



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:38 PM UTC

PDB ID : 6HXQ / pdb_00006hxq
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 types of validation reports are described at

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

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

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

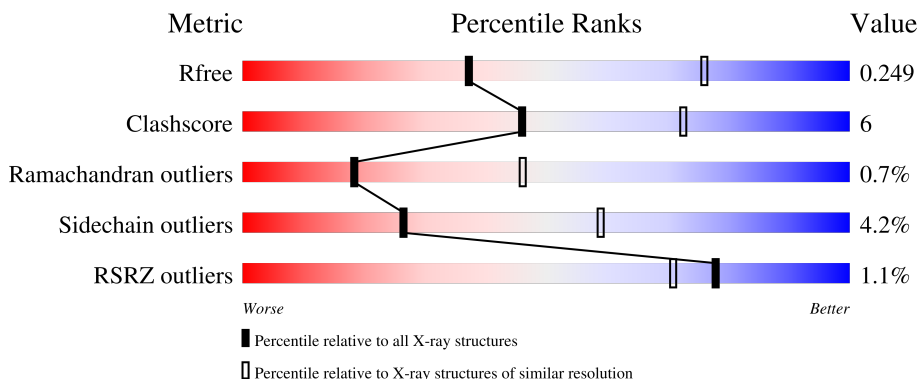
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

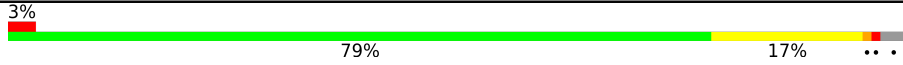
The reported resolution of this entry is 2.91 Å.

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}	180053	2995 (2.94-2.90)
Clashscore	190562	3213 (2.94-2.90)
Ramachandran outliers	187476	3128 (2.94-2.90)
Sidechain outliers	187428	3130 (2.94-2.90)
RSRZ outliers	180081	2995 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	353	 3% 79% 17% . .
1	C	353	 % 76% 19% . .
2	B	429	 76% 19% . .
2	D	429	 69% 24% . .

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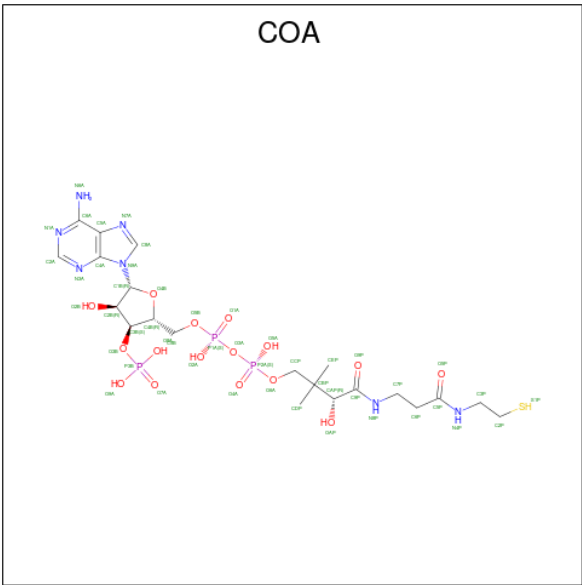
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	410	Total	C	N	O	S	0	0	0
			3191	2038	530	605	18			

- Molecule 3 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



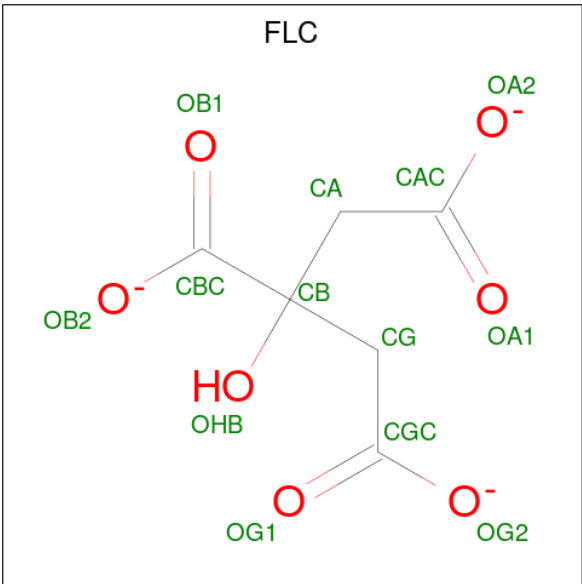
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			24	6	14	4		
3	A	1	Total	C	H	O	0	0
			24	6	14	4		
3	C	1	Total	C	H	O	0	0
			24	6	14	4		
3	C	1	Total	C	H	O	0	0
			24	6	14	4		

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



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
4	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 (CCD ID: FLC) (formula: C₆H₅O₇) (labeled as "Ligand of Interest" by depositor).

