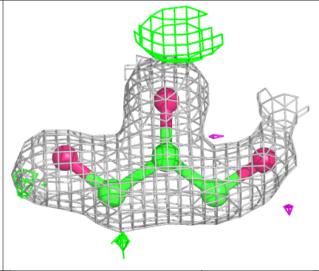


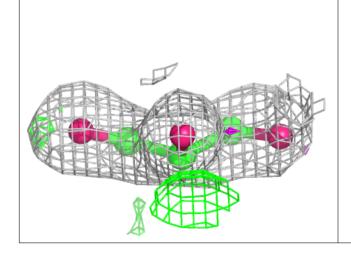


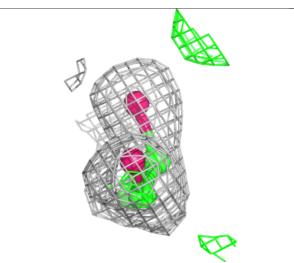


Electron density around GOL B 505:

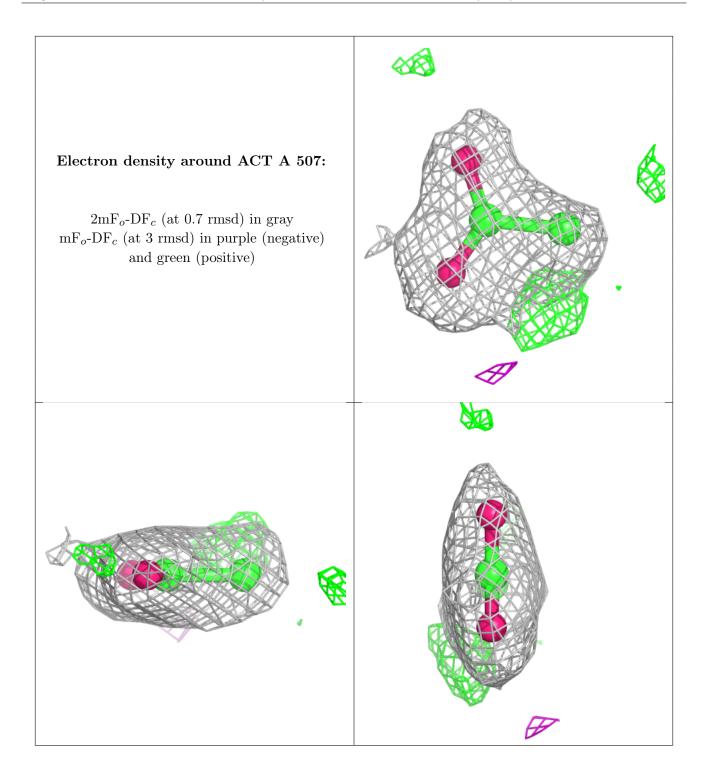
 $2 {
m mF}_o {
m -DF}_c$ (at 0.7 rmsd) in gray ${
m mF}_o {
m -DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)







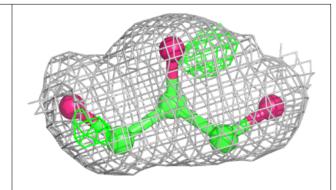


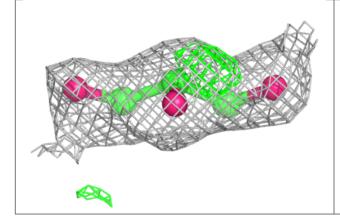


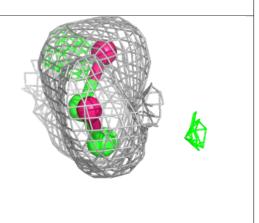


Electron density around GOL A 505:

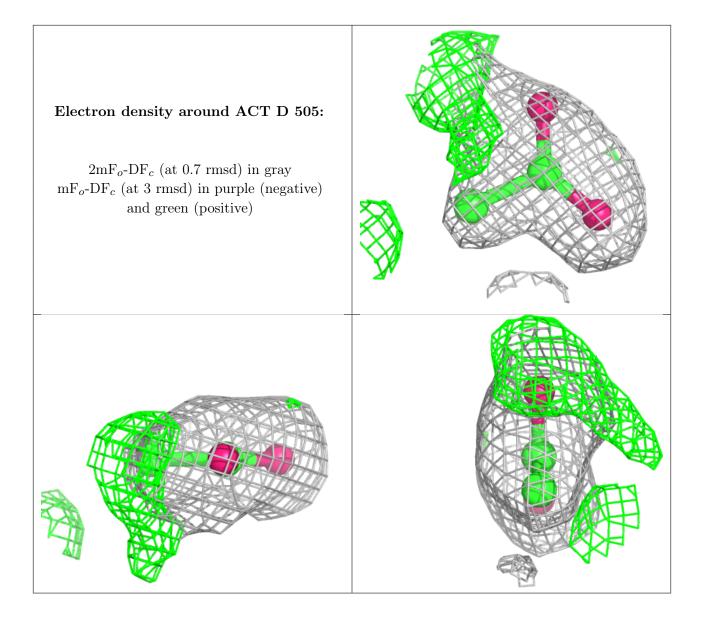
 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)



