



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 07:06 AM UTC

PDB ID : 8XXF / pdb_00008xxf
Title : TtCS, oxaloacetate, acetyl-CoA complex
Authors : Yang, L.; Fang, Y.J.
Deposited on : 2024-01-18
Resolution : 2.33 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:

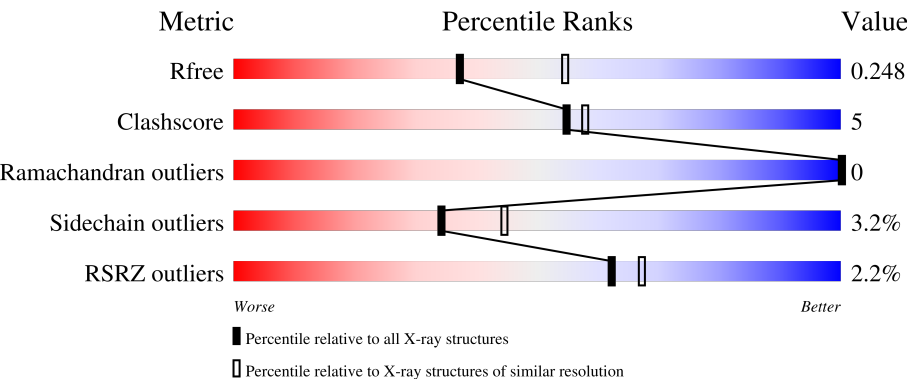
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal 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 i

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

The reported resolution of this entry is 2.33 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	3031 (2.36-2.32)
Clashscore	190562	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)
Sidechain outliers	187428	3095 (2.36-2.32)
RSRZ outliers	180081	3033 (2.36-2.32)

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	449	7% 82%14%..
1	B	449	% 88%11%. .
1	C	449	3% 84%13%..
1	D	449	88%10%. .
1	E	449	% 86%11%..

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Mol	Chain	Length	Quality of chain
1	F	449	82% 14% ••

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 22326 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 Citrate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	435	Total	C	N	O	S	0	0	0
			3502	2254	599	628	21			
1	B	449	Total	C	N	O	S	0	0	0
			3592	2309	616	646	21			
1	C	442	Total	C	N	O	S	0	0	0
			3537	2274	605	637	21			
1	D	440	Total	C	N	O	S	0	1	0
			3545	2280	610	634	21			
1	E	441	Total	C	N	O	S	0	0	0
			3531	2271	604	635	21			
1	F	441	Total	C	N	O	S	0	0	0
			3541	2277	608	635	21			

There are 42 discrepancies between the modelled and reference sequences:

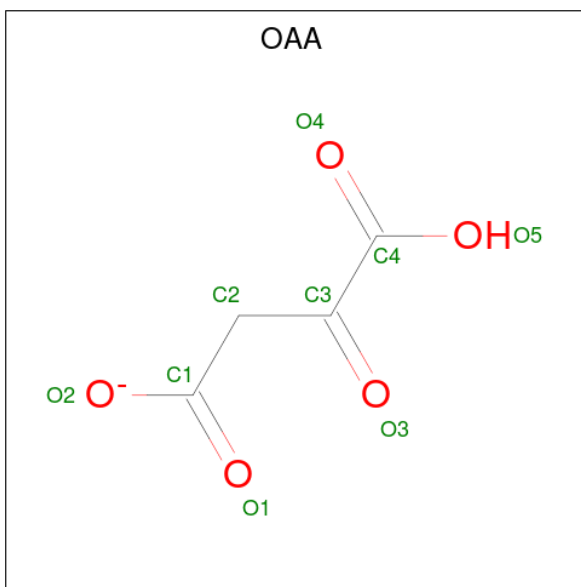
Chain	Residue	Modelled	Actual	Comment	Reference
A	443	LYS	-	expression tag	UNP A0A0S3QTD0
A	444	LEU	-	expression tag	UNP A0A0S3QTD0
A	445	ALA	-	expression tag	UNP A0A0S3QTD0
A	446	ALA	-	expression tag	UNP A0A0S3QTD0
A	447	ALA	-	expression tag	UNP A0A0S3QTD0
A	448	LEU	-	expression tag	UNP A0A0S3QTD0
A	449	GLU	-	expression tag	UNP A0A0S3QTD0
B	443	LYS	-	expression tag	UNP A0A0S3QTD0
B	444	LEU	-	expression tag	UNP A0A0S3QTD0
B	445	ALA	-	expression tag	UNP A0A0S3QTD0
B	446	ALA	-	expression tag	UNP A0A0S3QTD0
B	447	ALA	-	expression tag	UNP A0A0S3QTD0
B	448	LEU	-	expression tag	UNP A0A0S3QTD0
B	449	GLU	-	expression tag	UNP A0A0S3QTD0
C	443	LYS	-	expression tag	UNP A0A0S3QTD0
C	444	LEU	-	expression tag	UNP A0A0S3QTD0
C	445	ALA	-	expression tag	UNP A0A0S3QTD0