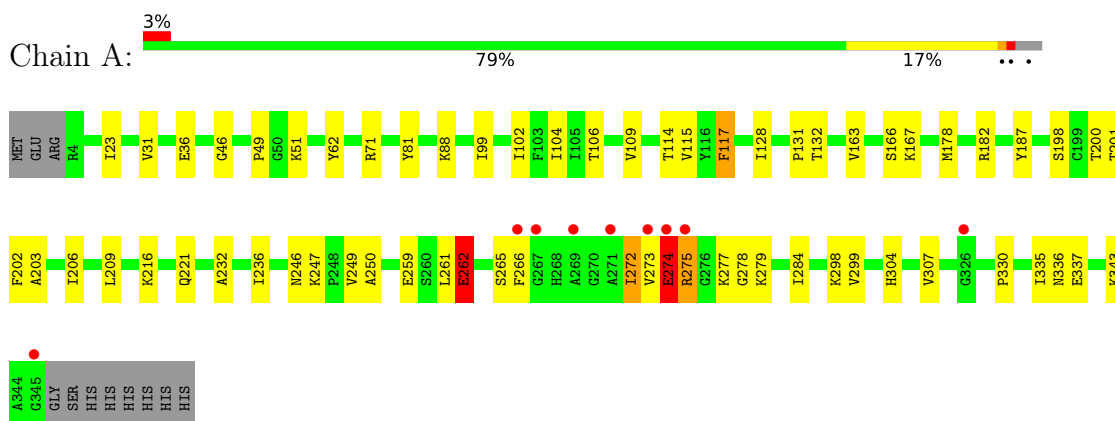


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	H	O	0	0
			18	6	5	7		

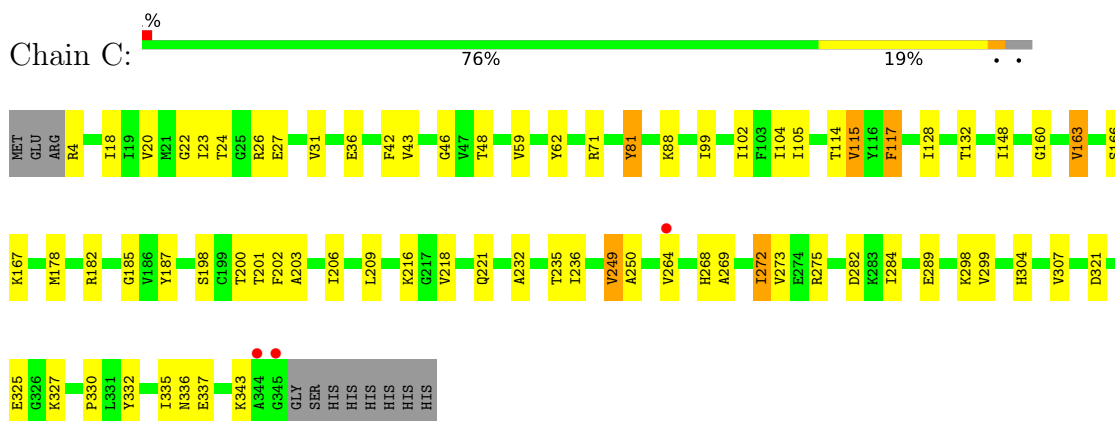
3 Residue-property plots [i](#)

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.

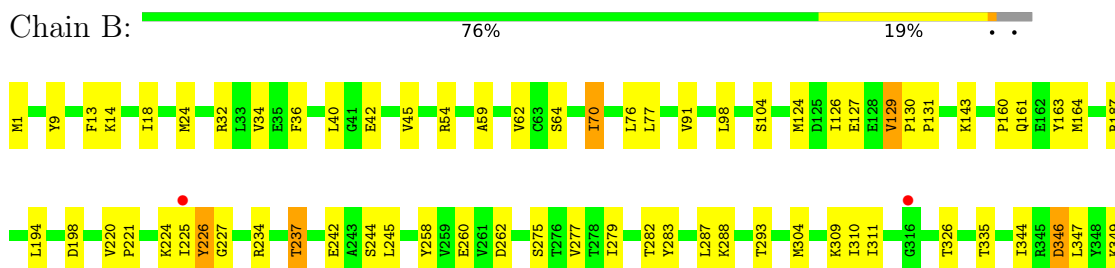
• Molecule 1: Citryl-CoA synthetase small subunit



