Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2023 – 02:07 AM EDT

PDB ID	:	7LON
Title	:	Ornithine Aminotransferase (OAT) cocrystallized with its inactivator - (1S,3 S)-3-amino-4-(difluoromethylene)cyclohexene-1-carboxylic acid
Authors	:	Butrin, A.; Zhu, W.; Liu, D.; Silverman, R.
Deposited on	:	2021-02-10
Resolution	:	1.95 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:

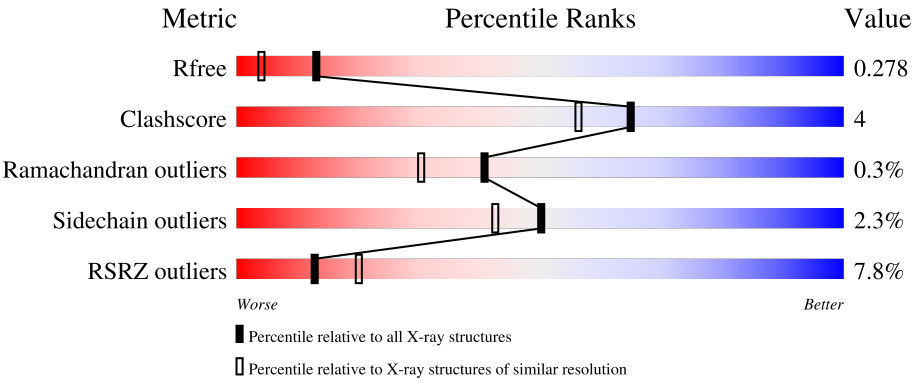
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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	404	12% 87% 12%
1	B	404	2% 87% 12%
1	C	404	9% 87% 12%

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	7QP	B	502	X	-	-	-
3	7QP	C	502	X	-	-	-

2 Entry composition

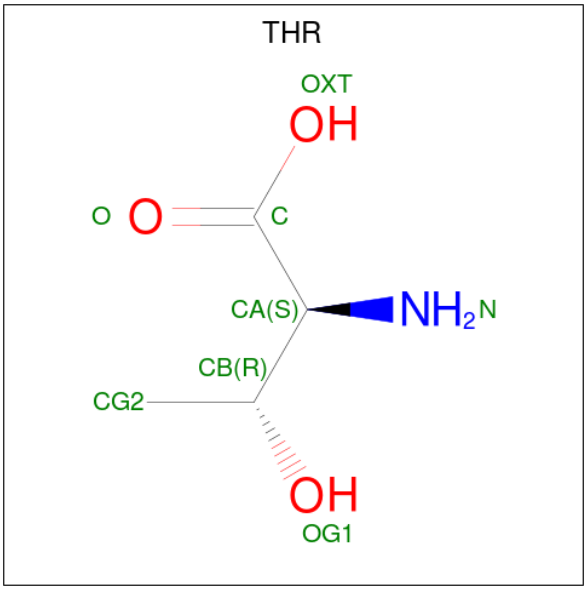
There are 4 unique types of molecules in this entry. The entry contains 10109 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Ornithine aminotransferase, mitochondrial.

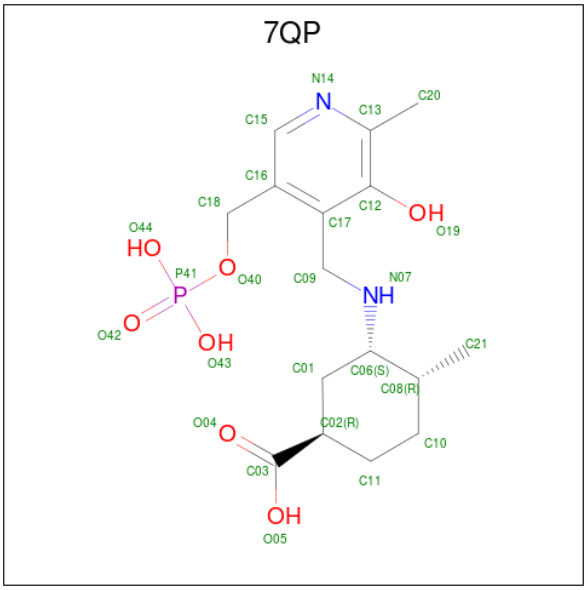
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	401	Total	C	N	O	S	0	1	0
			3148	2023	532	581	12			
1	A	401	Total	C	N	O	S	0	0	0
			3134	2015	526	581	12			
1	C	401	Total	C	N	O	S	0	2	0
			3154	2027	532	583	12			

- Molecule 2 is THREONINE (three-letter code: THR) (formula: $C_4H_9NO_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			7	4	1	2		
2	A	1	Total	C	N	O	0	0
			7	4	1	2		
2	C	1	Total	C	N	O	0	0
			7	4	1	2		

- Molecule 3 is (1R,3S,4R)-3-[({3-hydroxy-2-methyl-5-[(phosphonooxy)methyl]pyridin-4-yl}methyl)amino]-4-methylcyclohexane-1-carboxylic acid (three-letter code: 7QP) (formula: $C_{16}H_{25}N_2O_7P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	0	0
			26	16	2	7	1		
3	A	1	Total	C	N	O	P	0	0
			26	16	2	7	1		
3	C	1	Total	C	N	O	P	0	0
			26	16	2	7	1		

- Molecule 4 is water.

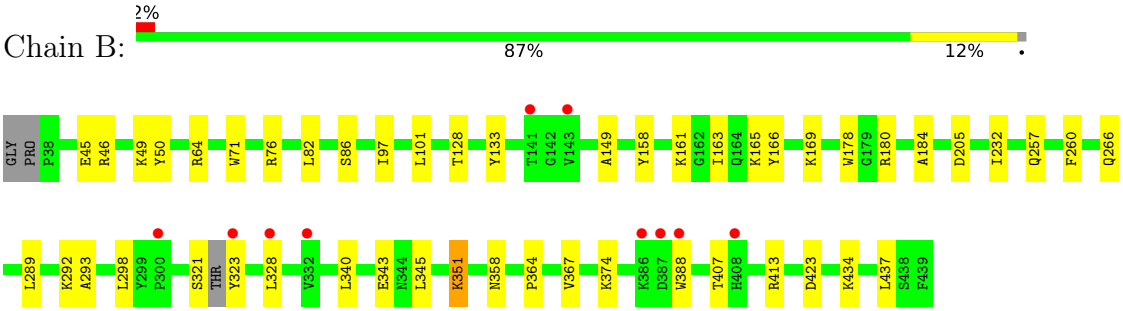
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	189	Total	O	0	0
			189	189		
4	A	190	Total	O	0	0
			190	190		
4	C	195	Total	O	0	0
			195	195		

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.

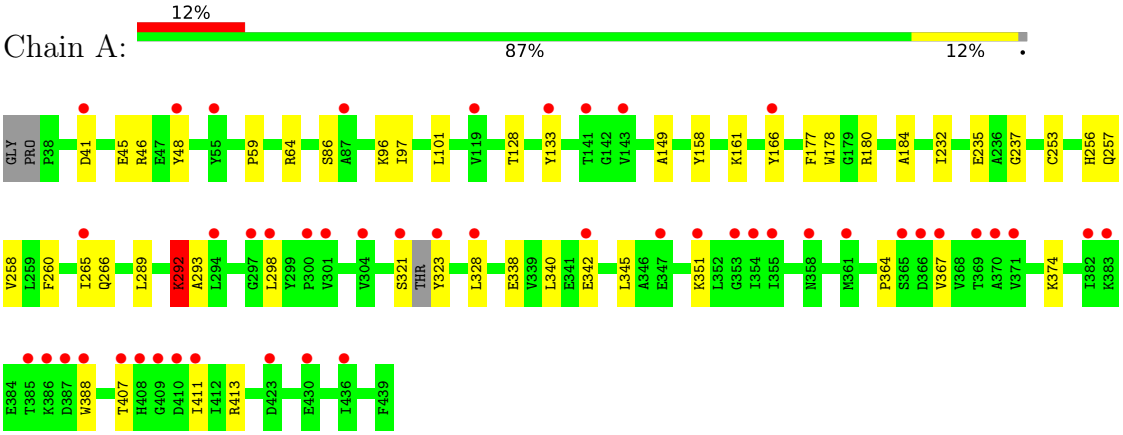
• Molecule 1: Ornithine aminotransferase, mitochondrial

Chain B:



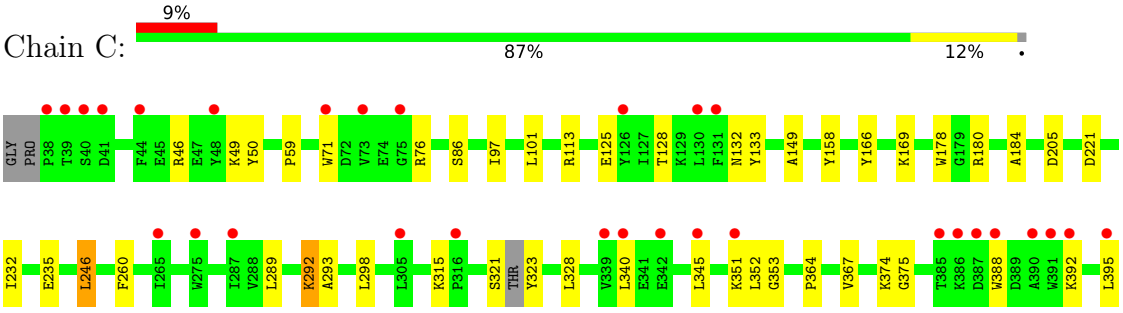
• Molecule 1: Ornithine aminotransferase, mitochondrial

