Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 07:15 AM BST

PDB ID	:	6HXQ
Title	:	Structure of citryl-CoA synthetase from Hydrogenobacter thermophilus
Authors	:	Verstraete, K.; Verschueren, K.
Deposited on	:	2018-10-17
Resolution	:	2.91 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 following versions of software and data (see references ⓘ) were used in the production of this report:

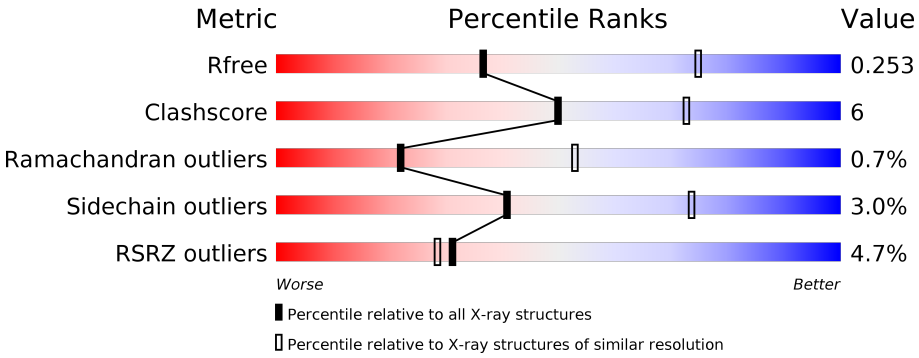
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.91 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	2307 (2.94-2.90)
Clashscore	141614	2531 (2.94-2.90)
Ramachandran outliers	138981	2462 (2.94-2.90)
Sidechain outliers	138945	2464 (2.94-2.90)
RSRZ outliers	127900	2248 (2.94-2.90)

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 on 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	353	5% 83% 13%
1	C	353	5% 80% 16%
2	B	429	3% 80% 14%
2	D	429	5% 74% 20%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11826 atoms, of which 125 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 Citryl-CoA synthetase small subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	342	Total	C	N	O	S	0	0	0
			2585	1649	440	489	7			
1	C	342	Total	C	N	O	S	0	0	0
			2585	1649	440	489	7			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	345	GLY	-	expression tag	UNP Q75VW6
A	346	GLY	-	expression tag	UNP Q75VW6
A	347	SER	-	expression tag	UNP Q75VW6
A	348	HIS	-	expression tag	UNP Q75VW6
A	349	HIS	-	expression tag	UNP Q75VW6
A	350	HIS	-	expression tag	UNP Q75VW6
A	351	HIS	-	expression tag	UNP Q75VW6
A	352	HIS	-	expression tag	UNP Q75VW6
A	353	HIS	-	expression tag	UNP Q75VW6
C	345	GLY	-	expression tag	UNP Q75VW6
C	346	GLY	-	expression tag	UNP Q75VW6
C	347	SER	-	expression tag	UNP Q75VW6
C	348	HIS	-	expression tag	UNP Q75VW6
C	349	HIS	-	expression tag	UNP Q75VW6
C	350	HIS	-	expression tag	UNP Q75VW6
C	351	HIS	-	expression tag	UNP Q75VW6
C	352	HIS	-	expression tag	UNP Q75VW6
C	353	HIS	-	expression tag	UNP Q75VW6

- Molecule 2 is a protein called Citryl-CoA synthetase large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	410	Total	C	N	O	S	0	0	0
			3191	2038	530	605	18			

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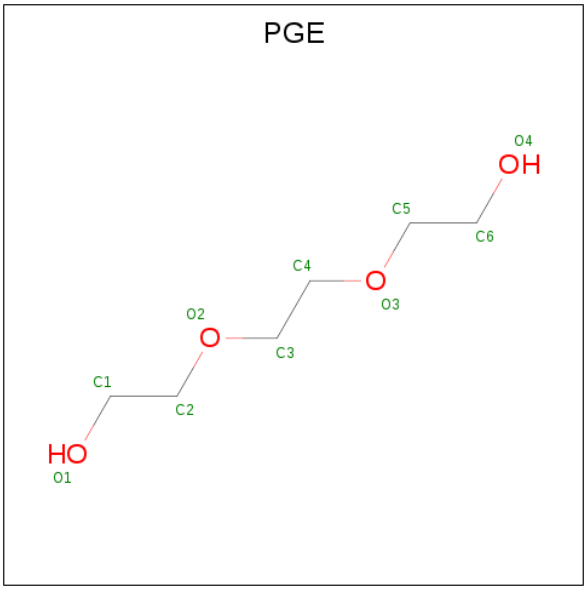
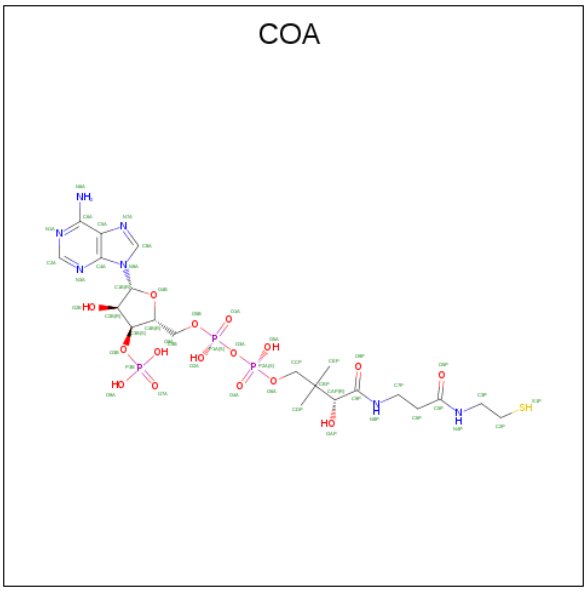
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	410	Total	C	N	O	S	0	0	0
			3191	2038	530	605	18			

- Molecule 3 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



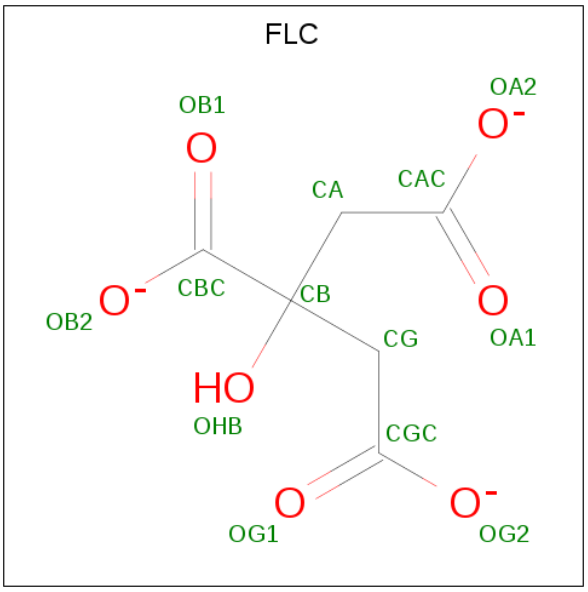
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			24	6	14	4		
3	A	1	Total	C	H	O	0	0
			24	6	14	4		
3	C	1	Total	C	H	O	0	0
			24	6	14	4		
3	C	1	Total	C	H	O	0	0
			24	6	14	4		

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



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
4	A	1	Total	C	H	N	O	P	S	0	0
			80	21	32	7	16	3	1		
4	C	1	Total	C	H	N	O	P	S	0	0
			80	21	32	7	16	3	1		

- Molecule 5 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7$) (labeled as "Ligand of Interest" by author).