• Molecule 1: Citryl-CoA synthetase small subunit

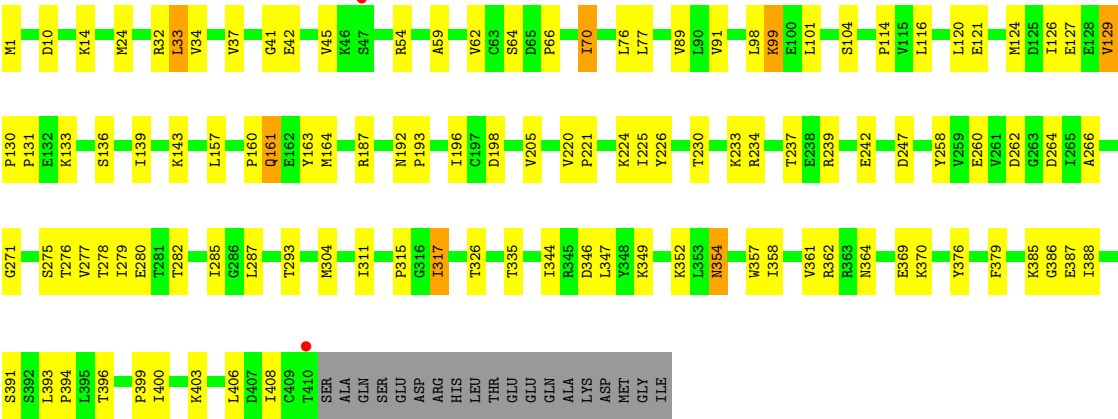


• Molecule 2: Citryl-CoA synthetase large subunit





● Molecule 2: Citryl-CoA synthetase large subunit



4 Data and refinement statistics

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) 99.9 (47.60-2.91)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.12 (at 2.91Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.189 , 0.223 0.209 , 0.249	Depositor DCC
R_{free} test set	2414 reflections (4.98%)	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 , 93.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	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.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.95	3/2639 (0.1%)	1.41	21/3582 (0.6%)
1	C	0.93	2/2639 (0.1%)	1.42	20/3582 (0.6%)
2	B	0.88	0/3253	1.38	24/4410 (0.5%)
2	D	0.88	0/3253	1.39	26/4410 (0.6%)
All	All	0.91	5/11784 (0.0%)	1.40	91/15984 (0.6%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	274	GLU	CA-C	5.40	1.60	1.52
1	A	277	LYS	CA-C	5.22	1.59	1.52
1	C	272	ILE	CA-C	5.08	1.57	1.52
1	C	104	ILE	CG1-CD1	-5.06	1.32	1.51
1	A	109	VAL	CA-C	5.04	1.57	1.53

All (91) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	226	TYR	N-CA-C	-7.80	99.29	110.59
1	A	272	ILE	CA-C-N	7.17	134.87	121.97
1	A	272	ILE	C-N-CA	7.17	134.87	121.97
1	A	167	LYS	N-CA-C	-7.10	103.47	111.14
1	A	246	ASN	CA-CB-CG	7.05	119.65	112.60
2	D	276	THR	CA-C-N	6.43	128.89	120.60
2	D	276	THR	C-N-CA	6.43	128.89	120.60
2	D	379	PHE	CA-CB-CG	6.36	120.16	113.80
2	B	194	LEU	N-CA-C	-6.28	97.46	108.20
1	C	167	LYS	N-CA-C	-6.28	104.06	111.03
2	B	379	PHE	CA-CB-CG	6.26	120.06	113.80
2	B	127	GLU	N-CA-C	-6.23	105.51	113.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	127	GLU	N-CA-C	-6.17	105.58	113.23
1	C	115	VAL	N-CA-CB	6.12	117.30	110.51
2	D	354	ASN	CA-CB-CG	6.11	118.71	112.60
1	C	337	GLU	CA-C-N	6.08	128.34	120.44
1	C	337	GLU	C-N-CA	6.08	128.34	120.44
2	D	242	GLU	CA-C-N	6.06	128.32	120.44
2	D	242	GLU	C-N-CA	6.06	128.32	120.44
2	B	354	ASN	CA-CB-CG	6.05	118.65	112.60
1	A	337	GLU	CA-C-N	6.02	128.27	120.44
1	A	337	GLU	C-N-CA	6.02	128.27	120.44
1	A	262	GLU	CB-CG-CD	5.95	122.72	112.60
2	B	14	LYS	CA-C-N	5.91	128.12	120.44
2	B	14	LYS	C-N-CA	5.91	128.12	120.44
2	B	226	TYR	N-CA-C	-5.88	101.81	110.52
1	A	261	LEU	CA-C-N	5.87	132.76	121.54
1	A	261	LEU	C-N-CA	5.87	132.76	121.54
1	A	115	VAL	N-CA-CB	5.87	117.02	110.51
2	D	14	LYS	CA-C-N	5.74	127.90	120.44
2	D	14	LYS	C-N-CA	5.74	127.90	120.44
2	B	310	ILE	CA-C-N	5.69	128.25	120.46
2	B	310	ILE	C-N-CA	5.69	128.25	120.46
1	A	247	LYS	N-CA-C	5.67	116.80	109.72
2	D	10	ASP	CA-CB-CG	5.65	118.25	112.60
1	A	274	GLU	CB-CG-CD	5.62	122.16	112.60
2	B	242	GLU	CA-C-N	5.59	127.71	120.44
2	B	242	GLU	C-N-CA	5.59	127.71	120.44
1	A	187	TYR	N-CA-C	-5.55	103.06	111.56
1	C	187	TYR	N-CA-C	-5.55	103.07	111.56
1	C	163	VAL	N-CA-CB	5.53	118.83	111.64
2	D	187	ARG	N-CA-C	-5.48	106.50	114.12
1	C	117	PHE	CA-CB-CG	5.41	119.21	113.80
1	C	321	ASP	CA-CB-CG	5.39	117.99	112.60
2	D	33	LEU	CA-C-N	5.34	127.49	120.60
2	D	33	LEU	C-N-CA	5.34	127.49	120.60
2	B	403	LYS	CA-C-N	5.34	127.69	120.38
2	B	403	LYS	C-N-CA	5.34	127.69	120.38
1	C	282	ASP	CA-C-N	5.34	127.38	120.44
1	C	282	ASP	C-N-CA	5.34	127.38	120.44
2	D	403	LYS	CA-C-N	5.33	127.69	120.38
2	D	403	LYS	C-N-CA	5.33	127.69	120.38
2	D	271	GLY	N-CA-C	5.32	119.57	112.65
1	A	51	LYS	CA-C-N	5.31	125.76	120.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	51	LYS	C-N-CA	5.31	125.76	120.98
2	B	187	ARG	N-CA-C	-5.30	106.75	114.12
2	D	386	GLY	N-CA-C	5.29	119.35	110.56
2	B	18	ILE	N-CA-C	-5.26	101.97	107.60
1	A	36	GLU	CB-CG-CD	5.25	121.53	112.60
1	C	36	GLU	CB-CG-CD	5.22	121.47	112.60
2	B	369	GLU	CA-C-N	5.21	127.22	120.44
2	B	369	GLU	C-N-CA	5.21	127.22	120.44
1	C	22	GLY	CA-C-N	5.21	128.70	120.47
1	C	22	GLY	C-N-CA	5.21	128.70	120.47
2	B	262	ASP	CA-CB-CG	5.20	117.80	112.60
2	B	283	TYR	CA-C-N	5.16	127.45	120.38
2	B	283	TYR	C-N-CA	5.16	127.45	120.38
1	C	200	THR	CA-C-N	5.15	131.39	122.64
1	C	200	THR	C-N-CA	5.15	131.39	122.64
2	D	344	ILE	CA-C-N	5.15	127.13	120.44
2	D	344	ILE	C-N-CA	5.15	127.13	120.44
2	B	227	GLY	N-CA-C	5.13	117.97	112.33
1	A	200	THR	CA-C-N	5.09	131.30	122.64
1	A	200	THR	C-N-CA	5.09	131.30	122.64
1	C	289	GLU	CB-CG-CD	5.09	121.25	112.60
2	B	344	ILE	CA-C-N	5.08	127.05	120.44
2	B	344	ILE	C-N-CA	5.08	127.05	120.44
1	A	209	LEU	CA-C-N	5.07	127.32	120.38
1	A	209	LEU	C-N-CA	5.07	127.32	120.38
2	D	264	ASP	CA-CB-CG	5.06	117.66	112.60
1	A	117	PHE	CA-CB-CG	5.05	118.85	113.80
2	B	386	GLY	N-CA-C	5.05	118.94	110.56
1	C	268	HIS	CA-C-N	5.05	127.36	120.54
1	C	268	HIS	C-N-CA	5.05	127.36	120.54
2	D	370	LYS	CA-C-N	5.05	125.54	119.94
2	D	370	LYS	C-N-CA	5.05	125.54	119.94
1	C	209	LEU	CA-C-N	5.04	127.74	120.38
1	C	209	LEU	C-N-CA	5.04	127.74	120.38
2	D	262	ASP	CA-CB-CG	5.03	117.63	112.60
2	D	369	GLU	CA-C-N	5.01	126.95	120.44
2	D	369	GLU	C-N-CA	5.01	126.95	120.44