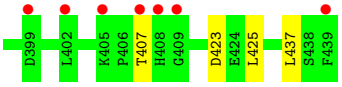
Chain A:



• Molecule 1: Ornithine aminotransferase, mitochondrial

Chain C:




D399
L402
K405
P406
T407
H408
G409
D423
E424
L425
L437
S438
F439

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 1 2	Depositor
Cell constants a, b, c, α, β, γ	192.02Å 192.02Å 57.06Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.05 – 1.95 49.05 – 1.95	Depositor EDS
% Data completeness (in resolution range)	94.4 (49.05-1.95) 94.9 (49.05-1.95)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.53 (at 1.95Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.243 , 0.278 0.246 , 0.278	Depositor DCC
R_{free} test set	4099 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å^2)	32.0	Xtriage
Anisotropy	0.169	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 53.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	10109	wwPDB-VP
Average B, all atoms (Å^2)	40.0	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 80.90 % 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 4.0202e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 7QP

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	0.49	0/3206	0.62	0/4351
1	B	0.57	0/3223	0.68	1/4372 (0.0%)
1	C	0.51	0/3229	0.64	1/4380 (0.0%)
All	All	0.52	0/9658	0.65	2/13103 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	221	ASP	CB-CG-OD1	5.25	123.03	118.30
1	B	165	LYS	C-N-CA	5.17	134.62	121.70

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	3134	0	3130	26	2
1	B	3148	0	3154	25	3
1	C	3154	0	3160	28	3
2	A	7	0	5	0	2
2	B	7	0	5	0	3
2	C	7	0	5	0	3

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	26	0	0	2	0
3	B	26	0	0	1	0
3	C	26	0	0	1	0
4	A	190	0	0	3	1
4	B	189	0	0	4	0
4	C	195	0	0	7	2
All	All	10109	0	9459	77	11

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

All (77) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:128:THR:OG1	4:C:601:HOH:O	1.75	0.99
1:C:113:ARG:NH1	4:C:602:HOH:O	1.96	0.97
1:C:125:GLU:HA	4:C:601:HOH:O	1.84	0.78
1:C:46[A]:ARG:NH1	4:C:603:HOH:O	2.17	0.77
1:A:161:LYS:HE3	1:A:257:GLN:HG3	1.71	0.72
1:A:48:TYR:OH	4:A:601:HOH:O	2.09	0.66
1:C:340:LEU:HD23	1:C:345:LEU:HD12	1.78	0.66
1:C:351:LYS:HG2	1:C:352:LEU:HD23	1.77	0.65
1:A:340:LEU:HD23	1:A:345:LEU:HD12	1.77	0.65
1:B:358:ASN:OD1	4:B:601:HOH:O	2.13	0.64
1:C:86:SER:O	1:C:293:ALA:HB2	2.01	0.60
1:C:158:TYR:OH	1:C:166:TYR:HA	2.02	0.60
1:B:364:PRO:HG2	1:B:367:VAL:HG22	1.84	0.59
1:C:97:ILE:HG22	1:C:298:LEU:HD22	1.84	0.59
1:A:97:ILE:HG22	1:A:298:LEU:HD22	1.83	0.59
1:B:97:ILE:HG22	1:B:298:LEU:HD22	1.83	0.58
1:B:257:GLN:NE2	4:B:604:HOH:O	2.28	0.57
1:A:237:GLY:HA3	1:A:411:ILE:HD13	1.85	0.57
1:A:256:HIS:O	1:A:257:GLN:HG2	2.03	0.57
1:A:178:TRP:CZ2	1:A:184:ALA:HA	2.40	0.56
1:B:158:TYR:OH	1:B:166:TYR:HA	2.06	0.55
1:A:41:ASP:O	1:A:45:GLU:HG2	2.05	0.55
1:C:178:TRP:CZ2	1:C:184:ALA:HA	2.41	0.55
1:A:149:ALA:HB2	1:A:289:LEU:HD21	1.89	0.55
1:A:232:ILE:HD11	1:A:374:LYS:HD2	1.88	0.55
1:A:158:TYR:OH	1:A:166:TYR:HA	2.07	0.55
1:C:149:ALA:HB2	1:C:289:LEU:HD21	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:437:LEU:HD12	1:A:64:ARG:HD2	1.90	0.54
1:B:86:SER:O	1:B:293:ALA:HB2	2.08	0.54
1:C:101:LEU:HD12	1:C:328:LEU:HD11	1.90	0.54
1:C:128:THR:HB	1:C:133:TYR:O	2.08	0.53
1:A:86:SER:O	1:A:293:ALA:HB2	2.09	0.53
1:C:246:LEU:HD22	4:C:696:HOH:O	2.09	0.52
1:C:392:LYS:HD3	1:C:395:LEU:HD12	1.90	0.52
1:B:343:GLU:OE2	4:B:603:HOH:O	2.20	0.50
1:C:49[B]:LYS:HD2	1:C:50:TYR:CZ	2.46	0.49
1:B:178:TRP:CZ2	1:B:184:ALA:HA	2.46	0.49
1:A:101:LEU:HD12	1:A:328:LEU:HD11	1.95	0.49
1:B:149:ALA:HB2	1:B:289:LEU:HD21	1.94	0.48
1:B:49:LYS:HD2	1:B:50:TYR:CZ	2.48	0.48
1:C:423:ASP:OD1	1:C:423:ASP:N	2.47	0.48
1:B:169:LYS:HD3	1:B:205:ASP:OD2	2.13	0.48
1:A:178:TRP:HA	3:A:502:7QP:C15	2.44	0.47
1:C:364:PRO:HG2	1:C:367:VAL:HG22	1.96	0.47
1:A:364:PRO:HG2	1:A:367:VAL:HG22	1.96	0.47
1:C:232:ILE:HD11	1:C:374:LYS:HD2	1.95	0.47
1:A:338:GLU:O	1:A:342:GLU:HG2	2.14	0.47
1:B:46[B]:ARG:HG2	4:B:731:HOH:O	2.15	0.46
1:B:101:LEU:HD12	1:B:328:LEU:HD11	1.98	0.46
1:B:434:LYS:HB2	4:A:606:HOH:O	2.14	0.46
1:C:178:TRP:HA	3:C:502:7QP:C15	2.46	0.46
1:B:64:ARG:HD2	1:C:437:LEU:HD12	1.96	0.46
1:A:265:ILE:O	1:A:292:LYS:HG3	2.16	0.46
1:B:161:LYS:HD3	1:B:163:ILE:HD11	1.98	0.46
1:B:266:GLN:OE1	1:B:413:ARG:NH2	2.44	0.45
1:A:46:ARG:HD3	4:A:738:HOH:O	2.16	0.45
1:A:161:LYS:CE	1:A:257:GLN:HG3	2.44	0.45
1:A:253:CYS:HB3	1:A:258:VAL:O	2.18	0.44
1:C:292:LYS:HB3	1:C:293:ALA:H	1.45	0.44
1:C:353:GLY:HA3	1:C:375:GLY:O	2.16	0.44
1:A:266:GLN:OE1	1:A:413:ARG:NH2	2.44	0.44
1:C:132:ASN:ND2	4:C:617:HOH:O	2.49	0.44
1:B:128:THR:HB	1:B:133:TYR:O	2.18	0.43
1:C:169:LYS:HD3	1:C:205:ASP:OD2	2.18	0.43
1:B:340:LEU:HD23	1:B:345:LEU:HD12	2.01	0.42
1:B:351:LYS:N	1:B:351:LYS:HD2	2.33	0.42
1:B:423:ASP:OD1	1:B:423:ASP:N	2.49	0.42
1:B:232:ILE:HD11	1:B:374:LYS:HD2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:71:TRP:HA	1:C:76:ARG:O	2.19	0.42
1:C:352:LEU:HB3	1:C:425:LEU:HD22	2.02	0.42
1:A:128:THR:HB	1:A:133:TYR:O	2.20	0.41
1:A:177:PHE:CE2	3:A:502:7QP:C01	3.03	0.41
1:A:256:HIS:C	1:A:257:GLN:HG2	2.41	0.41
1:A:96:LYS:HE3	1:A:342:GLU:OE2	2.21	0.41
1:B:71:TRP:HA	1:B:76:ARG:O	2.21	0.41
1:B:178:TRP:HA	3:B:502:7QP:C15	2.51	0.40
1:C:315:LYS:NZ	4:C:626:HOH:O	2.55	0.40

All (11) 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	Interatomic distance (Å)	Clash overlap (Å)
1:B:321:SER:C	2:B:501:THR:N[5_554]	1.43	0.77
1:B:323:TYR:N	2:B:501:THR:C[5_554]	1.43	0.77
1:A:321:SER:C	2:A:501:THR:N[4_554]	1.43	0.77
1:A:323:TYR:N	2:A:501:THR:C[4_554]	1.43	0.77
1:C:321:SER:C	2:C:501:THR:N[6_544]	1.43	0.77
1:C:323:TYR:N	2:C:501:THR:C[6_544]	1.43	0.77
1:B:321:SER:O	2:B:501:THR:N[5_554]	2.05	0.15
1:C:321:SER:O	2:C:501:THR:N[6_544]	2.06	0.14
4:A:779:HOH:O	4:A:782:HOH:O[4_554]	2.09	0.11
4:C:610:HOH:O	4:C:654:HOH:O[6_544]	2.17	0.03
4:C:760:HOH:O	4:C:762:HOH:O[1_554]	2.18	0.02