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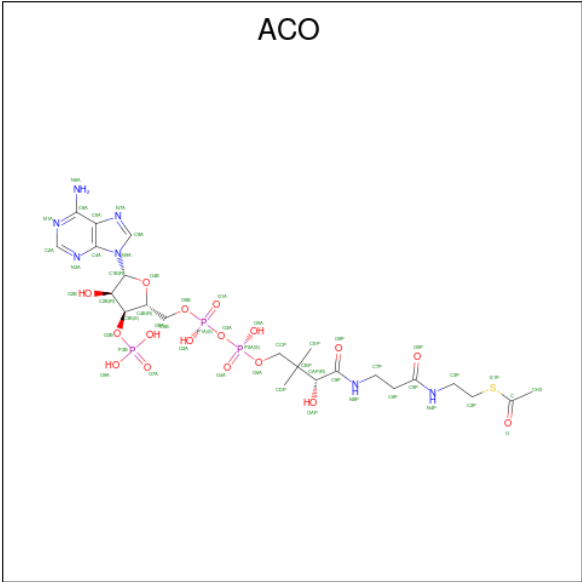
Chain	Residue	Modelled	Actual	Comment	Reference
C	446	ALA	-	expression tag	UNP A0A0S3QTD0
C	447	ALA	-	expression tag	UNP A0A0S3QTD0
C	448	LEU	-	expression tag	UNP A0A0S3QTD0
C	449	GLU	-	expression tag	UNP A0A0S3QTD0
D	443	LYS	-	expression tag	UNP A0A0S3QTD0
D	444	LEU	-	expression tag	UNP A0A0S3QTD0
D	445	ALA	-	expression tag	UNP A0A0S3QTD0
D	446	ALA	-	expression tag	UNP A0A0S3QTD0
D	447	ALA	-	expression tag	UNP A0A0S3QTD0
D	448	LEU	-	expression tag	UNP A0A0S3QTD0
D	449	GLU	-	expression tag	UNP A0A0S3QTD0
E	443	LYS	-	expression tag	UNP A0A0S3QTD0
E	444	LEU	-	expression tag	UNP A0A0S3QTD0
E	445	ALA	-	expression tag	UNP A0A0S3QTD0
E	446	ALA	-	expression tag	UNP A0A0S3QTD0
E	447	ALA	-	expression tag	UNP A0A0S3QTD0
E	448	LEU	-	expression tag	UNP A0A0S3QTD0
E	449	GLU	-	expression tag	UNP A0A0S3QTD0
F	443	LYS	-	expression tag	UNP A0A0S3QTD0
F	444	LEU	-	expression tag	UNP A0A0S3QTD0
F	445	ALA	-	expression tag	UNP A0A0S3QTD0
F	446	ALA	-	expression tag	UNP A0A0S3QTD0
F	447	ALA	-	expression tag	UNP A0A0S3QTD0
F	448	LEU	-	expression tag	UNP A0A0S3QTD0
F	449	GLU	-	expression tag	UNP A0A0S3QTD0

- Molecule 2 is OXALOACETATE ION (CCD ID: OAA) (formula: $C_4H_3O_5$) (labeled as "Ligand of Interest" by depositor).



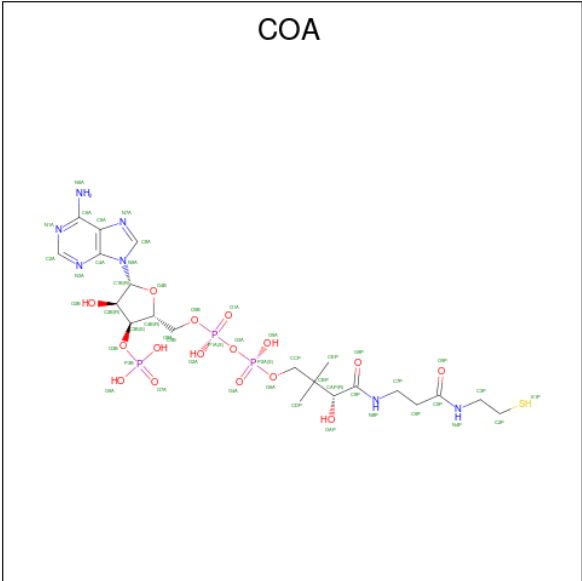
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			9	4	5		
2	B	1	Total	C	O	0	0
			9	4	5		
2	D	1	Total	C	O	0	0
			9	4	5		
2	E	1	Total	C	O	0	0
			9	4	5		
2	F	1	Total	C	O	0	0
			9	4	5		