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	36	0
2	D	3191	0	3244	50	0
3	A	20	28	28	1	0
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	137	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 (137) 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:178:MET:HE2	2:D:394:PRO:HB3	1.62	0.81
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:178:MET:HE2	2:B:394:PRO:HB3	1.67	0.76
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
2:B:24:MET:HE1	2:B:32:ARG:HB3	1.80	0.63
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:24:MET:HE1	2:D:32:ARG:HB3	1.81	0.61
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
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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
1:A:335:ILE:HD12	2:B:385:LYS:HB3	1.96	0.47
2:D:54:ARG:HB3	2:D:59:ALA:HB3	1.96	0.47
2:D:120:LEU:HG	2:D:157:LEU:HD23	1.95	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:45:VAL:HG22	2:D:91:VAL:HG22	1.98	0.45
2:D:121:GLU:HG3	2:D:133:LYS:HD2	1.97	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
1:A:274:GLU:HB3	1:A:278:GLY:HA3	2.01	0.42
2:B:98:LEU:HD11	2:B:198:ASP:HB2	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: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:81:TYR:CZ	1:C:105:ILE:HG21	2.56	0.41
1:C:115:VAL:HG11	2:D:114:PRO:HD3	2.03	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:258:TYR:CE2	2:D:260:GLU:HG2	2.54	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

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	340/353 (96%)	314 (92%)	22 (6%)	4 (1%)	10	32
1	C	340/353 (96%)	324 (95%)	15 (4%)	1 (0%)	36	64
2	B	408/429 (95%)	382 (94%)	23 (6%)	3 (1%)	18	46
2	D	408/429 (95%)	383 (94%)	23 (6%)	2 (0%)	24	53
All	All	1496/1564 (96%)	1403 (94%)	83 (6%)	10 (1%)	18	46

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

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%)	258 (96%)	11 (4%)	27	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	269/279 (96%)	260 (97%)	9 (3%)	33	65
2	B	347/363 (96%)	332 (96%)	15 (4%)	26	58
2	D	347/363 (96%)	330 (95%)	17 (5%)	22	52
All	All	1232/1284 (96%)	1180 (96%)	52 (4%)	26	59