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	397/404 (98%)	379 (96%)	16 (4%)	2 (0%)	29 17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	398/404 (98%)	379 (95%)	18 (4%)	1 (0%)	41 30
1	C	399/404 (99%)	381 (96%)	17 (4%)	1 (0%)	41 30
All	All	1194/1212 (98%)	1139 (95%)	51 (4%)	4 (0%)	41 30

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	292	LYS
1	A	292	LYS
1	A	59	PRO
1	C	59	PRO

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	333/337 (99%)	326 (98%)	7 (2%)	53 46
1	B	335/337 (99%)	328 (98%)	7 (2%)	53 46
1	C	336/337 (100%)	329 (98%)	7 (2%)	53 46
All	All	1004/1011 (99%)	983 (98%)	21 (2%)	50 46

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	45	GLU
1	B	82	LEU
1	B	180	ARG
1	B	260	PHE
1	B	351	LYS
1	B	388	TRP
1	B	407	THR
1	A	180	ARG
1	A	235	GLU
1	A	260	PHE

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Mol	Chain	Res	Type
1	A	292	LYS
1	A	351	LYS
1	A	388	TRP
1	A	407	THR
1	C	180	ARG
1	C	235	GLU
1	C	246	LEU
1	C	260	PHE
1	C	292	LYS
1	C	388	TRP
1	C	407	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	7QP	B	502	1,2	27,27,27	2.11	7 (25%)	33,39,39	3.59	10 (30%)
3	7QP	C	502	1,2	27,27,27	2.10	4 (14%)	33,39,39	2.68	12 (36%)
3	7QP	A	502	1,2	27,27,27	1.96	3 (11%)	33,39,39	3.16	12 (36%)
2	THR	C	501	3	5,6,7	0.67	0	6,7,9	1.62	1 (16%)
2	THR	A	501	3	5,6,7	0.67	0	6,7,9	1.89	1 (16%)
2	THR	B	501	3	5,6,7	0.98	0	6,7,9	4.05	3 (50%)

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	7QP	B	502	1,2	2/2/5/6	4/15/28/28	0/2/2/2
3	7QP	C	502	1,2	1/1/5/6	6/15/28/28	0/2/2/2
3	7QP	A	502	1,2	-	6/15/28/28	0/2/2/2
2	THR	C	501	3	-	4/5/6/8	-
2	THR	A	501	3	-	3/5/6/8	-
2	THR	B	501	3	-	1/5/6/8	-

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	7QP	C06-N07	-7.47	1.32	1.47
3	C	502	7QP	C06-N07	-7.46	1.32	1.47
3	B	502	7QP	C06-N07	-6.47	1.34	1.47
3	B	502	7QP	C09-C17	5.03	1.58	1.51
3	C	502	7QP	C09-C17	4.97	1.58	1.51
3	A	502	7QP	C09-C17	4.19	1.57	1.51
3	C	502	7QP	C02-C03	3.06	1.56	1.51
3	B	502	7QP	C09-N07	2.90	1.55	1.46
3	B	502	7QP	P41-O40	2.33	1.67	1.60
3	A	502	7QP	P41-O40	2.26	1.67	1.60
3	C	502	7QP	P41-O40	2.17	1.67	1.60
3	B	502	7QP	C01-C06	2.16	1.56	1.53
3	B	502	7QP	O04-C03	2.13	1.28	1.22
3	B	502	7QP	C02-C03	2.07	1.55	1.51

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	502	7QP	C10-C11-C02	-11.56	91.80	111.18
3	A	502	7QP	C09-C17-C12	8.88	129.54	120.04
3	B	502	7QP	C01-C02-C03	8.80	129.34	110.99
3	C	502	7QP	C10-C11-C02	-8.50	96.93	111.18
2	B	501	THR	OG1-CB-CA	-8.29	91.47	109.06
3	B	502	7QP	C01-C06-N07	7.85	129.55	112.11
3	A	502	7QP	C01-C02-C11	6.70	118.90	109.86
3	A	502	7QP	C09-C17-C16	-6.60	112.37	119.71
3	A	502	7QP	C17-C09-N07	6.27	129.04	111.78
3	B	502	7QP	C17-C09-N07	6.17	128.76	111.78
3	C	502	7QP	C01-C02-C03	5.83	123.16	110.99
3	A	502	7QP	C11-C10-C08	-5.16	104.48	112.22
3	B	502	7QP	C21-C08-C06	4.99	120.67	113.13
3	B	502	7QP	C21-C08-C10	-4.25	103.25	111.04
3	B	502	7QP	C11-C02-C03	-4.22	103.10	111.32
2	B	501	THR	O-C-CA	-4.21	113.75	124.78
3	C	502	7QP	C21-C08-C06	4.06	119.28	113.13
3	C	502	7QP	C11-C02-C03	-4.04	103.47	111.32
3	A	502	7QP	C21-C08-C06	-4.03	107.03	113.13
3	A	502	7QP	C21-C08-C10	3.97	118.32	111.04
2	A	501	THR	CB-CA-C	-3.93	105.50	111.77
3	C	502	7QP	C01-C06-N07	3.92	120.81	112.11
3	C	502	7QP	C17-C09-N07	3.90	122.51	111.78
3	A	502	7QP	C11-C02-C03	3.88	118.86	111.32
3	C	502	7QP	C09-C17-C12	3.82	124.13	120.04
3	B	502	7QP	C11-C10-C08	-3.64	106.77	112.22
3	A	502	7QP	C01-C06-N07	3.47	119.82	112.11
3	A	502	7QP	C09-N07-C06	-3.40	107.74	114.90
3	C	502	7QP	O05-C03-C02	3.13	122.41	114.21
2	B	501	THR	CB-CA-C	-3.06	106.89	111.77
3	B	502	7QP	C01-C02-C11	3.06	113.99	109.86
2	C	501	THR	O-C-CA	-2.96	117.03	124.78
3	C	502	7QP	C01-C02-C11	-2.36	106.68	109.86
3	C	502	7QP	C16-C15-N14	-2.22	120.13	123.82
3	C	502	7QP	O04-C03-C02	-2.17	117.63	122.93
3	C	502	7QP	C15-C16-C17	2.12	119.61	118.12
3	B	502	7QP	O44-P41-O40	2.11	112.34	106.73
3	A	502	7QP	C15-C16-C17	2.02	119.55	118.12
3	A	502	7QP	C16-C15-N14	-2.01	120.47	123.82

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	502	7QP	C02
3	B	502	7QP	C06
3	C	502	7QP	C06

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	THR	O-C-CA-CB
2	C	501	THR	O-C-CA-CB
2	C	501	THR	N-CA-CB-OG1
2	C	501	THR	C-CA-CB-OG1
3	B	502	7QP	N07-C09-C17-C16
3	B	502	7QP	N07-C09-C17-C12
3	B	502	7QP	C08-C06-N07-C09
3	A	502	7QP	N07-C09-C17-C16
3	C	502	7QP	N07-C09-C17-C16
3	C	502	7QP	C08-C06-N07-C09
3	B	502	7QP	C01-C06-N07-C09
3	C	502	7QP	C01-C06-N07-C09
3	A	502	7QP	C08-C06-N07-C09
3	A	502	7QP	C01-C06-N07-C09
2	A	501	THR	C-CA-CB-OG1
3	A	502	7QP	C18-O40-P41-O42
3	A	502	7QP	N07-C09-C17-C12
3	C	502	7QP	N07-C09-C17-C12
2	A	501	THR	N-CA-CB-OG1
3	C	502	7QP	C01-C02-C03-O04
2	C	501	THR	C-CA-CB-CG2
3	C	502	7QP	C01-C02-C03-O05
3	A	502	7QP	C01-C02-C03-O05
2	B	501	THR	O-C-CA-CB

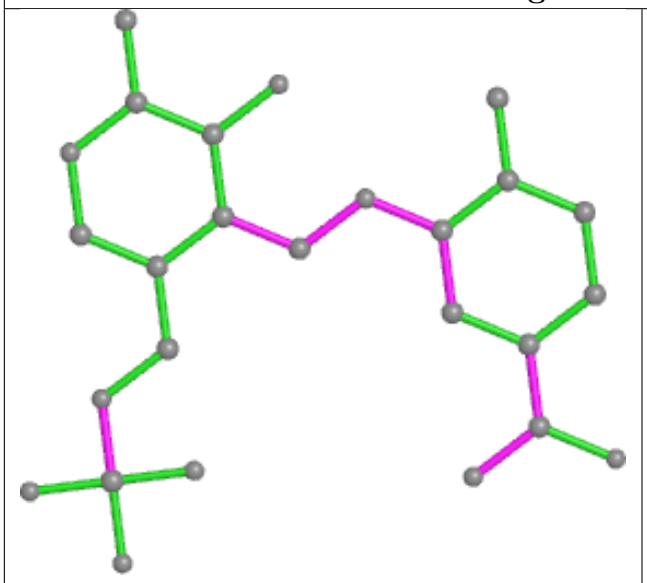
There are no ring outliers.