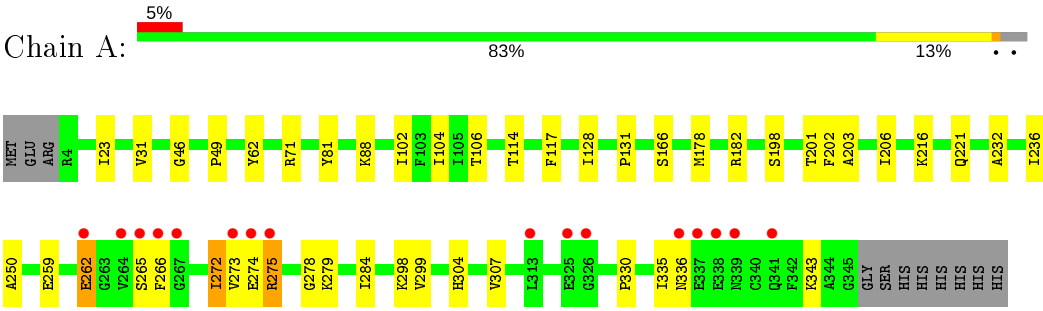
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	H	O	0	0
			18	6	5	7		

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.

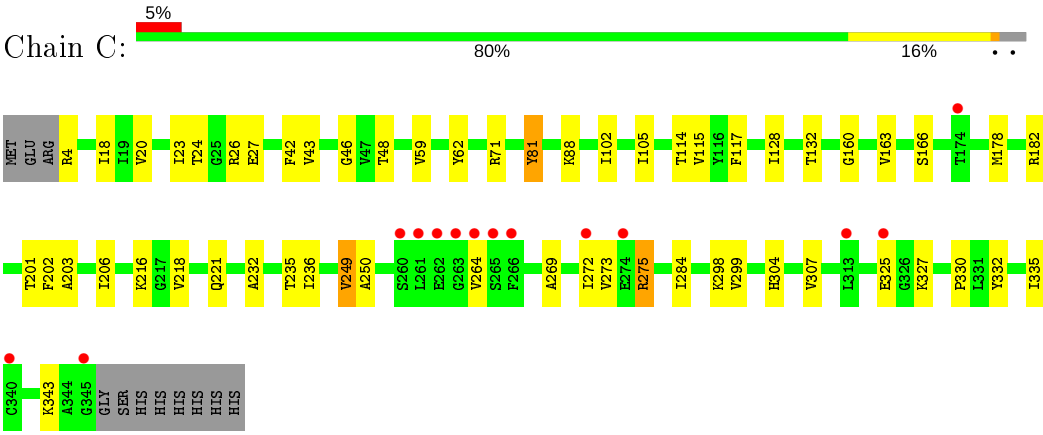
- Molecule 1: Citryl-CoA synthetase small subunit

Chain A:



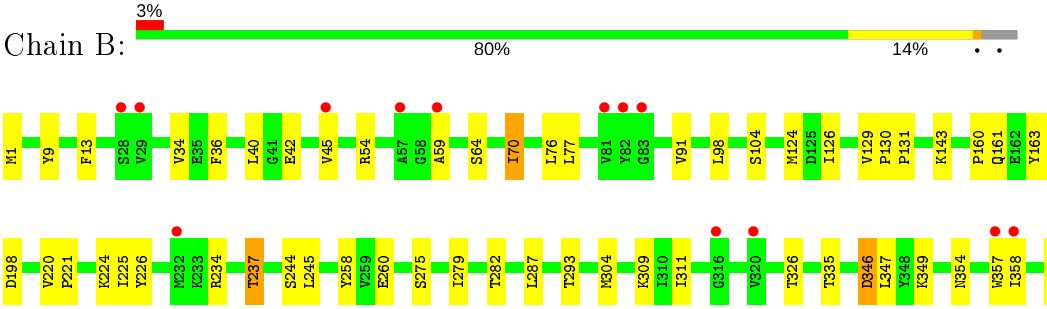
- Molecule 1: Citryl-CoA synthetase small subunit

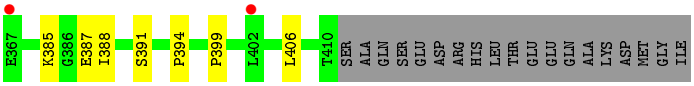
Chain C:



- Molecule 2: Citryl-CoA synthetase large subunit

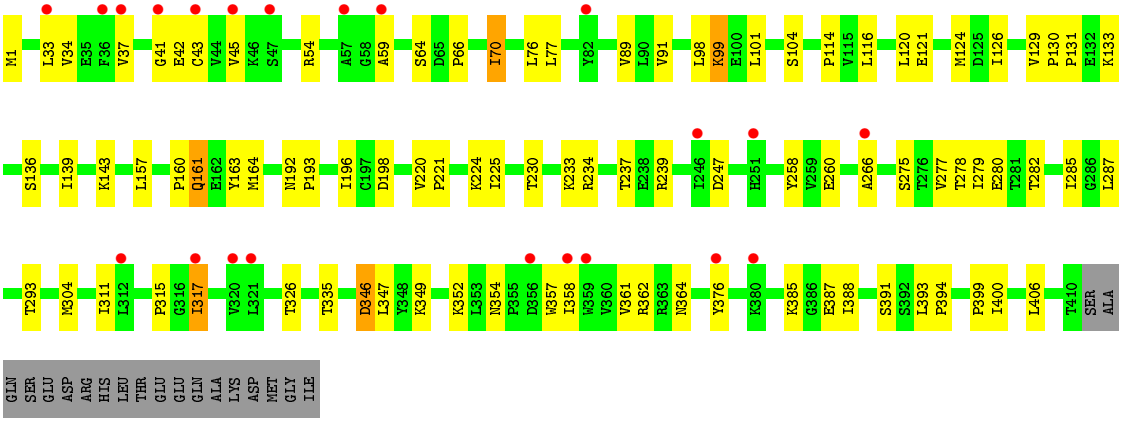
Chain B:





- Molecule 2: Citryl-CoA synthetase large subunit

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	118.50Å 127.03Å 143.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.60 – 2.91 47.60 – 2.91	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.60-2.91) 99.6 (47.60-2.91)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.12 (at 2.91Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.189 , 0.223 0.209 , 0.253	Depositor DCC
R_{free} test set	2413 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	78.9	Xtriage
Anisotropy	0.371	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 73.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	11826	wwPDB-VP
Average B, all atoms (Å^2)	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.55	0/2639	0.75	1/3582 (0.0%)
1	C	0.55	0/2639	0.74	0/3582
2	B	0.51	0/3253	0.72	1/4410 (0.0%)
2	D	0.51	0/3253	0.71	0/4410
All	All	0.53	0/11784	0.73	2/15984 (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	A	272	ILE	C-N-CA	5.27	134.87	121.70
2	B	194	LEU	N-CA-C	-5.01	97.46	111.00

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	2585	0	2589	25	0
1	C	2585	0	2589	34	0
2	B	3191	0	3244	35	0
2	D	3191	0	3244	49	0
3	A	20	28	28	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	20	28	28	1	0
4	A	48	32	32	1	0
4	C	48	32	32	1	0
5	B	13	5	5	0	0
All	All	11701	125	11791	135	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 6.