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	VAL
1	A	81	TYR
1	A	99	ILE
1	A	132	THR
1	A	163	VAL
1	A	198	SER
1	A	216	LYS
1	A	249	VAL
1	A	265	SER
1	A	274	GLU
1	A	275	ARG
2	B	1	MET
2	B	62	VAL
2	B	70	ILE
2	B	77	LEU
2	B	104	SER
2	B	129	VAL
2	B	143	LYS
2	B	226	TYR
2	B	237	THR
2	B	245	LEU
2	B	277	VAL
2	B	288	LYS
2	B	346	ASP
2	B	396	THR
2	B	408	ILE
1	C	4	ARG
1	C	31	VAL
1	C	81	TYR
1	C	99	ILE
1	C	148	ILE
1	C	163	VAL
1	C	198	SER

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Mol	Chain	Res	Type
1	C	216	LYS
1	C	249	VAL
2	D	1	MET
2	D	62	VAL
2	D	70	ILE
2	D	77	LEU
2	D	89	VAL
2	D	99	LYS
2	D	104	SER
2	D	129	VAL
2	D	143	LYS
2	D	161	GLN
2	D	205	VAL
2	D	247	ASP
2	D	277	VAL
2	D	280	GLU
2	D	317	ILE
2	D	396	THR
2	D	408	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	336	ASN
2	B	2	ASN
2	B	152	ASN
2	B	200	ASN
1	C	30	GLN
1	C	221	GLN
1	C	336	ASN
1	C	339	ASN
2	D	78	ASN
2	D	96	ASN
2	D	200	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	C	401	-	9,9,9	0.40	0	8,8,8	0.33	0
3	PGE	C	402	-	9,9,9	0.22	0	8,8,8	0.26	0
4	COA	A	403	-	47,50,50	0.63	1 (2%)	69,75,75	0.68	1 (1%)
3	PGE	A	401	-	9,9,9	0.46	0	8,8,8	0.48	0
4	COA	C	403	-	47,50,50	0.84	2 (4%)	69,75,75	0.75	1 (1%)
5	FLC	B	501	-	12,12,12	1.18	0	17,17,17	1.27	2 (11%)
3	PGE	A	402	-	9,9,9	0.28	0	8,8,8	0.17	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	PGE	C	401	-	-	2/7/7/7	-
3	PGE	C	402	-	-	2/7/7/7	-
4	COA	A	403	-	-	29/48/64/64	0/3/3/3
3	PGE	A	401	-	-	1/7/7/7	-
4	COA	C	403	-	-	22/48/64/64	0/3/3/3
5	FLC	B	501	-	-	3/16/16/16	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PGE	A	402	-	-	2/7/7/7	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	403	COA	P3B-O3B	4.21	1.66	1.59
4	A	403	COA	P3B-O3B	2.96	1.64	1.59
4	C	403	COA	P2A-O6A	2.65	1.69	1.59

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	501	FLC	OB2-CBC-CB	2.38	117.70	113.14
4	A	403	COA	CEP-CBP-CCP	2.19	111.84	108.22
4	C	403	COA	O6A-P2A-O4A	2.18	117.58	108.94
5	B	501	FLC	OB1-CBC-CB	-2.17	117.89	122.09

There are no chirality outliers.

All (61) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	403	COA	CCP-O6A-P2A-O3A
4	A	403	COA	CCP-O6A-P2A-O4A
4	A	403	COA	CCP-O6A-P2A-O5A
4	A	403	COA	CEP-CBP-CCP-O6A
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
4	C	403	COA	C5B-O5B-P1A-O1A
4	C	403	COA	CCP-O6A-P2A-O3A
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