- Molecule 3 is ACETYL COENZYME *A (CCD ID: ACO) (formula: $C_{23}H_{38}N_7O_{17}P_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	0	0
			51	23	7	17	3	1		
3	F	1	Total	C	N	O	P	S	0	0
			51	23	7	17	3	1		

- Molecule 4 is COENZYME A (CCD ID: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	D	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		

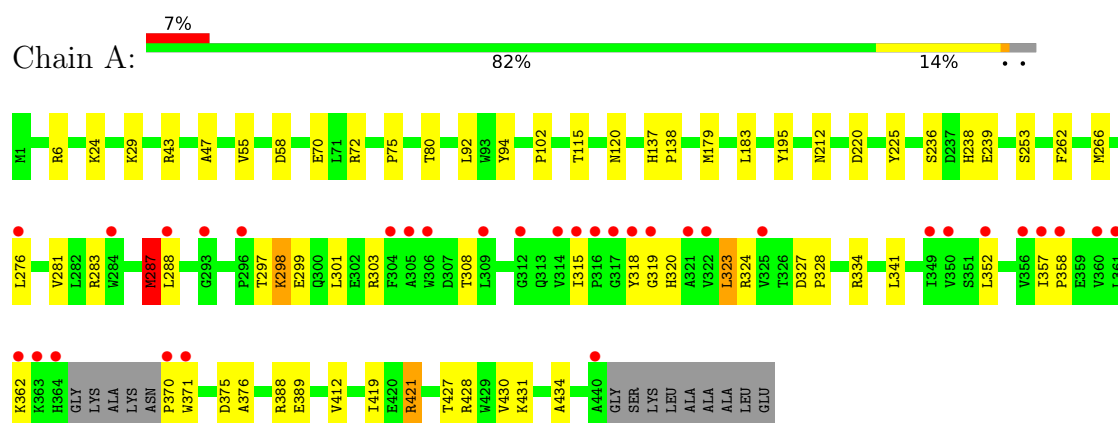
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	117	Total 117	O 117	0	0
5	B	152	Total 152	O 152	0	0
5	C	136	Total 136	O 136	0	0
5	D	164	Total 164	O 164	0	0
5	E	147	Total 147	O 147	0	0
5	F	167	Total 167	O 167	0	0

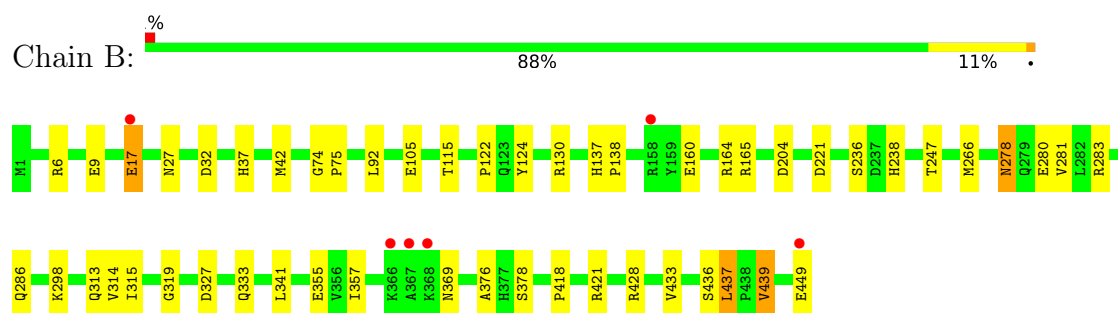
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