6 monomers are involved in 12 short contacts:

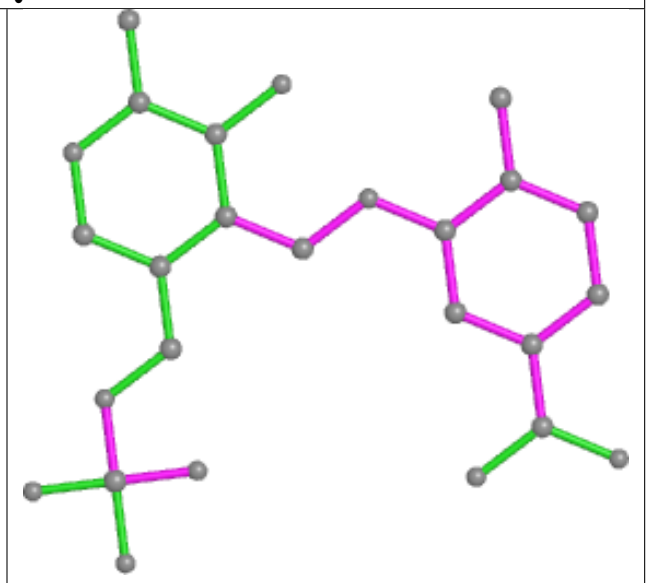
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	502	7QP	1	0
3	C	502	7QP	1	0
3	A	502	7QP	2	0
2	C	501	THR	0	3
2	A	501	THR	0	2
2	B	501	THR	0	3