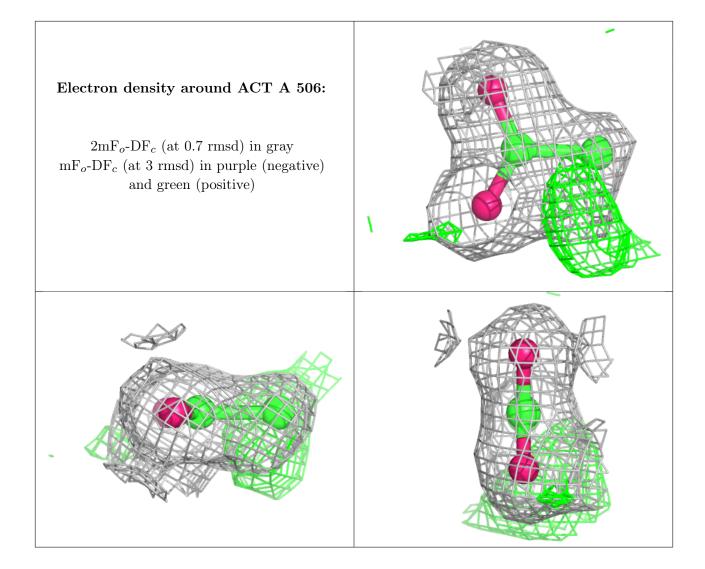








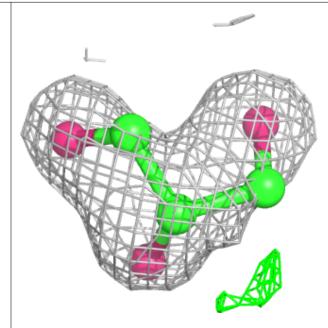


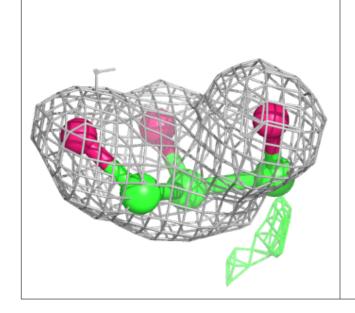


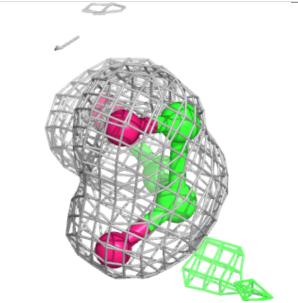


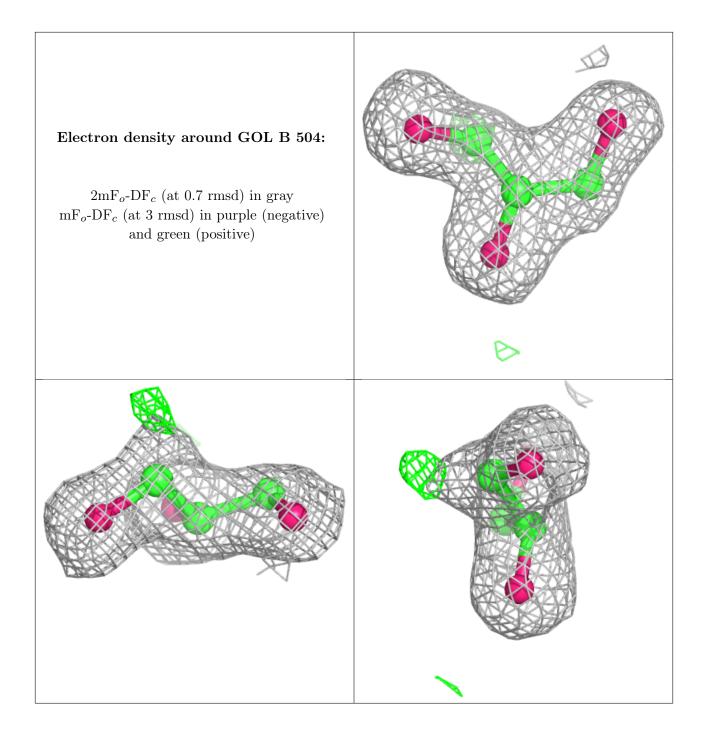
Electron density around GOL B 506:

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

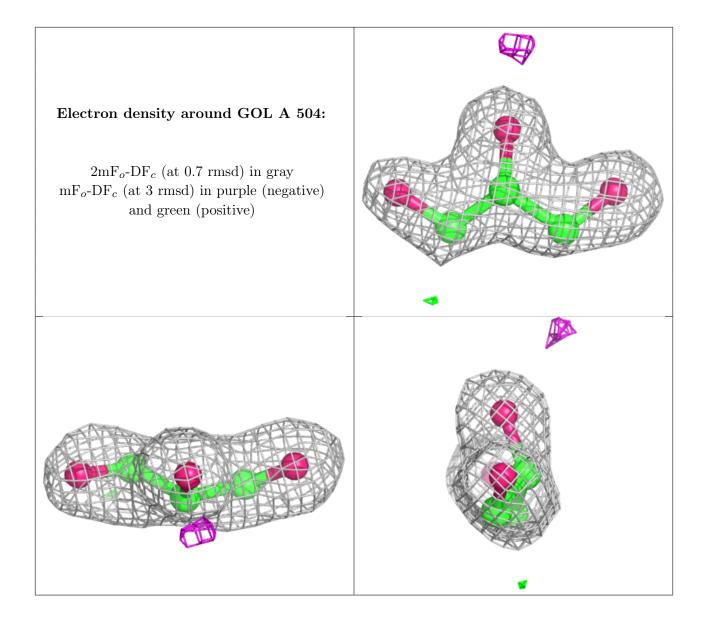








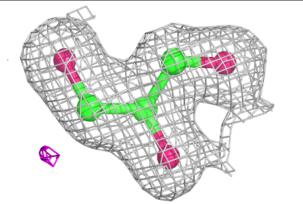


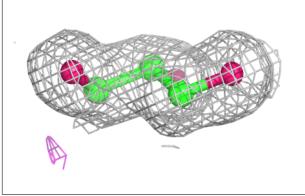


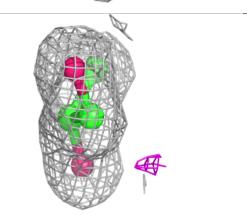


Electron density around GOL D 504:

 $2 {\rm mF}_o\text{-}{\rm DF}_c$ (at 0.7 rmsd) in gray ${\rm mF}_o\text{-}{\rm DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

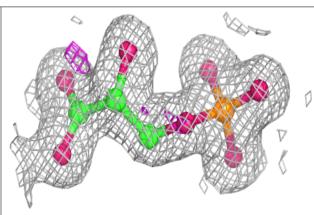


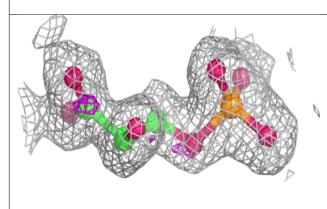


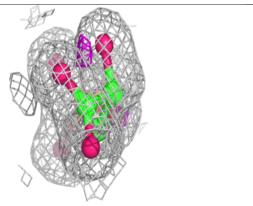


Electron density around 3PG B 502:

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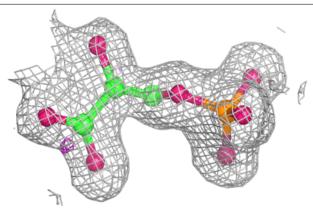


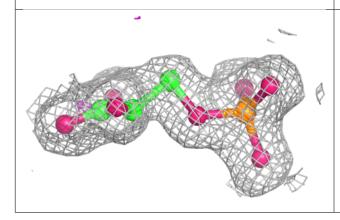


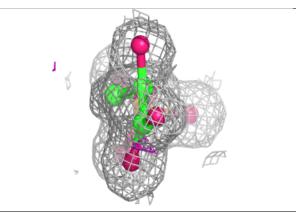


Electron density around 3PG B 503:

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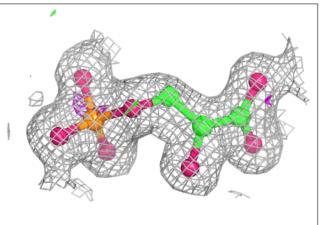


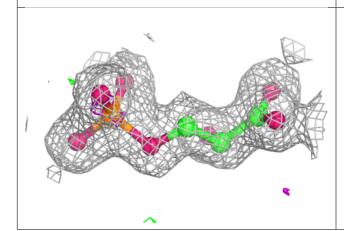


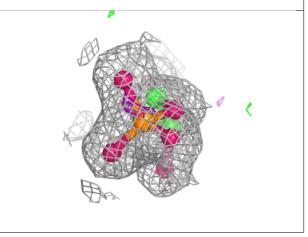


Electron density around 3PG C 502:

 $2 \text{mF}_o\text{-DF}_c$ (at 0.7 rmsd) in gray $\text{mF}_o\text{-DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)





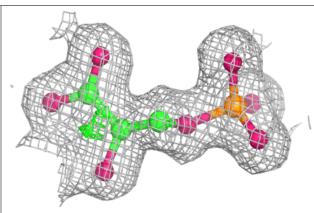


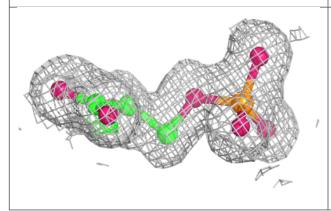


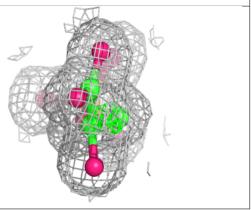
Electron density around 3PG C 503: 2mF_o-DF_c (at 0.7 rmsd) in gray mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

Electron density around 3PG D 503:

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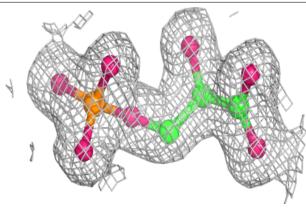


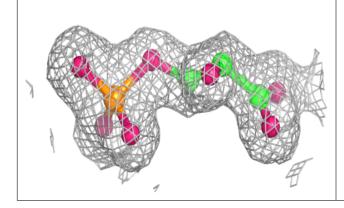


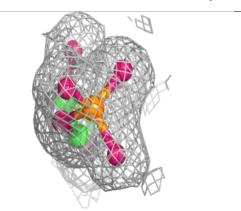


Electron density around 3PG A 502:

 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

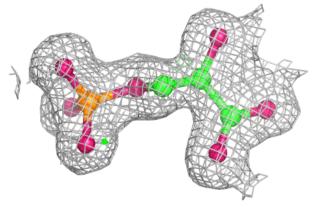


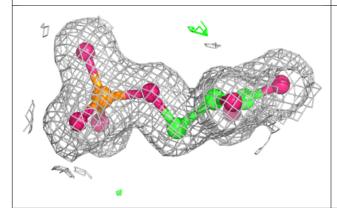


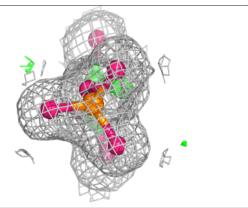


Electron density around 3PG A 503:

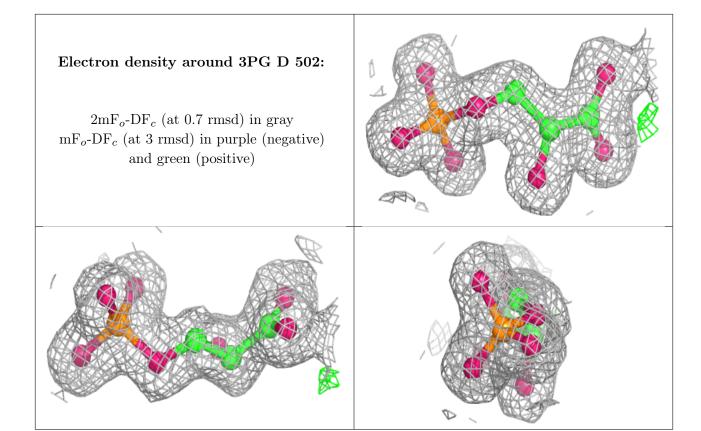
 $2 \text{mF}_o\text{-DF}_c$ (at 0.7 rmsd) in gray $\text{mF}_o\text{-DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)