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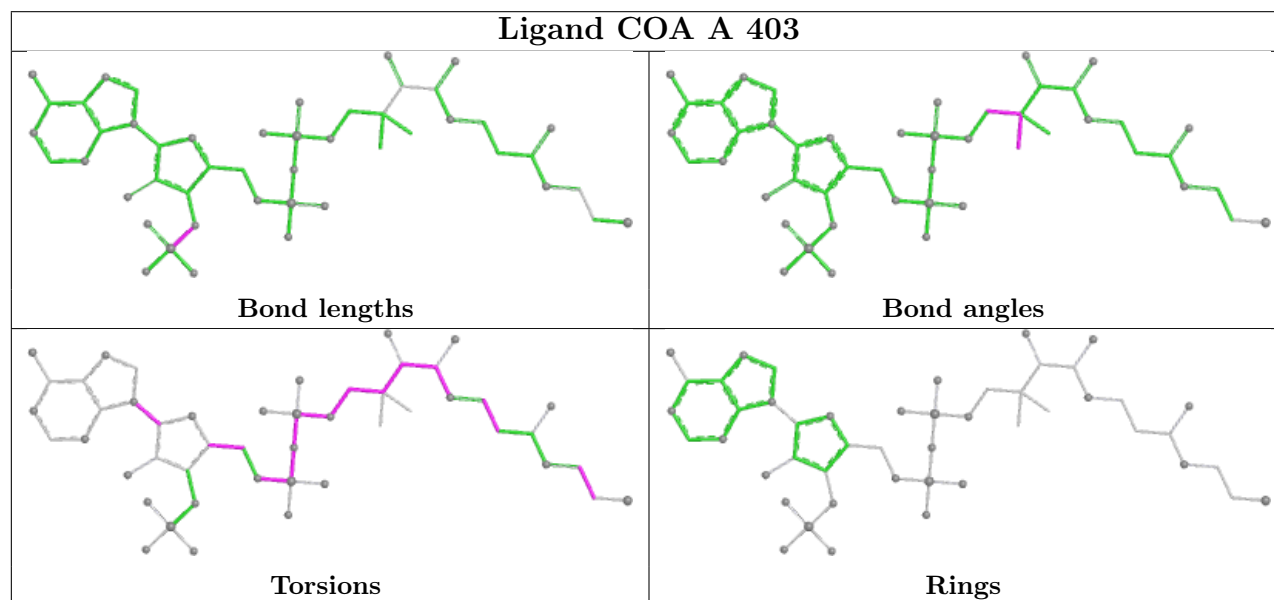
Mol	Chain	Res	Type	Atoms
4	C	403	COA	OAP-CAP-CBP-CEP
4	C	403	COA	C9P-CAP-CBP-CEP
4	C	403	COA	N8P-C9P-CAP-OAP
4	C	403	COA	C5P-C6P-C7P-N8P
4	C	403	COA	S1P-C2P-C3P-N4P
3	C	402	PGE	O2-C3-C4-O3
3	C	401	PGE	O3-C5-C6-O4
3	A	402	PGE	O1-C1-C2-O2
4	A	403	COA	O9P-C9P-N8P-C7P
4	A	403	COA	O9P-C9P-CAP-OAP
4	C	403	COA	O9P-C9P-CAP-OAP
4	C	403	COA	C2B-C1B-N9A-C8A
4	A	403	COA	OAP-CAP-CBP-CEP
4	A	403	COA	P2A-O3A-P1A-O5B
4	C	403	COA	P2A-O3A-P1A-O5B
3	A	402	PGE	C6-C5-O3-C4
3	A	401	PGE	C6-C5-O3-C4
4	A	403	COA	O4B-C4B-C5B-O5B
4	A	403	COA	C2B-C1B-N9A-C8A
4	C	403	COA	CBP-CCP-O6A-P2A
4	A	403	COA	CDP-CBP-CCP-O6A
5	B	501	FLC	CB-CA-CAC-OA2
4	A	403	COA	C5B-O5B-P1A-O1A
4	A	403	COA	C5B-O5B-P1A-O2A
4	A	403	COA	C5B-O5B-P1A-O3A
4	A	403	COA	OAP-CAP-CBP-CCP
4	C	403	COA	C5B-O5B-P1A-O2A
4	C	403	COA	C5B-O5B-P1A-O3A
5	B	501	FLC	OHB-CB-CG-CGC
4	A	403	COA	OAP-CAP-CBP-CDP
4	C	403	COA	C2B-C1B-N9A-C4A
4	A	403	COA	C3B-C4B-C5B-O5B
5	B	501	FLC	CB-CA-CAC-OA1
4	A	403	COA	O4B-C1B-N9A-C8A
3	C	402	PGE	O1-C1-C2-O2
4	C	403	COA	C4B-C5B-O5B-P1A
4	C	403	COA	O4B-C1B-N9A-C8A
3	C	401	PGE	O1-C1-C2-O2
4	A	403	COA	CBP-CCP-O6A-P2A
4	A	403	COA	N8P-C9P-CAP-CBP
4	A	403	COA	P1A-O3A-P2A-O5A