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

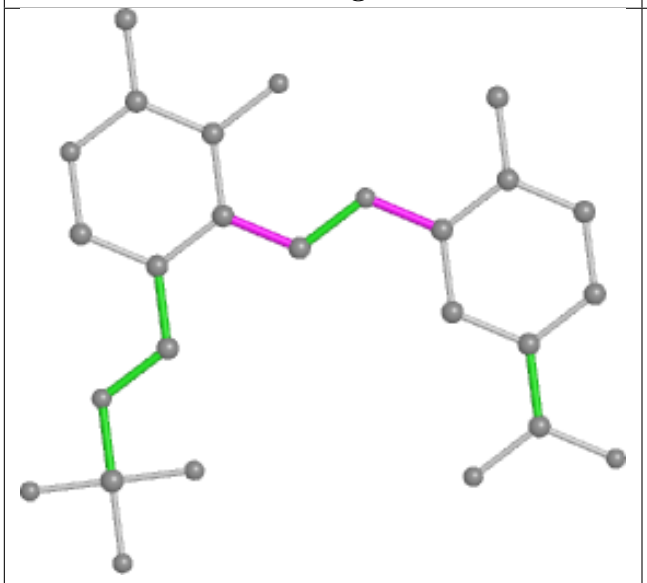
Ligand 7QP B 502



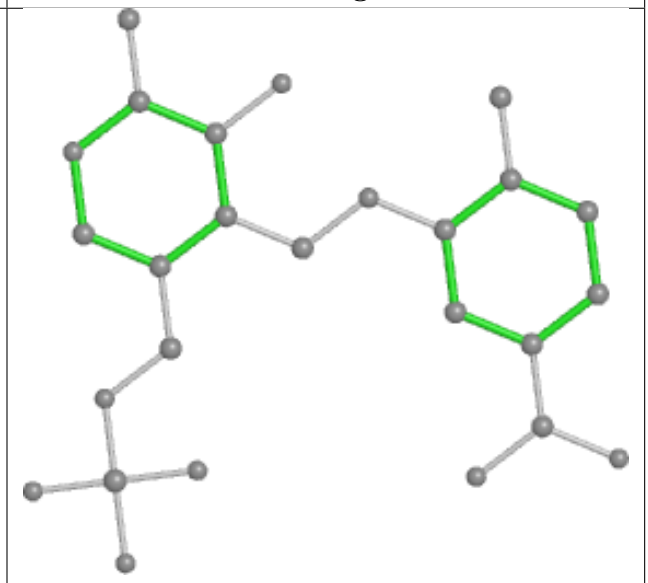
Bond lengths



Bond angles

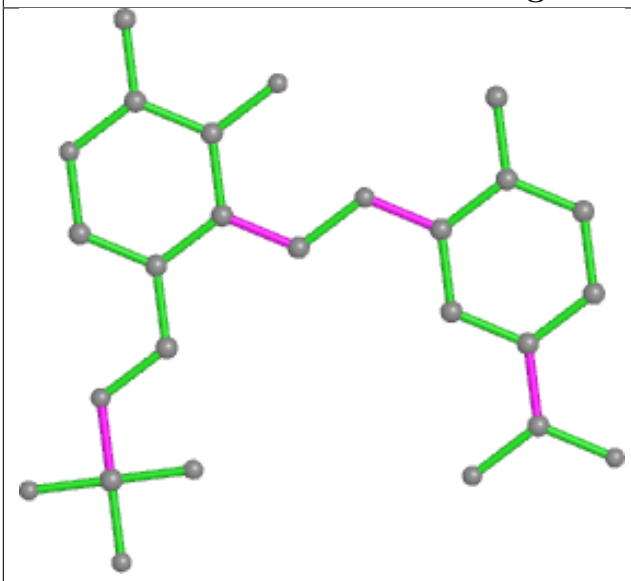


Torsions

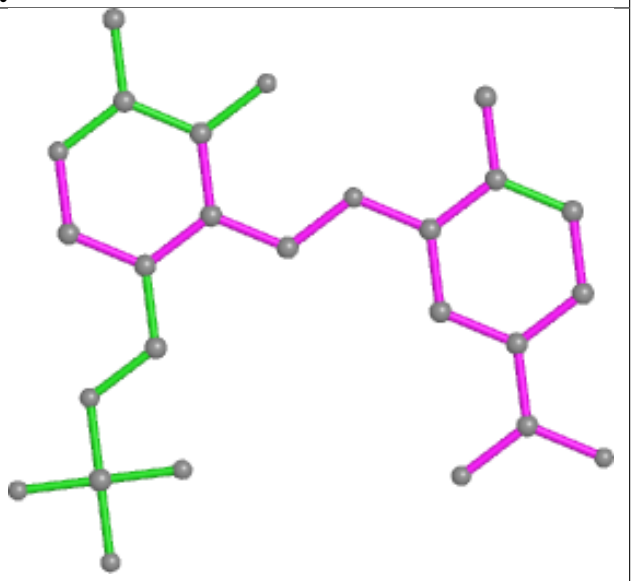


Rings

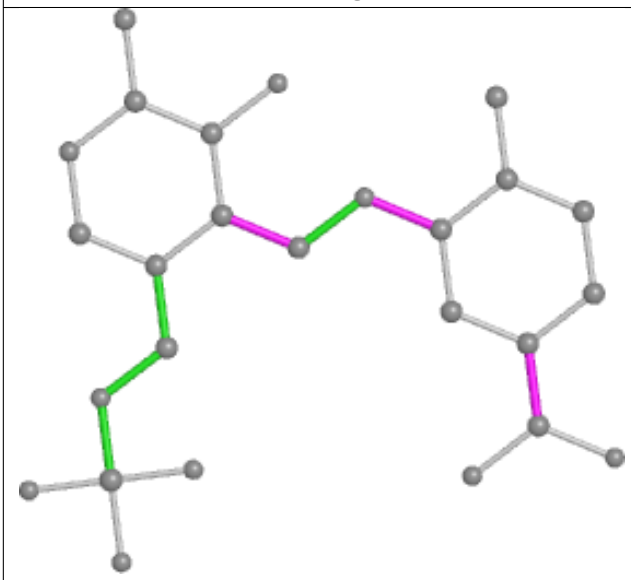
Ligand 7QP C 502



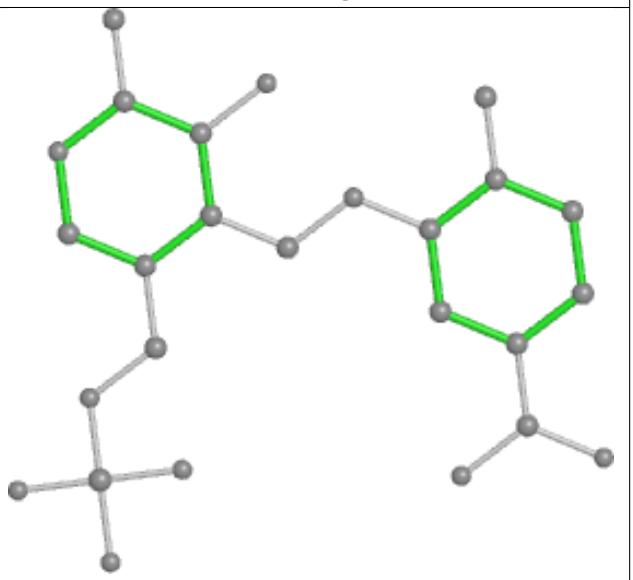
Bond lengths



Bond angles

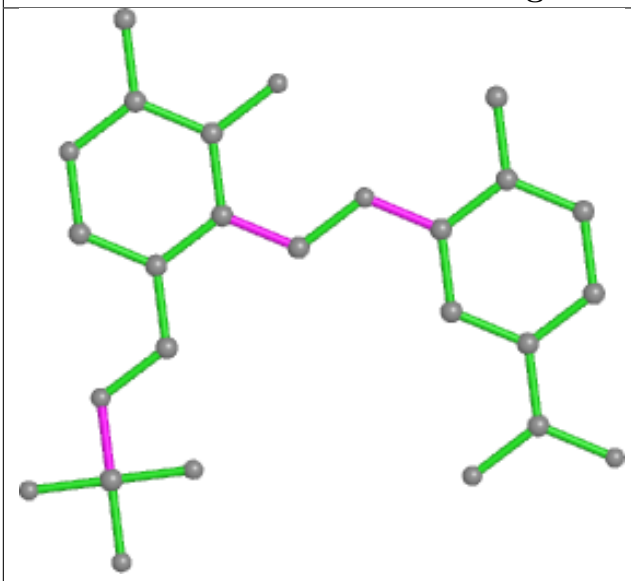


Torsions

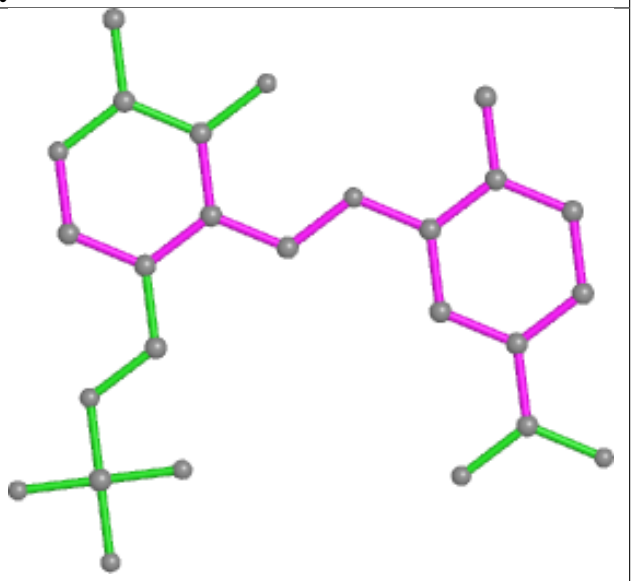


Rings

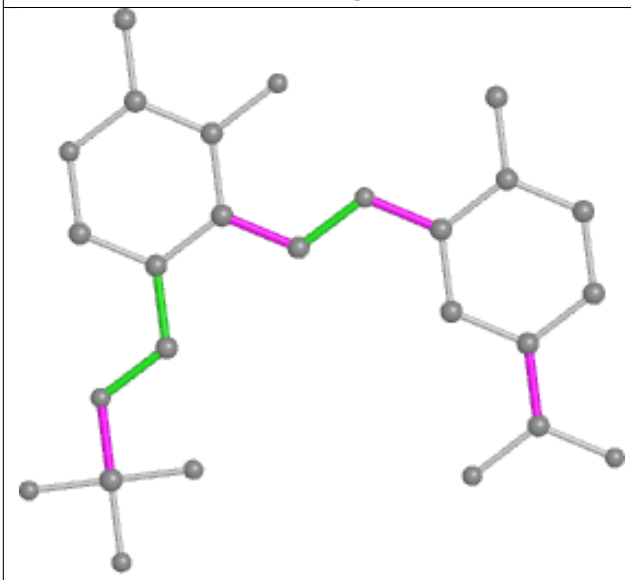
Ligand 7QP A 502



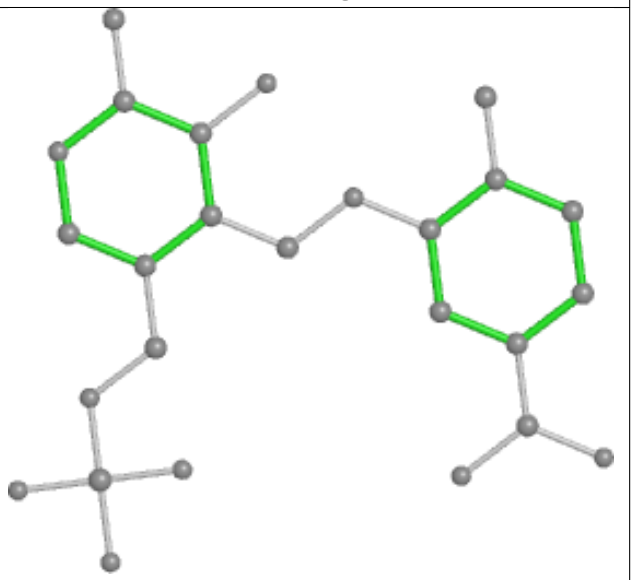
Bond lengths



Bond angles

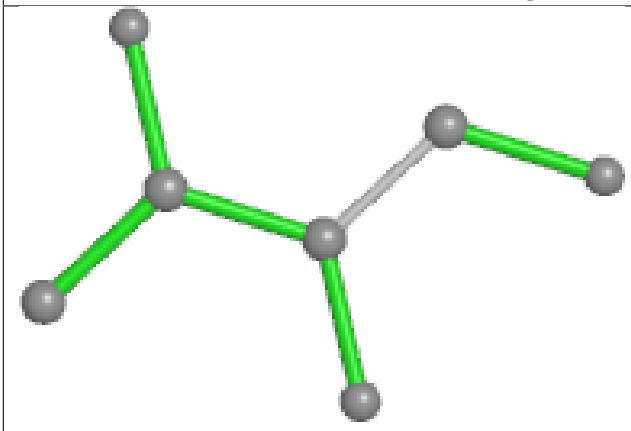


Torsions

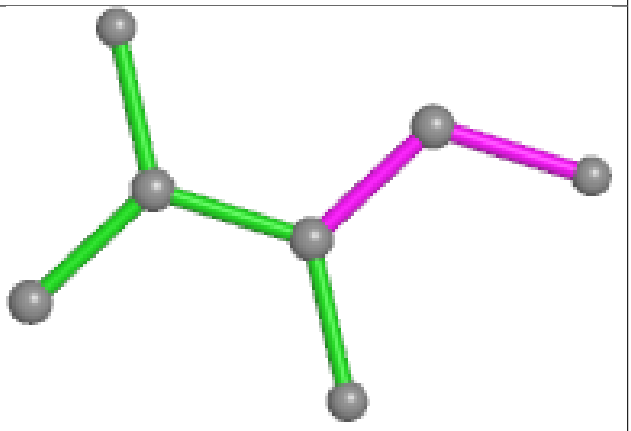


Rings

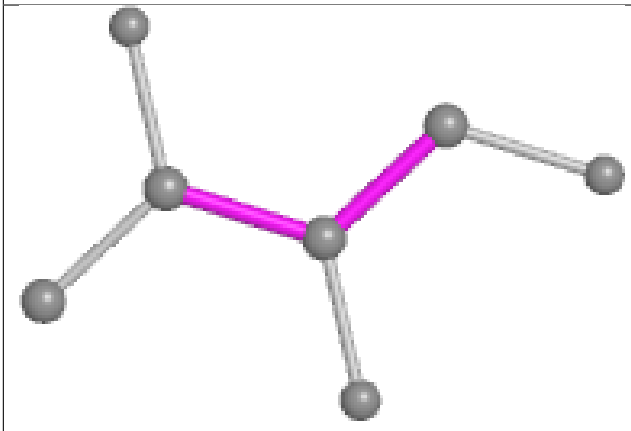
Ligand THR C 501



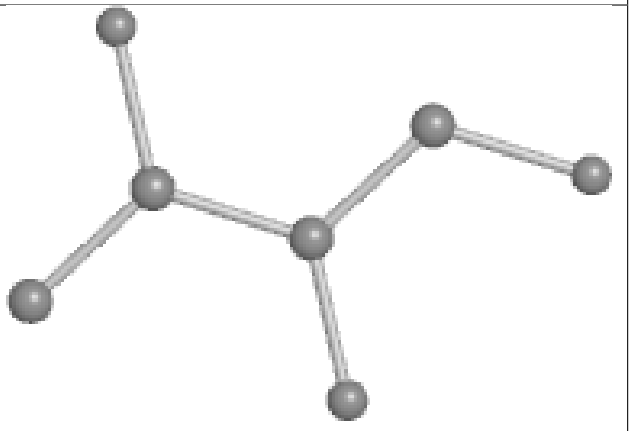
Bond lengths



Bond angles

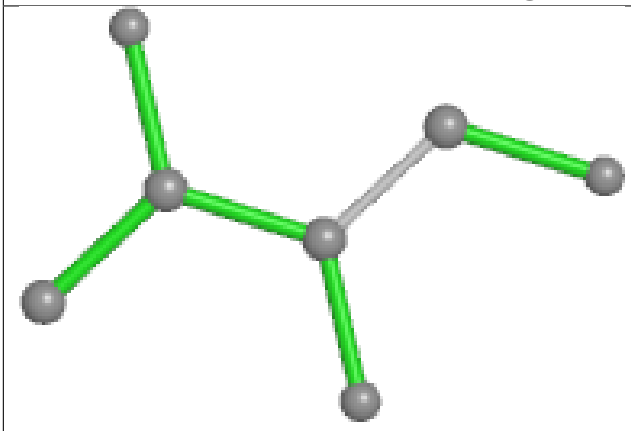


Torsions

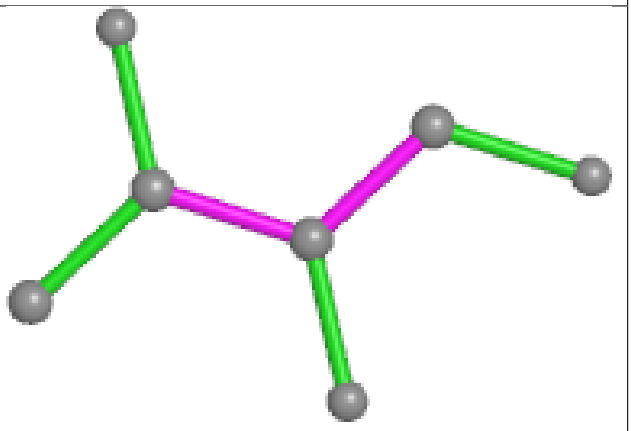


Rings

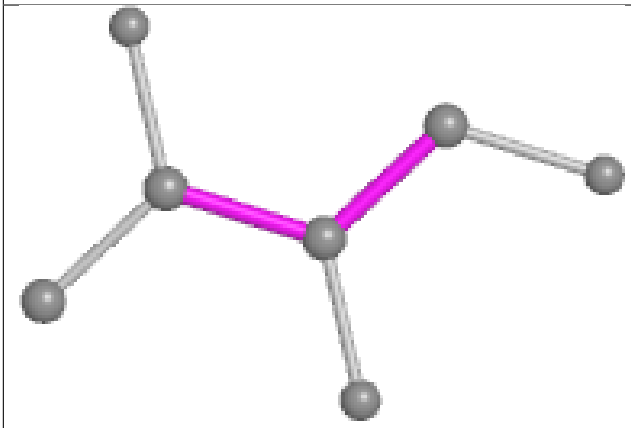
Ligand THR A 501



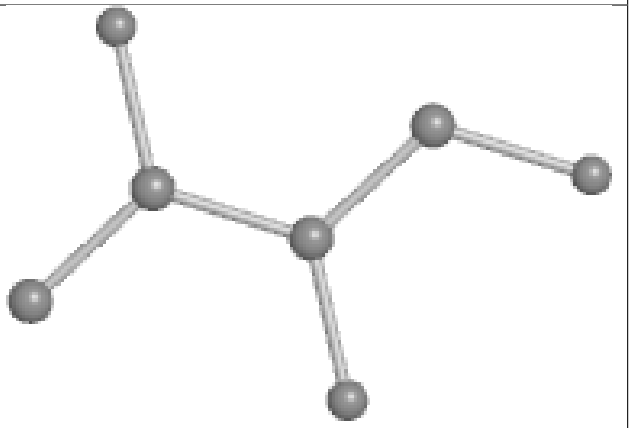
Bond lengths



Bond angles

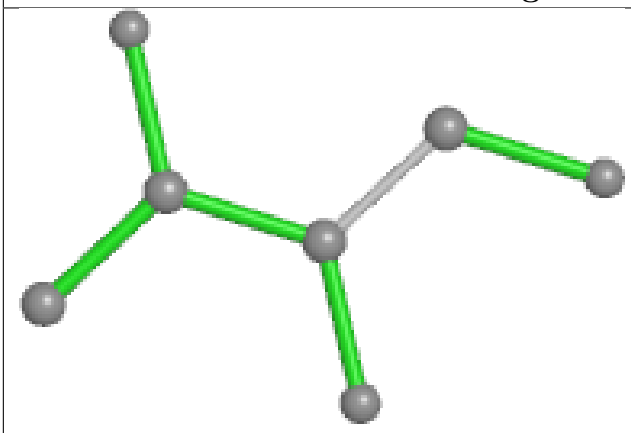


Torsions

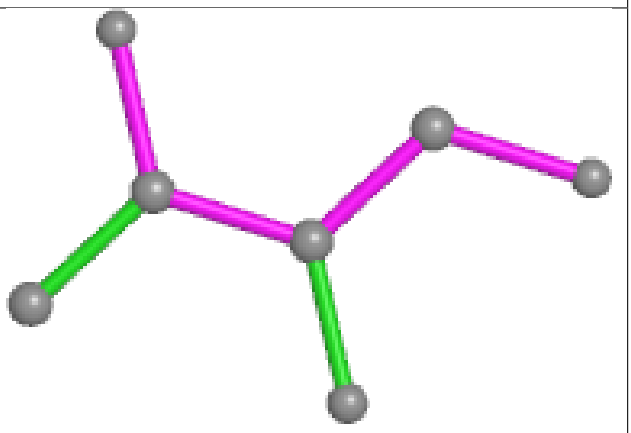


Rings

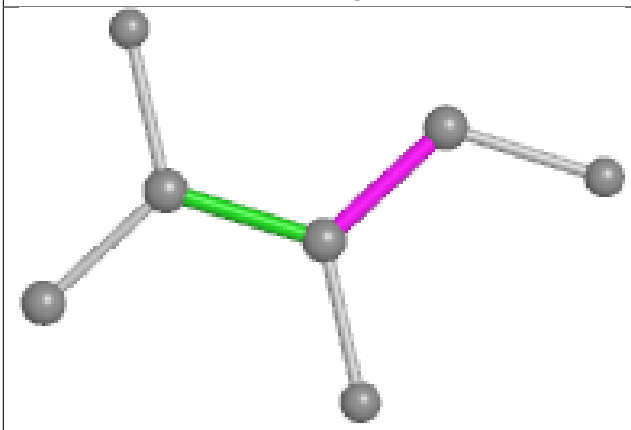
Ligand THR B 501



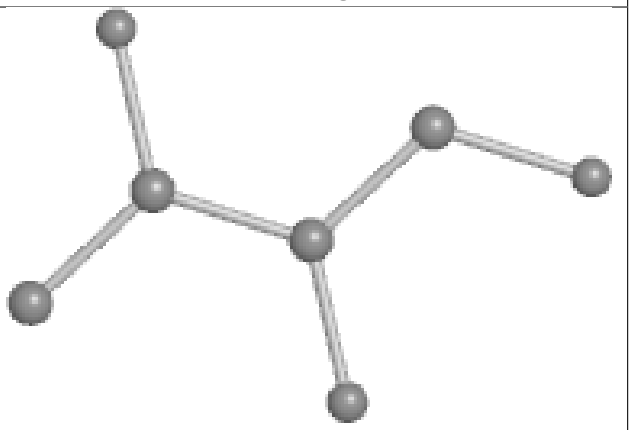
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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>2	OWAB(Å^2)	Q<0.9
1	A	401/404 (99%)	0.85	47 (11%) 4 7	29, 43, 67, 125	0
1	B	401/404 (99%)	0.09	10 (2%) 57 66	17, 28, 45, 97	0
1	C	401/404 (99%)	0.66	37 (9%) 9 14	27, 42, 61, 117	0
All	All	1203/1212 (99%)	0.53	94 (7%) 13 20	17, 38, 62, 125	0