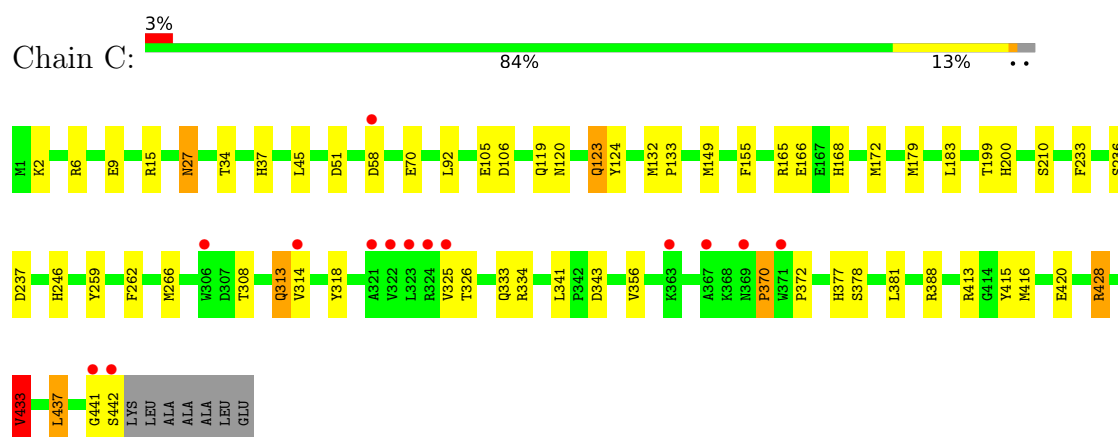
• Molecule 1: Citrate synthase



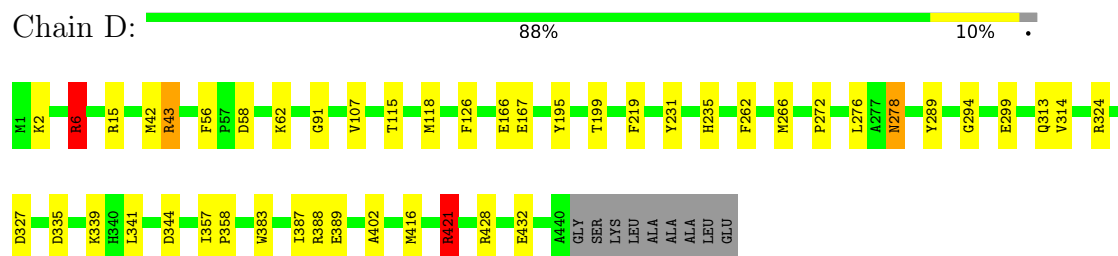
• Molecule 1: Citrate synthase



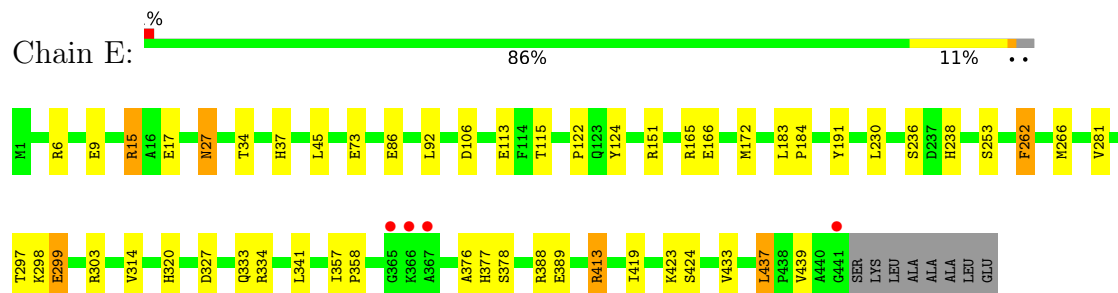
• Molecule 1: Citrate synthase



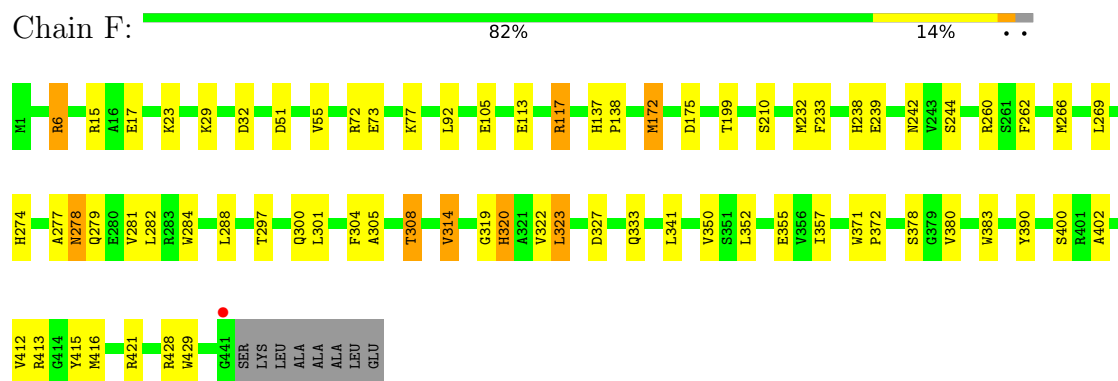
- Molecule 1: Citrate synthase



- Molecule 1: Citrate synthase



- Molecule 1: Citrate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	108.49Å 131.76Å 207.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.15 – 2.33 30.15 – 2.33	Depositor EDS
% Data completeness (in resolution range)	99.9 (30.15-2.33) 99.9 (30.15-2.33)	Depositor EDS
R_{merge}	0.32	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, R_{free}	0.187 , 0.245 0.194 , 0.248	Depositor DCC
R_{free} test set	6296 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	32.8	Xtriage
Anisotropy	0.107	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 40.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	22326	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.42% 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: OAA, COA, ACO

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	0.59	0/3597	1.17	7/4875 (0.1%)
1	B	0.61	0/3688	1.18	7/4999 (0.1%)
1	C	0.61	0/3633	1.19	15/4926 (0.3%)
1	D	0.60	0/3644	1.17	7/4938 (0.1%)
1	E	0.61	0/3627	1.15	8/4918 (0.2%)
1	F	0.62	0/3637	1.19	8/4929 (0.2%)
All	All	0.61	0/21826	1.17	52/29585 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
1	D	0	4
1	E	0	5
1	F	0	3
All	All	0	17

There are no bond length outliers.

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	433	VAL	N-CA-CB	-8.06	101.22	112.35
1	B	327	ASP	CA-CB-CG	7.56	120.16	112.60
1	D	327	ASP	CA-CB-CG	7.25	119.84	112.60
1	F	327	ASP	CA-CB-CG	7.00	119.60	112.60
1	D	6	ARG	CG-CD-NE	-6.85	96.94	112.00
1	D	6	ARG	N-CA-CB	-6.64	100.44	110.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	166	GLU	CB-CG-CD	6.35	123.39	112.60