All (135) 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:274:GLU:HG3	1:A:275:ARG:H	1.25	0.97
1:C:330:PRO:HG3	2:D:387:GLU:HG2	1.56	0.88
1:C:336:ASN:HB2	1:C:343:LYS:HG3	1.64	0.80
1:A:336:ASN:HB2	1:A:343:LYS:HG3	1.65	0.77
1:A:274:GLU:HG3	1:A:275:ARG:N	2.02	0.75
1:A:88:LYS:HE3	3:A:401:PGE:O2	1.88	0.74
2:D:275:SER:O	2:D:279:ILE:HG12	1.87	0.73
1:A:330:PRO:HG3	2:B:387:GLU:HG2	1.71	0.73
2:D:230:THR:HA	2:D:233:LYS:HE2	1.71	0.71
2:D:282:THR:HG22	2:D:399:PRO:HB3	1.73	0.69
2:D:346:ASP:HA	2:D:349:LYS:HE3	1.77	0.67
2:B:282:THR:HG22	2:B:399:PRO:HB3	1.78	0.66
2:B:275:SER:O	2:B:279:ILE:HG12	1.97	0.64
1:C:203:ALA:HB1	1:C:235:THR:HG21	1.81	0.62
1:A:202:PHE:O	1:A:206:ILE:HG12	1.99	0.62
2:D:293:THR:HG21	2:D:311:ILE:HD11	1.81	0.61
1:C:202:PHE:O	1:C:206:ILE:HG12	2.00	0.61
2:B:364:ASN:HD22	2:B:391:SER:HB2	1.65	0.61
2:D:364:ASN:HD22	2:D:391:SER:HB2	1.68	0.58
1:A:259:GLU:OE1	1:A:279:LYS:HB2	2.03	0.58
1:A:104:ILE:HB	1:A:131:PRO:HA	1.85	0.58
2:D:42:GLU:HG3	2:D:64:SER:HA	1.86	0.57
1:A:304:HIS:O	1:A:307:VAL:HG12	2.05	0.57
1:A:262:GLU:HA	1:A:272:ILE:HD12	1.85	0.57
1:C:304:HIS:O	1:C:307:VAL:HG12	2.05	0.56
1:C:62:TYR:HE2	1:C:71:ARG:HD3	1.70	0.56
2:D:161:GLN:HA	2:D:164:MET:HG2	1.88	0.56
2:D:278:THR:O	2:D:282:THR:HG23	2.06	0.56
1:C:232:ALA:O	1:C:236:ILE:HG12	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:TYR:HE2	1:A:71:ARG:HD3	1.70	0.55
2:B:346:ASP:HA	2:B:349:LYS:HE3	1.88	0.55
2:B:42:GLU:HG3	2:B:64:SER:HA	1.87	0.55
2:D:101:LEU:HD23	2:D:120:LEU:HA	1.87	0.55
2:B:326:THR:HG23	2:B:364:ASN:HB3	1.89	0.55
2:B:161:GLN:HA	2:B:164:MET:HG2	1.90	0.54
2:D:354:ASN:HB3	2:D:357:TRP:CE2	2.43	0.54
1:A:232:ALA:O	1:A:236:ILE:HG12	2.07	0.54
2:B:54:ARG:HB3	2:B:59:ALA:HB3	1.89	0.54
1:C:160:GLY:HA3	1:C:185:GLY:HA3	1.89	0.54
1:A:106:THR:HG23	4:A:403:COA:H133	1.90	0.53
2:B:354:ASN:HB3	2:B:357:TRP:CE2	2.44	0.52
2:B:361:VAL:CG1	2:B:388:ILE:HG12	2.39	0.52
2:D:160:PRO:HB2	2:D:163:TYR:HD2	1.75	0.51
2:D:361:VAL:CG1	2:D:388:ILE:HG12	2.39	0.51
1:A:284:ILE:HG23	1:A:299:VAL:HG11	1.91	0.51
2:B:160:PRO:HB2	2:B:163:TYR:HD2	1.75	0.51
1:C:284:ILE:HG23	1:C:299:VAL:HG11	1.92	0.51
2:D:326:THR:HG23	2:D:364:ASN:HB3	1.91	0.51
1:C:178:MET:HE2	2:D:394:PRO:HB3	1.92	0.51
1:C:182:ARG:HG3	1:C:307:VAL:HG21	1.93	0.51
1:C:81:TYR:CE1	1:C:105:ILE:HG21	2.45	0.50
1:A:114:THR:HA	1:A:117:PHE:CZ	2.47	0.50
2:B:59:ALA:HA	2:B:76:LEU:HD21	1.94	0.50
2:D:358:ILE:HD12	2:D:406:LEU:HD23	1.93	0.49
1:C:335:ILE:HD12	2:D:385:LYS:HB3	1.94	0.49
2:D:239:ARG:NH2	2:D:315:PRO:HD3	2.27	0.49
1:C:269:ALA:O	1:C:273:VAL:HG12	2.13	0.49
1:C:26:ARG:HH11	1:C:27:GLU:HB2	1.78	0.49
1:C:114:THR:HA	1:C:117:PHE:CZ	2.48	0.48
1:A:23:ILE:HG21	1:A:46:GLY:HA3	1.94	0.48
2:D:258:TYR:HE2	2:D:260:GLU:HG2	1.78	0.48
1:A:182:ARG:HG3	1:A:307:VAL:HG21	1.94	0.48
1:C:88:LYS:HE3	3:C:401:PGE:O3	2.13	0.48
2:D:221:PRO:HG2	2:D:224:LYS:HD2	1.95	0.48
2:D:285:ILE:HD13	2:D:400:ILE:HA	1.96	0.48
2:D:282:THR:HG22	2:D:399:PRO:CB	2.41	0.48
1:A:201:THR:HG22	1:A:203:ALA:H	1.79	0.48
2:D:59:ALA:HA	2:D:76:LEU:HD21	1.96	0.48
2:B:304:MET:HG3	2:B:335:THR:HA	1.96	0.48
2:B:126:ILE:HA	2:B:129:VAL:HG12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:358:ILE:HD12	2:B:406:LEU:HD23	1.95	0.47
2:D:234:ARG:HH22	2:D:237:THR:HG23	1.79	0.47
2:D:120:LEU:HG	2:D:157:LEU:HD23	1.95	0.47
2:D:54:ARG:HB3	2:D:59:ALA:HB3	1.96	0.47
1:A:335:ILE:HD12	2:B:385:LYS:HB3	1.96	0.47
2:B:258:TYR:HE2	2:B:260:GLU:HG2	1.80	0.47
1:C:20:VAL:HB	1:C:23:ILE:HD12	1.96	0.47
1:C:218:VAL:HB	1:C:249:VAL:HB	1.97	0.47
2:D:98:LEU:HD11	2:D:198:ASP:HB2	1.97	0.47
2:D:304:MET:HG3	2:D:335:THR:HA	1.97	0.47
1:A:259:GLU:HA	1:A:272:ILE:HD13	1.97	0.46
2:B:234:ARG:HH12	2:B:237:THR:HG22	1.81	0.46
2:D:114:PRO:HG2	2:D:139:ILE:HB	1.97	0.46
2:D:347:LEU:HD23	2:D:352:LYS:HB2	1.97	0.46
2:D:364:ASN:HD22	2:D:391:SER:H	1.63	0.46
2:B:309:LYS:HE2	2:B:347:LEU:HG	1.96	0.45
1:C:23:ILE:HG21	1:C:46:GLY:HA3	1.99	0.45
1:C:332:TYR:HB3	2:D:376:TYR:CD1	2.51	0.45
2:D:121:GLU:HG3	2:D:133:LYS:HD2	1.97	0.45
2:D:45:VAL:HG22	2:D:91:VAL:HG22	1.98	0.45
2:D:126:ILE:HA	2:D:129:VAL:HG12	1.97	0.45
1:C:272:ILE:HA	1:C:275:ARG:HG3	1.98	0.45
2:B:36:PHE:CZ	2:B:40:LEU:HD11	2.52	0.45
2:B:364:ASN:HD22	2:B:391:SER:H	1.65	0.45
1:A:166:SER:OG	1:A:221:GLN:HG3	2.16	0.44
2:B:130:PRO:HA	2:B:131:PRO:HD3	1.91	0.44
2:B:221:PRO:HG2	2:B:224:LYS:HD2	1.99	0.44
1:C:102:ILE:HB	1:C:128:ILE:HG12	1.99	0.44
2:D:266:ALA:HB2	2:D:317:ILE:HD13	1.98	0.44
1:A:178:MET:HE2	2:B:394:PRO:HB3	2.00	0.43
2:D:116:LEU:O	2:D:136:SER:HA	2.19	0.43
1:C:18:ILE:HD12	1:C:42:PHE:HB3	2.00	0.43
1:C:201:THR:HG22	1:C:203:ALA:H	1.82	0.43
2:D:220:VAL:HB	2:D:225:ILE:HD11	2.00	0.43
1:C:166:SER:OG	1:C:221:GLN:HG3	2.18	0.43
2:B:220:VAL:HB	2:B:225:ILE:HD11	1.99	0.43
2:B:364:ASN:ND2	2:B:391:SER:HB2	2.33	0.43
2:B:34:VAL:HA	2:B:70:ILE:HD11	2.01	0.42
1:C:132:THR:HG22	4:C:403:COA:H22	2.01	0.42
2:D:362:ARG:HG3	2:D:393:LEU:HD23	2.01	0.42
1:A:102:ILE:HB	1:A:128:ILE:HG12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:GLU:HB3	1:A:278:GLY:HA3	2.01	0.42
2:B:258:TYR:CE2	2:B:260:GLU:HG2	2.54	0.42
2:B:293:THR:HG21	2:B:311:ILE:HD11	2.01	0.42
2:B:98:LEU:HD11	2:B:198:ASP:HB2	2.01	0.42
2:D:99:LYS:HB3	2:D:196:ILE:HD12	2.00	0.42
2:B:13:PHE:N	2:B:13:PHE:HD1	2.18	0.42
1:A:250:ALA:HA	1:A:298:LYS:O	2.20	0.42
2:D:364:ASN:ND2	2:D:391:SER:HB2	2.34	0.42
1:C:43:VAL:HG12	1:C:59:VAL:HG11	2.02	0.41
2:B:13:PHE:N	2:B:13:PHE:CD1	2.86	0.41
1:C:160:GLY:HA3	1:C:185:GLY:CA	2.50	0.41
2:D:130:PRO:HA	2:D:131:PRO:HD3	1.91	0.41
2:B:9:TYR:HA	2:B:13:PHE:HB2	2.02	0.41
2:B:45:VAL:HG22	2:B:91:VAL:HG22	2.02	0.41
1:C:115:VAL:HG11	2:D:114:PRO:HD3	2.03	0.41
2:D:258:TYR:CE2	2:D:260:GLU:HG2	2.54	0.41
1:C:81:TYR:CZ	1:C:105:ILE:HG21	2.56	0.41
2:D:33:LEU:O	2:D:37:VAL:HG23	2.21	0.41
2:D:41:GLY:HA2	2:D:66:PRO:HG3	2.03	0.41
2:D:34:VAL:HA	2:D:70:ILE:HD11	2.01	0.40
1:C:24:THR:OG1	1:C:48:THR:HG21	2.21	0.40
2:D:192:ASN:HA	2:D:193:PRO:HA	1.77	0.40
1:C:250:ALA:HA	1:C:298:LYS:O	2.21	0.40
1:C:325:GLU:HB2	1:C:327:LYS:HE3	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	340/353 (96%)	314 (92%)	22 (6%)	4 (1%)	13 38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	C	340/353 (96%)	324 (95%)	15 (4%)	1 (0%)	41 70
2	B	408/429 (95%)	382 (94%)	23 (6%)	3 (1%)	22 53
2	D	408/429 (95%)	383 (94%)	23 (6%)	2 (0%)	29 60
All	All	1496/1564 (96%)	1403 (94%)	83 (6%)	10 (1%)	22 53