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	387	ASP	9.1
1	A	387	ASP	6.8
1	A	367	VAL	6.8
1	B	387	ASP	6.5
1	A	388	TRP	6.3
1	C	386	LYS	5.4
1	B	386	LYS	5.3
1	A	41	ASP	5.2
1	C	41	ASP	5.1
1	A	354	ILE	5.0
1	A	365	SER	4.7
1	A	48	TYR	4.1
1	A	361	MET	3.9
1	C	40	SER	3.8
1	C	73	VAL	3.8
1	C	408	HIS	3.8
1	C	388	TRP	3.7
1	C	399	ASP	3.5
1	A	430	GLU	3.4
1	C	38	PRO	3.4
1	A	141	THR	3.3
1	A	436	ILE	3.3
1	A	358	ASN	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	388	TRP	3.3
1	A	366	ASP	3.3
1	C	48	TYR	3.2
1	A	408	HIS	3.2
1	A	328	LEU	3.1
1	C	345	LEU	3.1
1	A	342	GLU	3.1
1	A	301	VAL	3.1
1	C	385	THR	3.0
1	B	332	VAL	3.0
1	A	383	LYS	2.9
1	A	298	LEU	2.9
1	C	126	TYR	2.9
1	A	321	SER	2.9
1	C	75	GLY	2.9
1	C	439	PHE	2.9
1	B	328	LEU	2.8
1	A	371	VAL	2.8
1	A	300	PRO	2.8
1	A	423	ASP	2.8
1	C	340	LEU	2.8
1	A	294	LEU	2.8
1	A	411	ILE	2.8
1	C	44	PHE	2.7
1	B	323	TYR	2.7
1	C	130	LEU	2.7
1	C	392	LYS	2.7
1	A	409	GLY	2.7
1	A	385	THR	2.7
1	A	370	ALA	2.6
1	C	391	TRP	2.6
1	A	304	VAL	2.6
1	C	265	ILE	2.6
1	C	39	THR	2.5
1	C	287	ILE	2.5
1	A	55	TYR	2.5
1	A	347	GLU	2.5
1	B	300	PRO	2.5
1	C	275	TRP	2.5
1	B	143	VAL	2.5
1	A	323	TYR	2.5
1	A	353	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	402	LEU	2.5
1	A	386	LYS	2.5
1	C	316	PRO	2.4
1	A	119	VAL	2.4
1	A	351	LYS	2.4
1	A	410	ASP	2.4
1	C	71	TRP	2.4
1	A	297	GLY	2.4
1	C	342	GLU	2.4
1	A	369	THR	2.3
1	A	143	VAL	2.3
1	A	265	ILE	2.3
1	C	390	ALA	2.3
1	C	305	LEU	2.2
1	A	133	TYR	2.2
1	C	407	THR	2.2
1	C	351	LYS	2.2
1	C	409	GLY	2.2
1	C	131	PHE	2.2
1	C	339	VAL	2.2
1	C	405	LYS	2.1
1	A	87	ALA	2.1
1	C	395	LEU	2.1
1	A	355	ILE	2.1
1	A	407	THR	2.0
1	A	166	TYR	2.0
1	A	382	ILE	2.0
1	B	141	THR	2.0
1	B	408	HIS	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