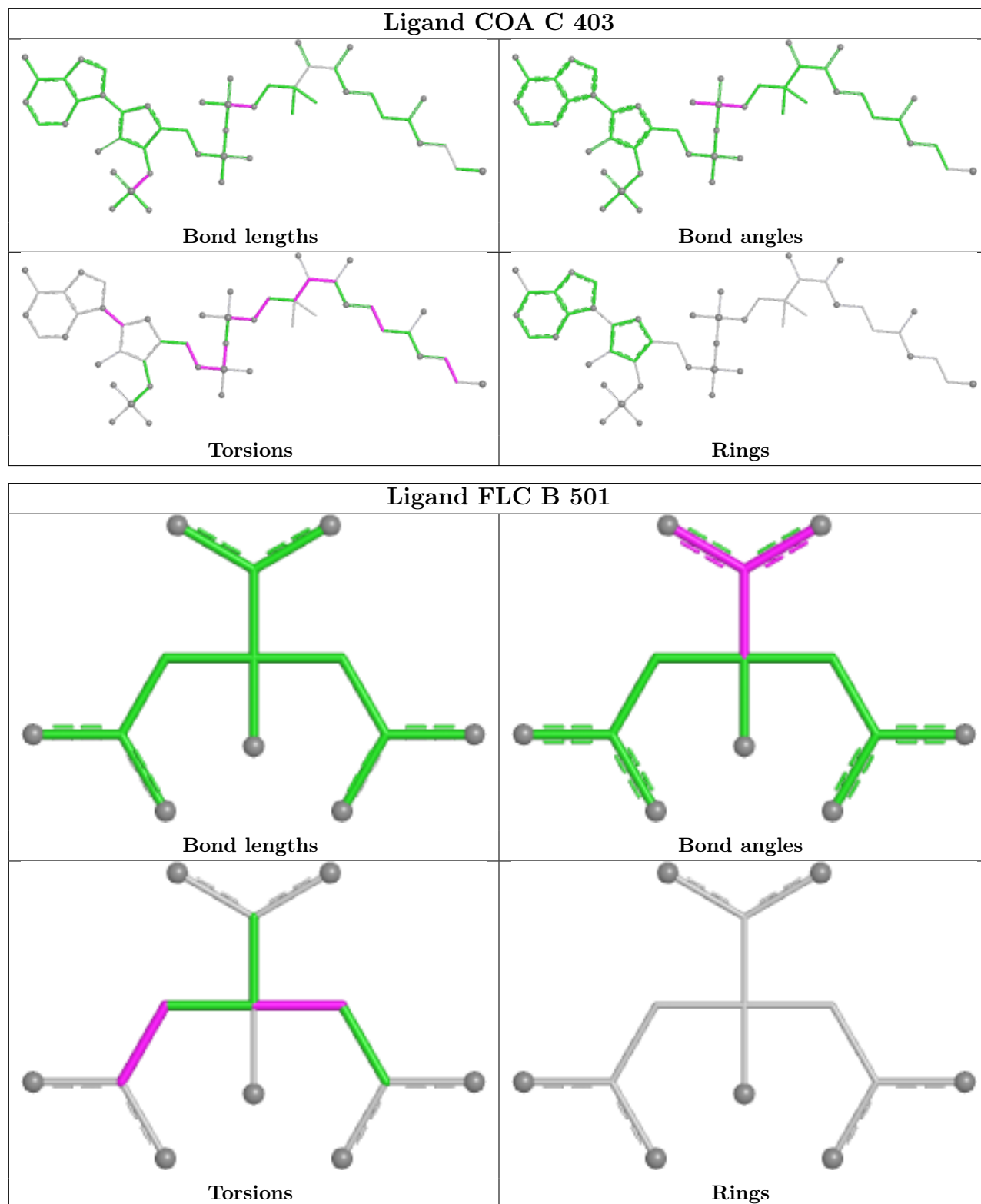
There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	401	PGE	1	0
4	A	403	COA	1	0
3	A	401	PGE	1	0
4	C	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 than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers ⓘ

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 [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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	342/353 (96%)	-0.11	9 (2%) 57 47	50, 82, 147, 171	0
1	C	342/353 (96%)	-0.16	3 (0%) 81 74	50, 83, 149, 196	0
2	B	410/429 (95%)	-0.13	2 (0%) 87 83	52, 101, 150, 179	0
2	D	410/429 (95%)	-0.06	2 (0%) 87 83	58, 107, 153, 180	0
All	All	1504/1564 (96%)	-0.11	16 (1%) 78 71	50, 93, 151, 196	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	273	VAL	5.1
1	A	274	GLU	3.0
1	A	266	PHE	2.9
1	A	269	ALA	2.7
1	C	344	ALA	2.7
2	B	225	ILE	2.6
1	C	264	VAL	2.5
1	A	275	ARG	2.3
1	A	271	ALA	2.3
2	B	316	GLY	2.3
1	C	345	GLY	2.3
1	A	267	GLY	2.2
2	D	47	SER	2.2
1	A	345	GLY	2.2
2	D	410	THR	2.1
1	A	326	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