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	273	VAL
2	B	124	MET
2	D	287	LEU
1	A	262	GLU
2	B	287	LEU
2	D	124	MET
2	B	244	SER
1	A	266	PHE
1	C	264	VAL
1	A	49	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	269/279 (96%)	262 (97%)	7 (3%)	46 76
1	C	269/279 (96%)	262 (97%)	7 (3%)	46 76
2	B	347/363 (96%)	338 (97%)	9 (3%)	46 76
2	D	347/363 (96%)	333 (96%)	14 (4%)	31 63
All	All	1232/1284 (96%)	1195 (97%)	37 (3%)	41 73

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	VAL

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Mol	Chain	Res	Type
1	A	81	TYR
1	A	198	SER
1	A	216	LYS
1	A	249	VAL
1	A	265	SER
1	A	275	ARG
2	B	1	MET
2	B	70	ILE
2	B	77	LEU
2	B	104	SER
2	B	143	LYS
2	B	226	TYR
2	B	237	THR
2	B	245	LEU
2	B	346	ASP
1	C	4	ARG
1	C	81	TYR
1	C	163	VAL
1	C	198	SER
1	C	216	LYS
1	C	249	VAL
1	C	275	ARG
2	D	1	MET
2	D	43	CYS
2	D	70	ILE
2	D	77	LEU
2	D	89	VAL
2	D	99	LYS
2	D	104	SER
2	D	143	LYS
2	D	161	GLN
2	D	247	ASP
2	D	277	VAL
2	D	280	GLU
2	D	317	ILE
2	D	346	ASP

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

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 monosaccharides in this entry.