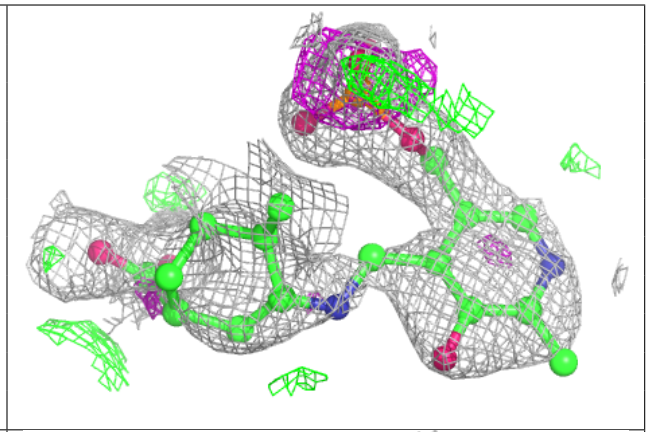
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

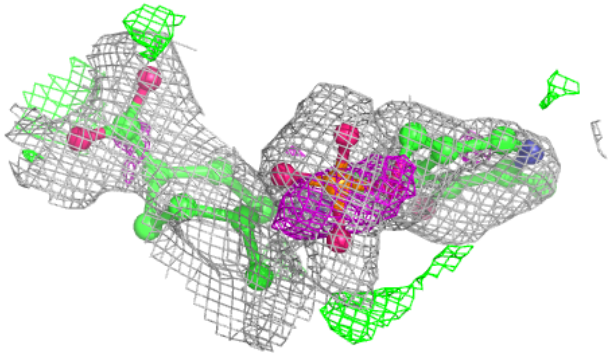
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	7QP	C	502	26/26	0.81	0.22	49,58,67,69	0
3	7QP	A	502	26/26	0.83	0.21	47,56,65,65	0
3	7QP	B	502	26/26	0.88	0.17	26,35,46,48	0
2	THR	C	501	7/8	0.90	0.20	46,49,54,58	0
2	THR	A	501	7/8	0.92	0.20	45,46,55,59	0
2	THR	B	501	7/8	0.96	0.17	22,25,31,32	0

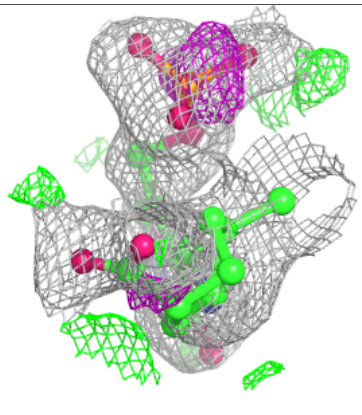
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 7QP C 502:

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

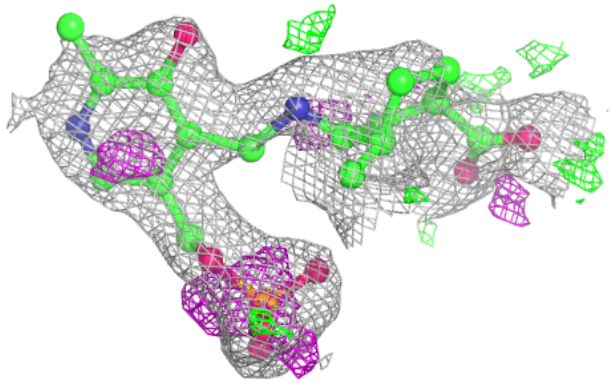


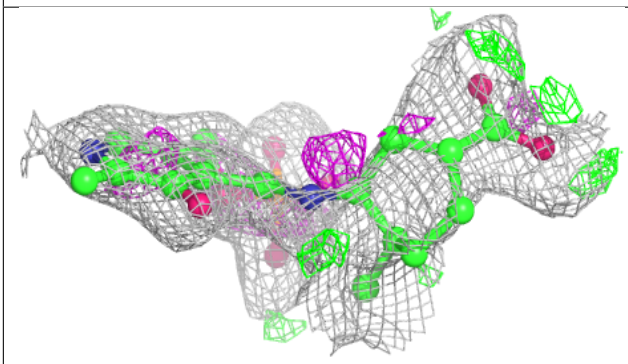


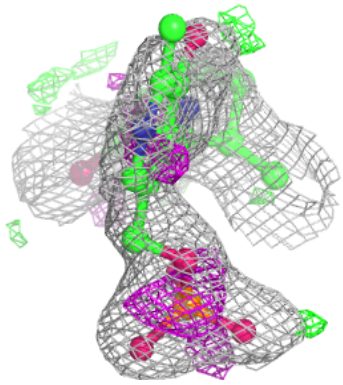


Electron density around 7QP A 502:

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

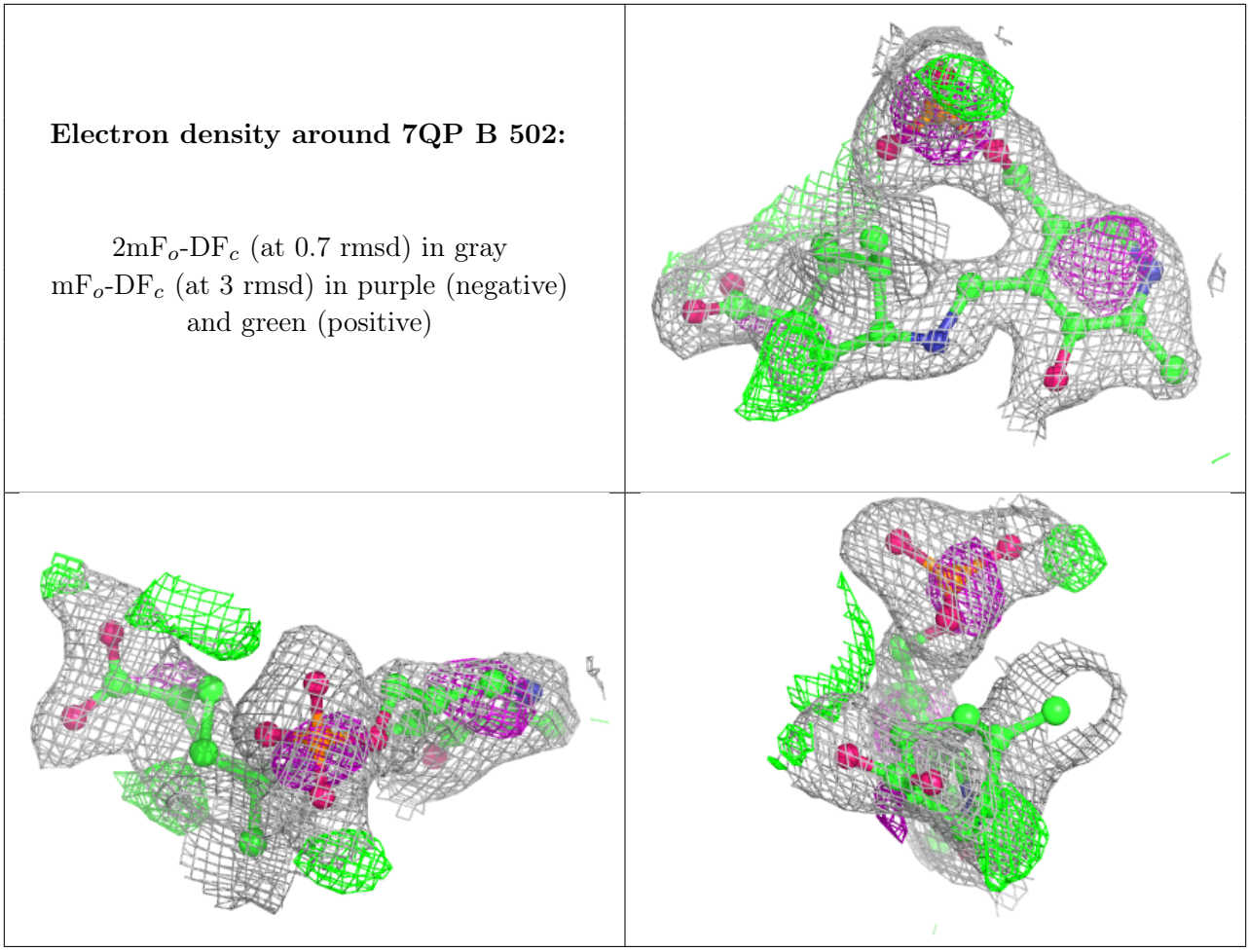






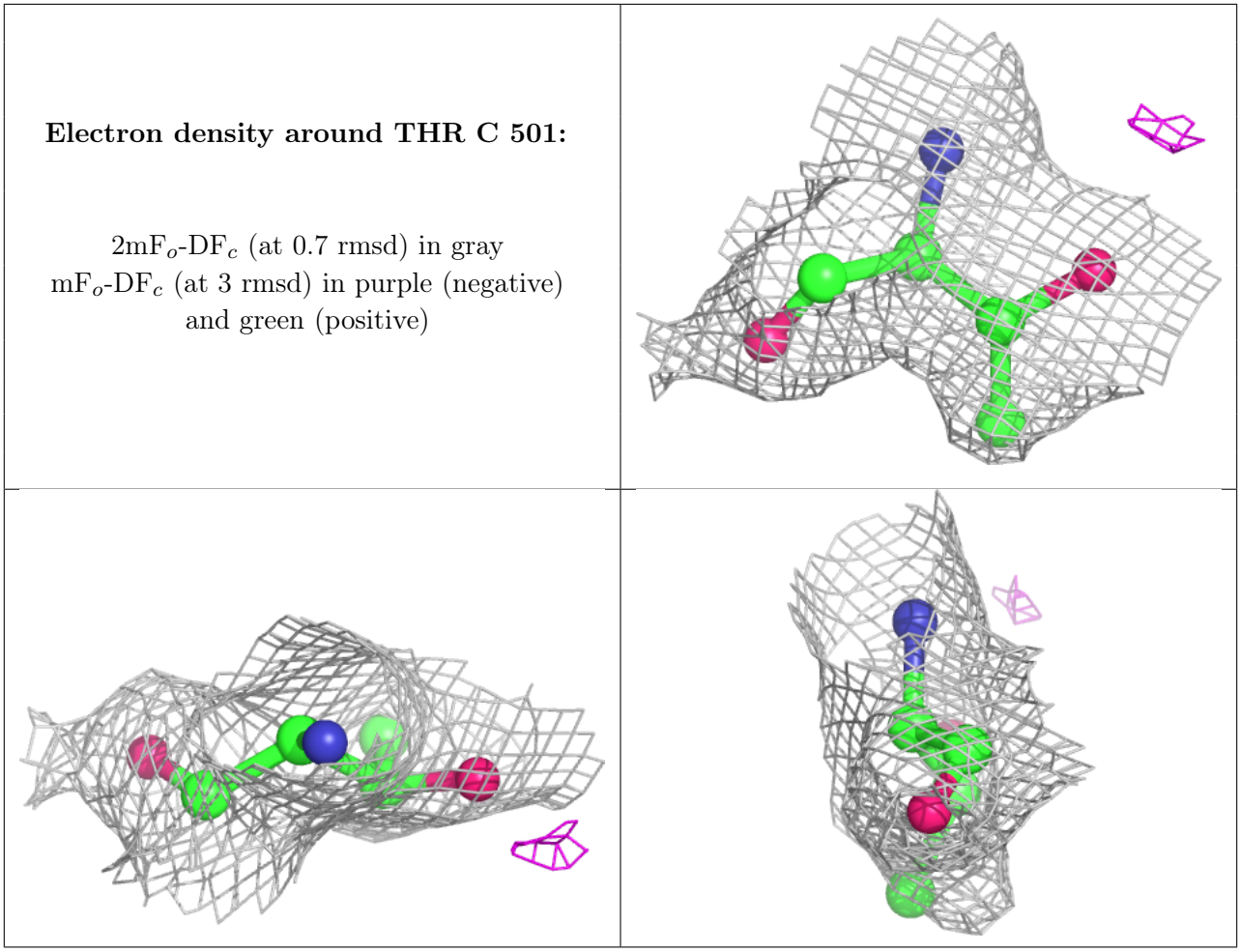
Electron density around 7QP B 502:

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



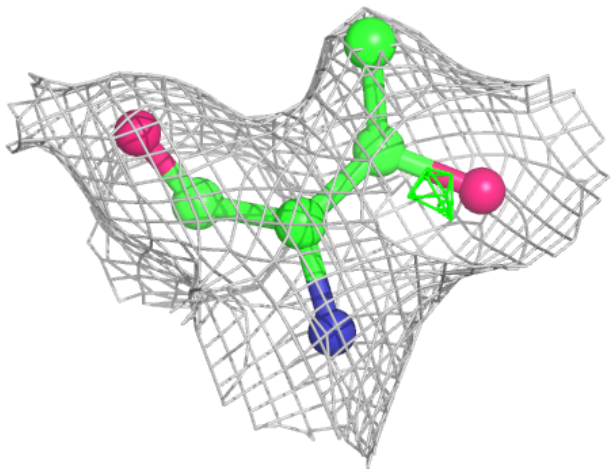
Electron density around THR C 501:

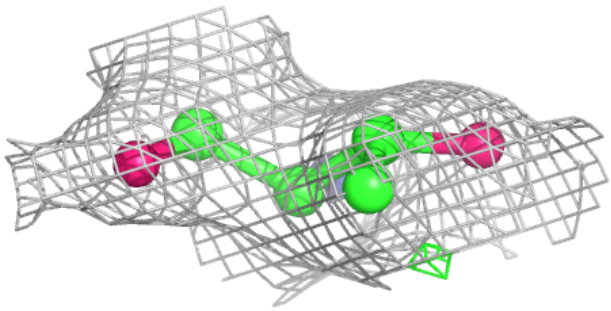
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

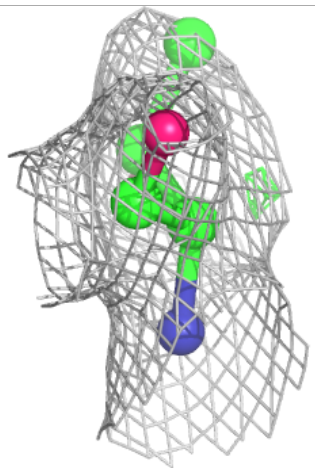


Electron density around THR A 501:

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

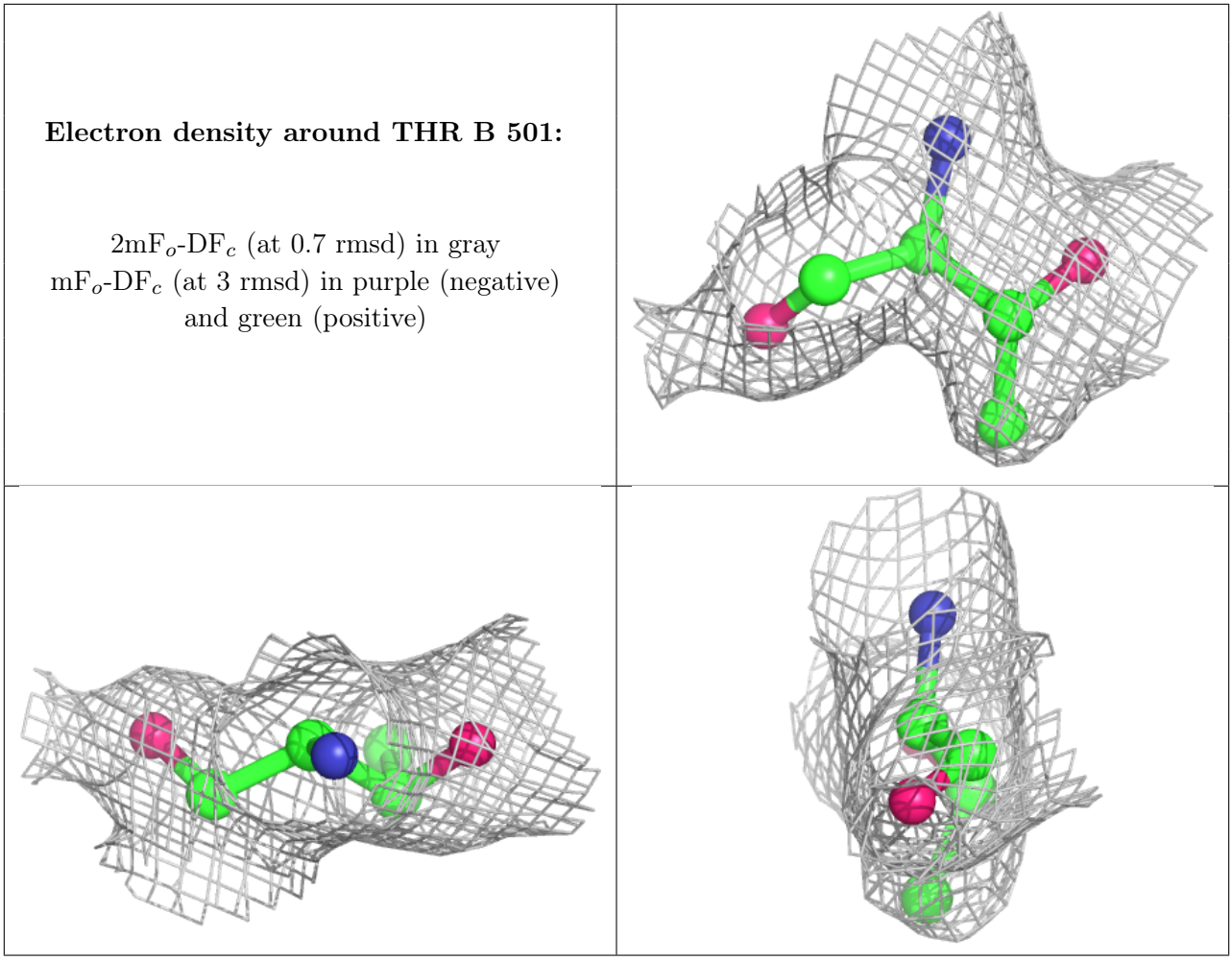






Electron density around THR B 501:

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



6.5 Other polymers (i)

There are no such residues in this entry.