1	F	314	VAL	N-CA-CB	-6.27	99.52	110.49
1	C	70	GLU	CB-CA-C	-6.25	97.98	110.42
1	C	199	THR	CA-CB-OG1	-6.14	100.39	109.60
1	B	130	ARG	N-CA-CB	6.12	119.76	110.28
1	E	262	PHE	CA-CB-CG	-6.06	107.74	113.80
1	A	80	THR	CA-CB-OG1	-5.98	100.64	109.60
1	F	320	HIS	CA-CB-CG	-5.93	107.87	113.80
1	A	375	ASP	CA-CB-CG	5.85	118.45	112.60
1	C	166	GLU	CB-CG-CD	5.83	122.52	112.60
1	C	370	PRO	N-CA-CB	-5.63	97.10	101.83
1	F	6	ARG	CG-CD-NE	-5.62	99.64	112.00
1	F	260	ARG	CD-NE-CZ	5.61	132.25	124.40
1	E	115	THR	CA-CB-OG1	-5.57	101.24	109.60
1	C	237	ASP	CA-CB-CG	5.53	118.13	112.60
1	B	32	ASP	CA-CB-CG	5.52	118.12	112.60
1	C	356	VAL	CA-C-N	5.52	124.75	120.33
1	C	356	VAL	C-N-CA	5.52	124.75	120.33
1	B	439	VAL	N-CA-CB	5.51	116.73	110.72
1	C	200	HIS	CA-CB-CG	-5.50	108.30	113.80
1	C	119	GLN	CB-CA-C	-5.47	99.21	109.72
1	F	6	ARG	N-CA-CB	-5.44	102.11	110.16
1	A	287	MET	CG-SD-CE	5.42	112.82	100.90
1	C	343	ASP	CA-CB-CG	5.40	118.00	112.60
1	F	175	ASP	CA-CB-CG	5.39	117.99	112.60
1	A	283	ARG	CA-C-N	5.38	127.93	120.29
1	A	283	ARG	C-N-CA	5.38	127.93	120.29
1	D	58	ASP	CA-CB-CG	5.36	117.96	112.60
1	A	318	TYR	CB-CA-C	5.33	119.36	109.70
1	B	278	ASN	CB-CA-C	5.33	120.79	110.46
1	E	320	HIS	CB-CA-C	5.32	118.61	109.51
1	A	58	ASP	CA-CB-CG	5.24	117.84	112.60
1	D	126	PHE	CA-CB-CG	-5.22	108.58	113.80
1	E	15	ARG	CB-CA-C	5.22	119.14	110.90
1	E	113	GLU	N-CA-CB	-5.21	102.45	110.16
1	C	124	TYR	N-CA-CB	5.21	118.24	110.22
1	C	388	ARG	CB-CA-C	-5.13	101.81	110.64
1	C	433	VAL	N-CA-CB	-5.12	105.29	112.35
1	E	327	ASP	CA-CB-CG	5.10	117.70	112.60
1	C	326	THR	CA-CB-OG1	-5.09	101.96	109.60
1	E	106	ASP	CA-CB-CG	5.08	117.68	112.60
1	B	247	THR	CA-CB-OG1	-5.06	102.01	109.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	335	ASP	CA-CB-CG	5.04	117.64	112.60
1	F	357	ILE	N-CA-CB	5.04	113.67	110.50
1	D	344	ASP	CA-CB-CG	5.03	117.63	112.60
1	C	233	PHE	N-CA-CB	-5.01	102.60	109.91