5.6 Ligand geometry

7 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	PGE	A	402	-	9,9,9	0.28	0	8,8,8	0.17	0
3	PGE	C	401	-	9,9,9	0.40	0	8,8,8	0.33	0
4	COA	C	403	-	41,50,50	0.95	2 (4%)	52,75,75	0.86	2 (3%)
3	PGE	A	401	-	9,9,9	0.46	0	8,8,8	0.48	0
5	FLC	B	501	-	3,12,12	0.47	0	3,17,17	1.82	2 (66%)
3	PGE	C	402	-	9,9,9	0.22	0	8,8,8	0.27	0
4	COA	A	403	-	41,50,50	0.75	1 (2%)	52,75,75	0.85	2 (3%)

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	PGE	A	402	-	-	2/7/7/7	-
3	PGE	C	401	-	-	2/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	COA	C	403	-	-	20/44/64/64	0/3/3/3
3	PGE	A	401	-	-	1/7/7/7	-
5	FLC	B	501	-	-	1/6/16/16	-
3	PGE	C	402	-	-	2/7/7/7	-
4	COA	A	403	-	-	26/44/64/64	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	403	COA	P3B-O3B	4.02	1.66	1.59
4	A	403	COA	P3B-O3B	2.86	1.64	1.59
4	C	403	COA	P2A-O6A	2.58	1.69	1.59

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	C	403	COA	C5A-C6A-N6A	2.60	124.30	120.35
4	A	403	COA	C5A-C6A-N6A	2.37	123.96	120.35
5	B	501	FLC	CB-CA-CAC	2.28	118.64	114.98
4	A	403	COA	CEP-CBP-CCP	2.22	111.84	108.23
4	C	403	COA	O6A-P2A-O4A	2.18	117.58	109.07
5	B	501	FLC	CB-CG-CGC	2.12	118.38	114.98

There are no chirality outliers.

All (54) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	403	COA	CCP-O6A-P2A-O4A
4	C	403	COA	CCP-O6A-P2A-O5A
4	C	403	COA	OAP-CAP-CBP-CCP
4	C	403	COA	C9P-CAP-CBP-CCP
4	C	403	COA	OAP-CAP-CBP-CDP
4	C	403	COA	C9P-CAP-CBP-CDP
4	C	403	COA	OAP-CAP-CBP-CEP
4	C	403	COA	C9P-CAP-CBP-CEP
4	C	403	COA	N8P-C9P-CAP-OAP
4	C	403	COA	C5P-C6P-C7P-N8P
4	C	403	COA	S1P-C2P-C3P-N4P
4	A	403	COA	CCP-O6A-P2A-O4A
4	A	403	COA	CCP-O6A-P2A-O5A

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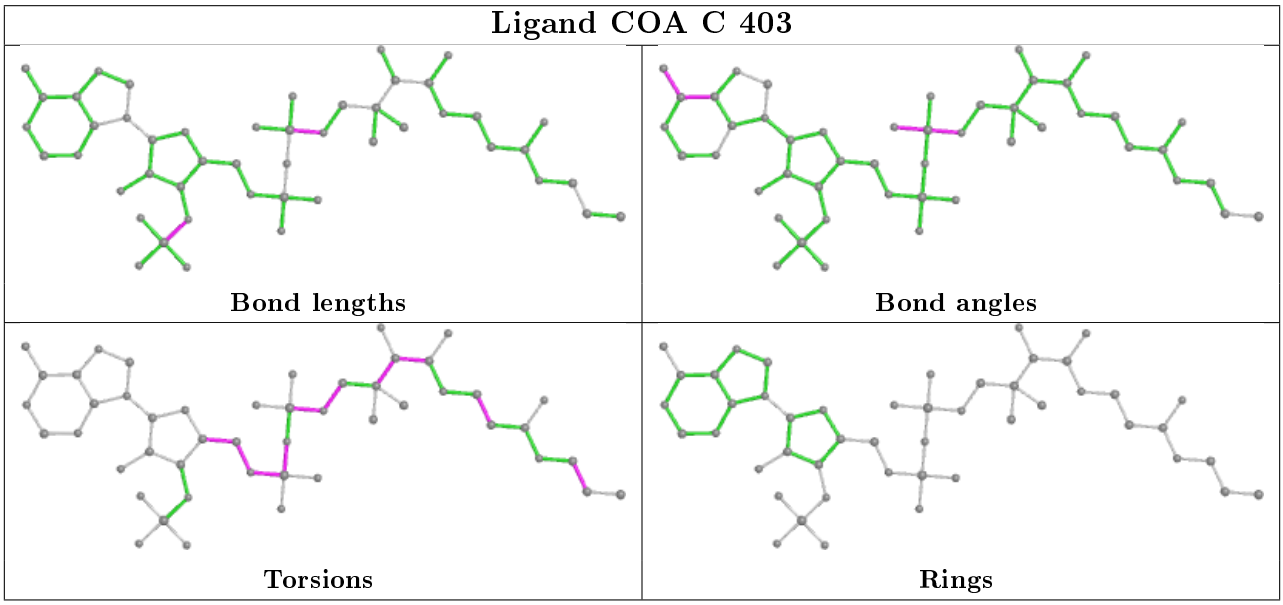
Mol	Chain	Res	Type	Atoms
4	A	403	COA	CAP-CBP-CCP-O6A
4	A	403	COA	C9P-CAP-CBP-CCP
4	A	403	COA	C9P-CAP-CBP-CDP
4	A	403	COA	C9P-CAP-CBP-CEP
4	A	403	COA	N8P-C9P-CAP-OAP
4	A	403	COA	CAP-C9P-N8P-C7P
4	A	403	COA	C5P-C6P-C7P-N8P
4	A	403	COA	S1P-C2P-C3P-N4P
3	C	402	PGE	O2-C3-C4-O3
3	C	401	PGE	O3-C5-C6-O4
3	A	402	PGE	O1-C1-C2-O2
4	A	403	COA	O4B-C4B-C5B-O5B
4	A	403	COA	O9P-C9P-N8P-C7P
4	C	403	COA	O9P-C9P-CAP-OAP
4	A	403	COA	O9P-C9P-CAP-OAP
4	A	403	COA	CEP-CBP-CCP-O6A
4	A	403	COA	OAP-CAP-CBP-CEP
4	C	403	COA	P2A-O3A-P1A-O5B
4	A	403	COA	P2A-O3A-P1A-O5B
3	A	401	PGE	C6-C5-O3-C4
3	A	402	PGE	C6-C5-O3-C4
4	C	403	COA	C5B-O5B-P1A-O3A
4	A	403	COA	C5B-O5B-P1A-O3A
4	A	403	COA	CCP-O6A-P2A-O3A
4	C	403	COA	CBP-CCP-O6A-P2A
4	C	403	COA	C5B-O5B-P1A-O1A
4	C	403	COA	C5B-O5B-P1A-O2A
4	A	403	COA	C5B-O5B-P1A-O2A
5	B	501	FLC	OHB-CB-CG-CGC
4	A	403	COA	C3B-C4B-C5B-O5B
4	A	403	COA	OAP-CAP-CBP-CCP
4	A	403	COA	CDP-CBP-CCP-O6A
4	A	403	COA	OAP-CAP-CBP-CDP
4	C	403	COA	C4B-C5B-O5B-P1A
4	C	403	COA	CCP-O6A-P2A-O3A
4	A	403	COA	C3B-O3B-P3B-O8A
3	C	402	PGE	O1-C1-C2-O2
3	C	401	PGE	O1-C1-C2-O2
4	A	403	COA	CBP-CCP-O6A-P2A
4	A	403	COA	C5B-O5B-P1A-O1A
4	C	403	COA	O4B-C4B-C5B-O5B