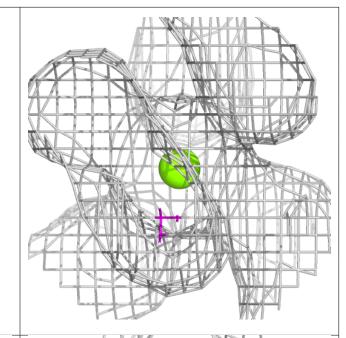


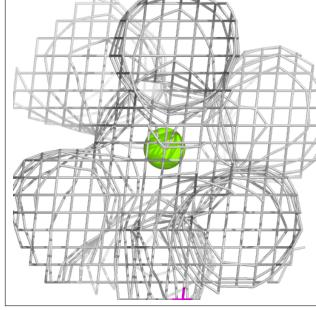
Electron density around MG A 501: $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_{o}\text{-}\mathrm{DF}_{c}$ (at 3 rmsd) in purple (negative) and green (positive)

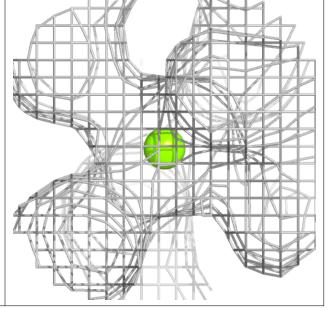


Electron density around MG B 501:

 $2 {
m mF}_o {
m -DF}_c$ (at 0.7 rmsd) in gray ${
m mF}_o {
m -DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

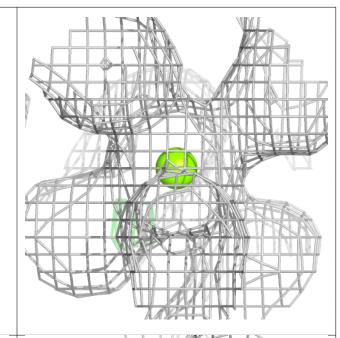


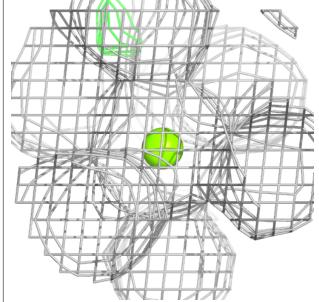


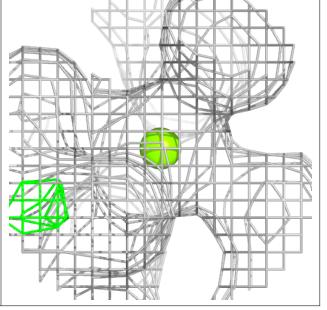


Electron density around MG D 501:

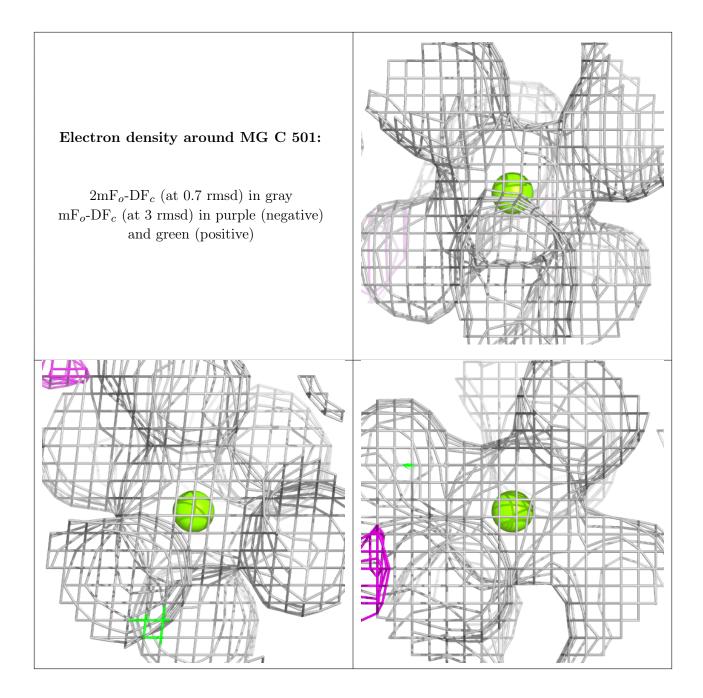
 $2 {
m mF}_o {
m -DF}_c$ (at 0.7 rmsd) in gray ${
m mF}_o {
m -DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)











6.5 Other polymers (i)

There are no such residues in this entry.