There are no chirality outliers.

All (17) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	334	ARG	Sidechain
1	A	388	ARG	Sidechain
1	A	421	ARG	Sidechain
1	A	6	ARG	Sidechain
1	A	72	ARG	Sidechain
1	D	324	ARG	Sidechain
1	D	421	ARG	Sidechain
1	D	43	ARG	Sidechain
1	D	6	ARG	Sidechain
1	E	151	ARG	Sidechain
1	E	303	ARG	Sidechain
1	E	388	ARG	Sidechain
1	E	413	ARG	Sidechain
1	E	73	GLU	Peptide
1	F	117	ARG	Sidechain
1	F	413	ARG	Sidechain
1	F	6	ARG	Sidechain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3502	0	3459	42	0
1	B	3592	0	3552	27	0
1	C	3537	0	3485	37	0
1	D	3545	0	3512	27	0
1	E	3531	0	3480	27	0
1	F	3541	0	3502	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	9	0	2	0	0
2	B	9	0	2	1	0
2	D	9	0	2	0	0
2	E	9	0	2	1	0
2	F	9	0	2	3	0
3	A	51	0	34	15	0
3	F	51	0	34	7	0
4	D	48	0	32	1	0
5	A	117	0	0	2	0
5	B	152	0	0	6	0
5	C	136	0	0	7	0
5	D	164	0	0	2	0
5	E	147	0	0	2	0
5	F	167	0	0	1	0
All	All	22326	0	21100	205	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 5.