There are no ring outliers.

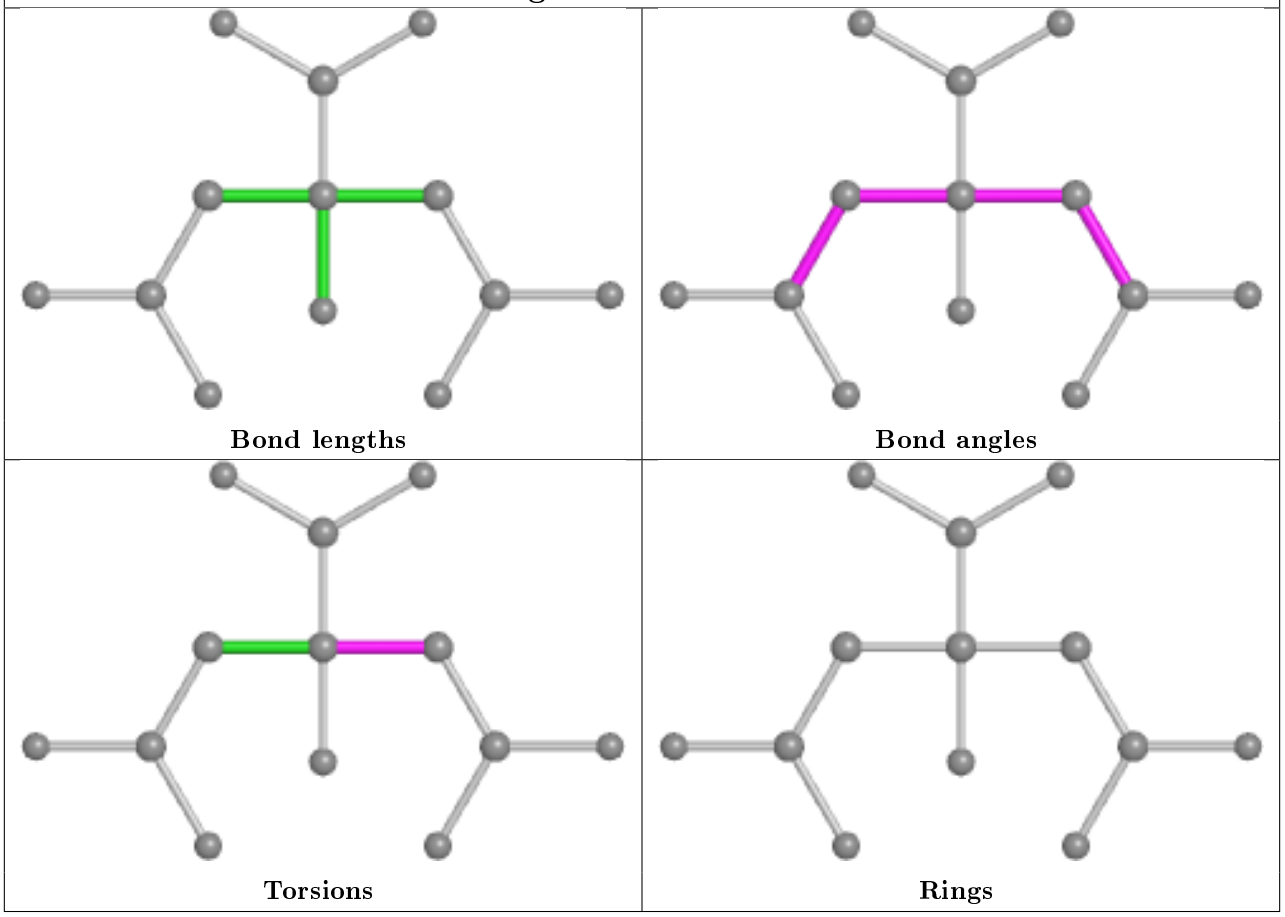
4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	401	PGE	1	0
4	C	403	COA	1	0
3	A	401	PGE	1	0
4	A	403	COA	1	0

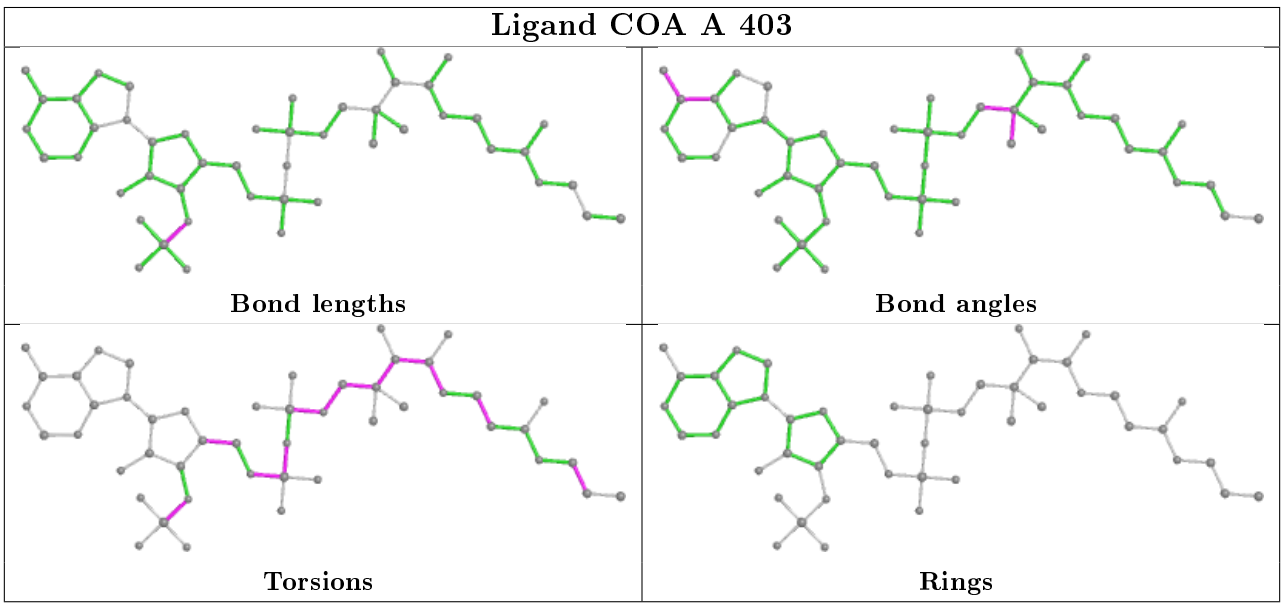
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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 FLC B 501