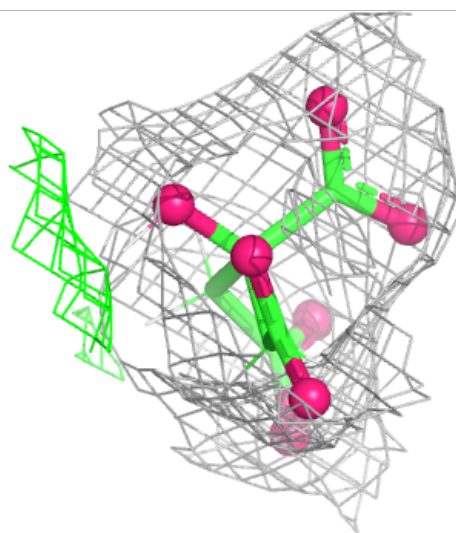
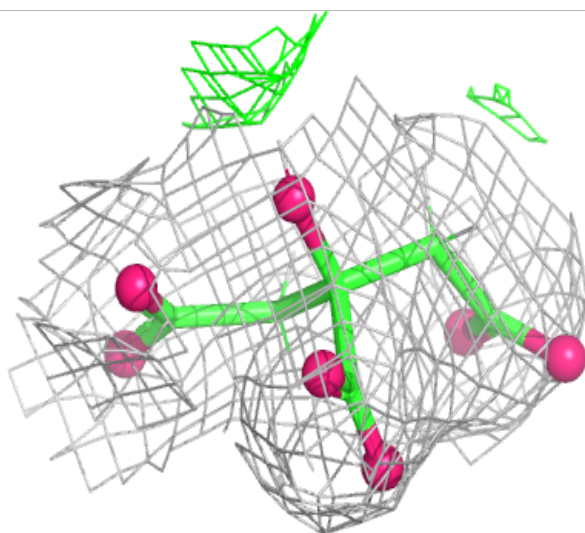
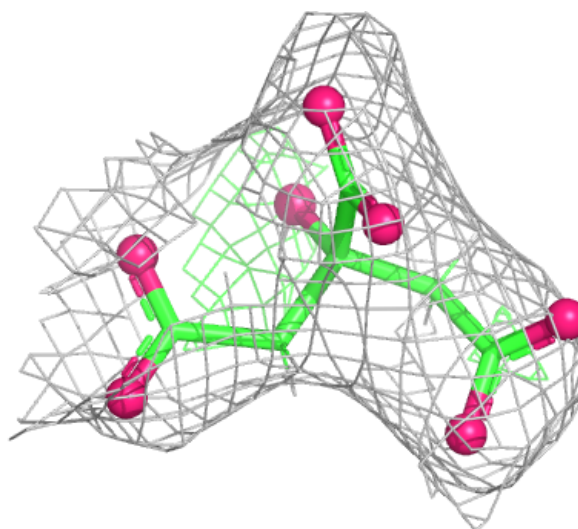
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	FLC	B	501	13/13	0.83	0.09	91,103,106,107	0
4	COA	C	403	48/48	0.89	0.10	77,96,121,126	0
4	COA	A	403	48/48	0.90	0.10	87,97,119,124	0
3	PGE	A	402	10/10	0.91	0.11	94,106,113,113	0
3	PGE	C	402	10/10	0.92	0.08	90,93,97,97	0
3	PGE	C	401	10/10	0.92	0.08	63,78,83,86	0
3	PGE	A	401	10/10	0.93	0.09	80,83,85,86	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.

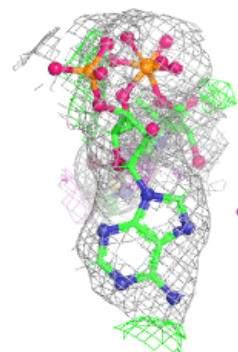
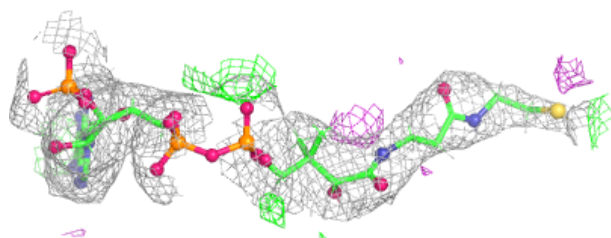
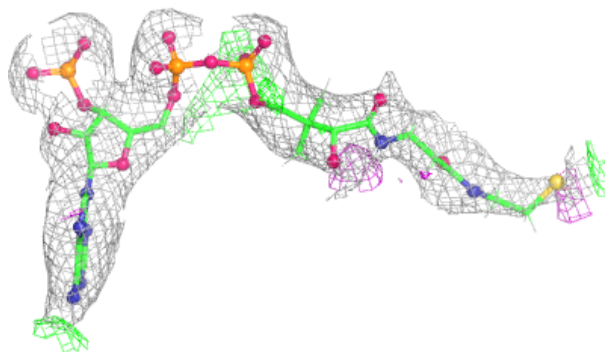
Electron density around FLC B 501:

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

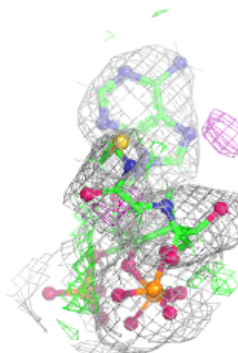
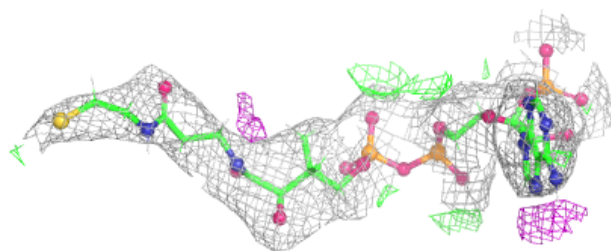
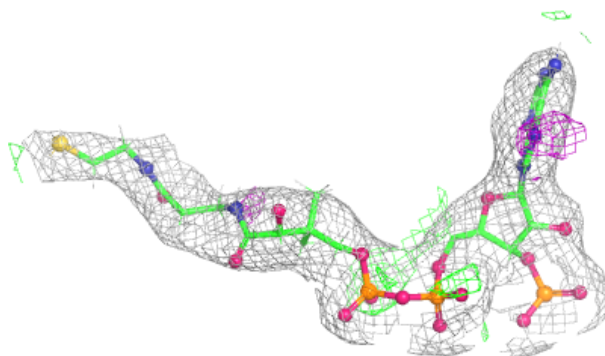


Electron density around COA C 403:

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

**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)



6.5 Other polymers [i](#)

There are no such residues in this entry.