All (205) 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:D:167:GLU:HG3	5:D:755:HOH:O	1.55	1.06
1:A:43:ARG:HH11	3:A:502:ACO:CCP	1.70	1.05
3:A:502:ACO:H72	3:A:502:ACO:H21	1.38	1.04
1:C:2:LYS:HB3	5:C:614:HOH:O	1.59	1.01
1:A:43:ARG:HH11	3:A:502:ACO:H121	1.34	0.90
1:A:43:ARG:HH11	3:A:502:ACO:H122	1.40	0.83
1:F:297:THR:H	1:F:300:GLN:HE21	1.29	0.80
1:F:274:HIS:ND1	3:F:502:ACO:HH31	1.97	0.80
1:A:43:ARG:NH1	3:A:502:ACO:H121	1.97	0.79
1:A:43:ARG:HE	3:A:502:ACO:H121	1.52	0.75
1:C:92:LEU:HD21	1:C:236:SER:OG	1.87	0.75
1:C:120:ASN:HA	1:F:199:THR:HG21	1.69	0.74
1:D:421:ARG:HD2	2:F:501:OAA:O1	1.88	0.74
1:D:278:ASN:C	1:D:278:ASN:HD22	1.98	0.71
1:F:304:PHE:O	1:F:308:THR:HG22	1.90	0.71
1:F:282:LEU:HD21	1:F:383:TRP:CE3	2.26	0.71
1:F:284:TRP:HE1	1:F:308:THR:HG21	1.57	0.70
1:F:274:HIS:HA	3:F:502:ACO:HH32	1.77	0.66
1:E:27:ASN:C	1:E:27:ASN:HD22	2.03	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:242:ASN:HB3	2:F:501:OAA:H21	1.80	0.63
1:A:301:LEU:HD22	1:A:352:LEU:HD23	1.78	0.63
1:F:238:HIS:O	1:F:239:GLU:HB2	1.99	0.63
1:F:278:ASN:HD22	1:F:279:GLN:N	1.96	0.63
1:B:74:GLY:HA2	5:B:615:HOH:O	1.97	0.63
1:A:43:ARG:NE	3:A:502:ACO:H121	2.13	0.62
1:B:37:HIS:HE1	5:B:722:HOH:O	1.81	0.62
1:F:172:MET:HA	1:F:172:MET:HE3	1.81	0.62
1:F:262:PHE:CE1	1:F:266:MET:HE3	2.35	0.61
1:E:34:THR:H	1:E:37:HIS:HD2	1.46	0.61
1:E:333:GLN:HE22	1:E:378:SER:HB3	1.66	0.60
1:A:281:VAL:HG11	1:A:376:ALA:HA	1.83	0.60
1:C:2:LYS:HD2	5:C:614:HOH:O	2.00	0.60
1:F:297:THR:HG22	1:F:300:GLN:HG3	1.84	0.60
3:A:502:ACO:H32	1:B:165:ARG:HH21	1.66	0.60
1:A:43:ARG:CZ	3:A:502:ACO:H121	2.32	0.59
1:F:55:VAL:HG23	1:F:239:GLU:HG3	1.84	0.59
1:F:333:GLN:HE22	1:F:378:SER:HB3	1.67	0.59
1:A:55:VAL:HG23	1:A:239:GLU:HG3	1.85	0.59
1:A:120:ASN:HA	1:D:199:THR:HG21	1.85	0.58
1:C:428:ARG:NH2	5:C:503:HOH:O	2.36	0.57
1:D:278:ASN:C	1:D:278:ASN:ND2	2.62	0.57
1:F:305:ALA:O	1:F:308:THR:HG23	2.05	0.57
3:F:502:ACO:H141	3:F:502:ACO:H32	1.86	0.57
1:E:262:PHE:CZ	1:E:266:MET:HE3	2.40	0.57
1:A:299:GLU:OE2	1:A:303:ARG:NH1	2.35	0.56
1:F:269:LEU:HA	1:F:274:HIS:CD2	2.40	0.56
1:B:164:ARG:NH2	5:B:602:HOH:O	2.38	0.56
3:A:502:ACO:H133	1:B:418:PRO:HG3	1.87	0.56
1:C:123:GLN:HG2	5:C:501:HOH:O	2.06	0.55
1:D:272:PRO:HA	1:D:276:LEU:HG	1.89	0.55
1:B:266:MET:HA	1:B:266:MET:HE2	1.89	0.55
1:C:428:ARG:HD3	5:C:525:HOH:O	2.06	0.54
1:D:262:PHE:CE1	1:D:266:MET:HE3	2.42	0.54
1:A:315:ILE:HG21	1:A:357:ILE:HG21	1.90	0.54
1:F:274:HIS:HA	3:F:502:ACO:CH3	2.37	0.53
1:F:15:ARG:NE	1:F:416:MET:HE3	2.23	0.53
1:E:165:ARG:HD2	5:E:700:HOH:O	2.08	0.53
1:C:433:VAL:HG12	1:C:437:LEU:HD22	1.91	0.52
1:F:320:HIS:CG	1:F:323:LEU:HB2	2.44	0.52