Ligand COA A 403



5.7 Other polymers (i)

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	342/353 (96%)	0.25	17 (4%)	28	25	50, 82, 147, 171	0
1	C	342/353 (96%)	0.16	17 (4%)	28	25	50, 83, 149, 196	0
2	B	410/429 (95%)	0.26	15 (3%)	41	38	52, 101, 150, 179	0
2	D	410/429 (95%)	0.36	22 (5%)	25	22	58, 107, 153, 180	0
All	All	1504/1564 (96%)	0.26	71 (4%)	31	28	50, 93, 151, 196	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	266	PHE	5.9
1	A	274	GLU	4.7
1	C	263	GLY	4.7
1	C	261	LEU	4.4
1	C	339	ASN	4.2
1	C	262	GLU	4.1
1	A	326	GLY	3.9
1	C	265	SER	3.9
2	D	251	HIS	3.6
2	B	320	VAL	3.5
2	D	320	VAL	3.5
1	C	274	GLU	3.5
1	C	260	SER	3.4
1	A	325	GLU	3.3
2	D	312	LEU	3.3
2	D	33	LEU	3.2
1	C	272	ILE	3.2
2	D	45	VAL	3.1
1	C	345	GLY	3.1
2	D	358	ILE	3.1
1	C	264	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	338	GLU	3.0
1	A	245	TRP	3.0
2	B	45	VAL	2.9
1	A	341	GLN	2.9
2	D	317	ILE	2.9
2	B	358	ILE	2.8
1	A	273	VAL	2.8
2	B	81	VAL	2.8
2	D	359	TRP	2.8
2	D	43	CYS	2.8
2	B	316	GLY	2.7
2	D	47	SER	2.7
1	C	266	PHE	2.7
1	C	325	GLU	2.5
1	C	340	CYS	2.5
2	D	376	TYR	2.5
2	D	41	GLY	2.5
2	D	380	LYS	2.4
1	A	267	GLY	2.4
2	B	82	TYR	2.4
2	D	37	VAL	2.4
1	A	337	GLU	2.4
2	D	246	ILE	2.4
1	A	275	ARG	2.3
1	A	336	ASN	2.3
2	B	28	SER	2.3
1	C	338	GLU	2.3
2	B	57	ALA	2.3
2	B	357	TRP	2.3
1	C	337	GLU	2.2
2	D	356	ASP	2.2
2	B	402	LEU	2.2
1	A	264	VAL	2.2
2	D	57	ALA	2.2
2	D	82	TYR	2.2
1	A	262	GLU	2.1
2	B	232	MET	2.1
2	D	266	ALA	2.1
2	D	321	LEU	2.1
2	B	29	VAL	2.1
2	B	83	GLY	2.1
2	D	36	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	174	THR	2.1
2	D	59	ALA	2.1
2	B	367	GLU	2.1
1	A	313	LEU	2.0
1	C	313	LEU	2.0
1	A	265	SER	2.0
1	A	339	ASN	2.0
2	B	59	ALA	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)

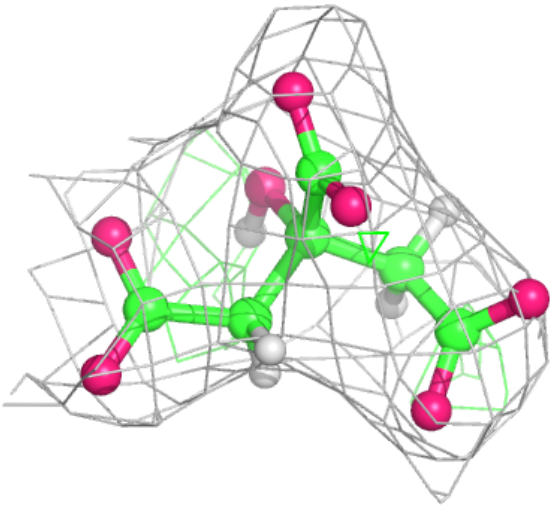
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

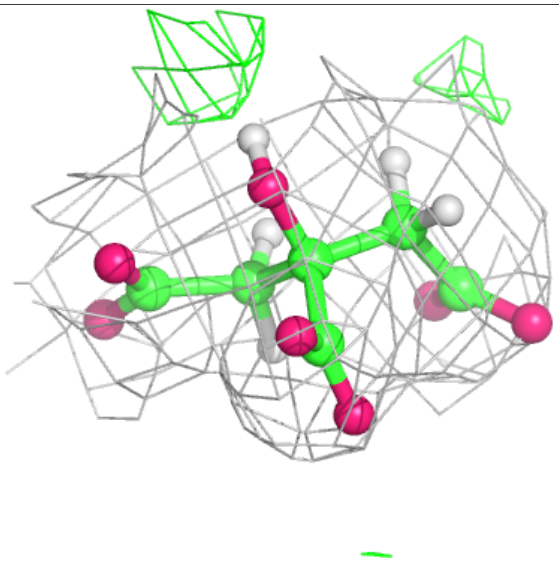
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	PGE	A	402	10/10	0.79	0.27	94,106,113,113	0
3	PGE	C	402	10/10	0.82	0.23	90,93,97,97	0
5	FLC	B	501	13/13	0.85	0.21	91,103,106,107	0
3	PGE	C	401	10/10	0.91	0.20	63,78,83,86	0
3	PGE	A	401	10/10	0.91	0.22	80,83,85,86	0
4	COA	A	403	48/48	0.93	0.19	87,97,119,124	0
4	COA	C	403	48/48	0.94	0.18	77,96,121,126	0

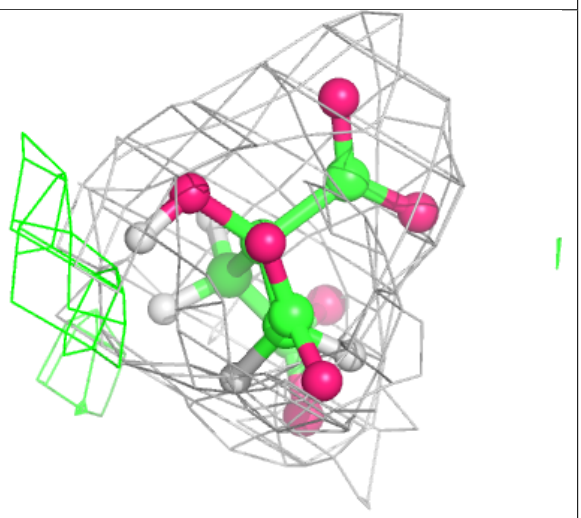
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FLC B 501:

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

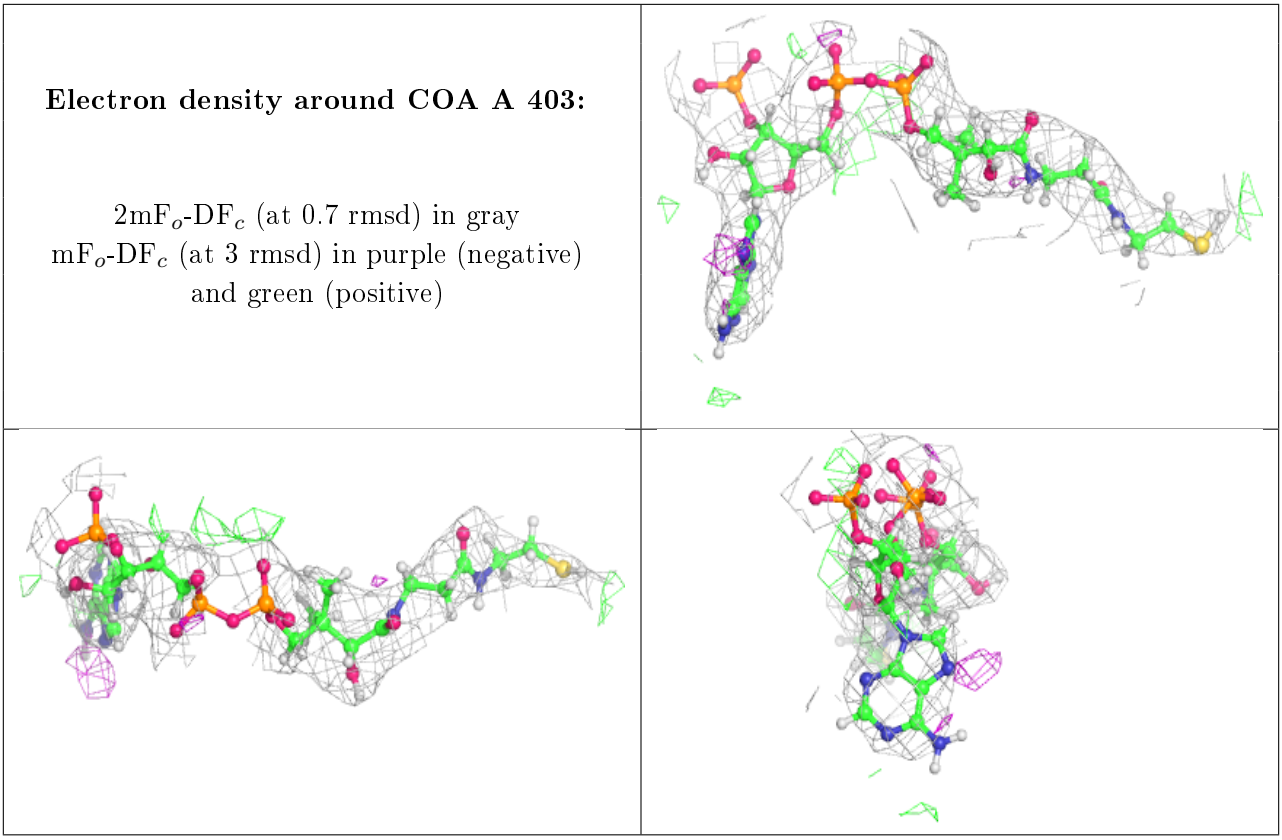






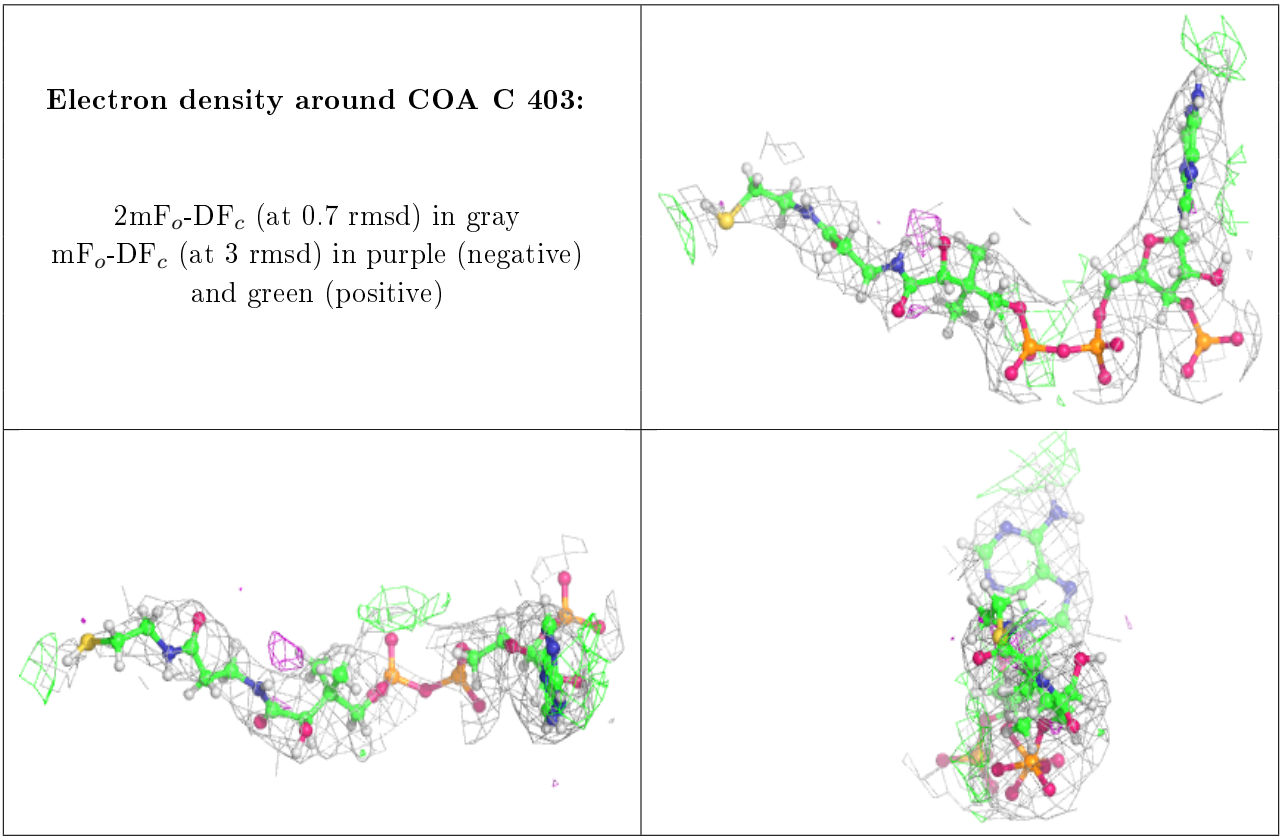
Electron density around COA A 403:

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



Electron density around COA C 403:

$2mF_o$-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.