1:B:6:ARG:NH1	1:B:9:GLU:OE2	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:333:GLN:HE22	1:C:378:SER:HA	1.74	0.52
1:F:297:THR:HG23	1:F:300:GLN:H	1.75	0.52
1:A:362:LYS:NZ	5:A:602:HOH:O	2.34	0.52
1:C:45:LEU:HD21	1:E:45:LEU:HD21	1.91	0.52
1:D:166:GLU:CD	1:D:416:MET:HE1	2.35	0.51
1:D:231:TYR:CE2	1:D:235:HIS:CE1	2.98	0.51
1:A:281:VAL:HG21	1:A:376:ALA:HA	1.93	0.51
1:A:430:VAL:O	1:A:434:ALA:HB2	2.11	0.51
1:C:155:PHE:CD2	1:C:172:MET:HE2	2.45	0.51
1:D:167:GLU:CG	5:D:755:HOH:O	2.34	0.51
1:F:232:MET:HA	1:F:400:SER:HB2	1.93	0.51
1:A:92:LEU:HD21	1:A:236:SER:OG	2.11	0.51
1:E:238:HIS:HD1	2:E:501:OAA:C3	2.23	0.51
1:C:58:ASP:O	1:C:325:VAL:CG2	2.59	0.50
1:B:75:PRO:C	5:B:615:HOH:O	2.54	0.50
1:E:15:ARG:HD2	5:E:682:HOH:O	2.12	0.50
1:E:262:PHE:CE1	1:E:266:MET:HE3	2.47	0.50
1:F:428:ARG:HD3	1:F:429:TRP:N	2.27	0.49
1:D:2:LYS:O	1:D:6:ARG:HB2	2.12	0.49
1:D:195:TYR:CG	1:D:389:GLU:HG2	2.47	0.49
1:E:357:ILE:N	1:E:358:PRO:CD	2.75	0.49
1:F:51:ASP:OD2	1:F:415:TYR:OH	2.30	0.49
1:B:75:PRO:HA	5:B:615:HOH:O	2.12	0.49
1:B:122:PRO:HB3	1:B:124:TYR:CE2	2.48	0.49
1:E:433:VAL:HG12	1:E:437:LEU:HD13	1.95	0.49
1:B:333:GLN:HE22	1:B:378:SER:HB3	1.77	0.49
1:D:15:ARG:HD3	1:D:416:MET:HE3	1.94	0.48
1:E:281:VAL:HG11	1:E:376:ALA:HA	1.95	0.48
1:A:262:PHE:CE1	1:A:266:MET:HE3	2.49	0.48
1:D:15:ARG:CD	1:D:416:MET:HE3	2.44	0.48
1:E:27:ASN:C	1:E:27:ASN:ND2	2.71	0.48
1:A:319:GLY:HA2	5:A:698:HOH:O	2.13	0.48
3:A:502:ACO:H142	3:A:502:ACO:O2A	2.13	0.48
1:E:34:THR:H	1:E:37:HIS:CD2	2.27	0.48
1:E:183:LEU:N	1:E:184:PRO:CD	2.77	0.48
1:A:266:MET:HA	1:A:266:MET:HE2	1.96	0.47
1:C:6:ARG:NH1	1:C:9:GLU:OE2	2.47	0.47
1:D:42:MET:O	1:D:43:ARG:C	2.58	0.47
1:C:51:ASP:OD2	1:C:415:TYR:OH	2.28	0.47
1:C:441:GLY:O	1:C:442:SER:C	2.58	0.47
1:C:333:GLN:HE21	1:C:381:LEU:HD12	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:502:ACO:H141	3:F:502:ACO:H62	1.96	0.47
1:A:238:HIS:O	1:A:239:GLU:HB2	2.14	0.47
1:A:315:ILE:HD13	1:A:357:ILE:HG23	1.97	0.47
3:A:502:ACO:H133	1:B:418:PRO:CG	2.45	0.47
1:A:253:SER:HB2	1:A:419:ILE:HA	1.97	0.47
1:D:56:PHE:CE1	1:D:62:LYS:HD2	2.50	0.47
1:C:58:ASP:O	1:C:325:VAL:HG21	2.15	0.46
1:B:281:VAL:HG11	1:B:376:ALA:HA	1.97	0.46
1:A:370:PRO:HG2	1:A:371:TRP:CD1	2.51	0.46
1:D:262:PHE:CZ	1:D:402:ALA:HB2	2.50	0.46
1:F:278:ASN:HD22	1:F:279:GLN:H	1.63	0.46
1:D:289:TYR:CE1	1:D:294:GLY:HA2	2.51	0.46
1:F:262:PHE:CZ	1:F:402:ALA:HB2	2.51	0.46
1:F:350:VAL:CG2	1:F:380:VAL:HG11	2.45	0.46
1:C:246:HIS:NE2	1:C:420:GLU:OE1	2.33	0.46
1:F:297:THR:HG22	1:F:300:GLN:CG	2.45	0.46
1:C:132:MET:O	1:C:133:PRO:C	2.58	0.46
1:F:92:LEU:HD22	1:F:233:PHE:CD1	2.51	0.46
1:A:43:ARG:NH1	3:A:502:ACO:CCP	2.52	0.46
1:C:179:MET:O	1:C:183:LEU:HG	2.16	0.46
1:C:262:PHE:CE1	1:C:266:MET:HE3	2.52	0.45
1:D:383:TRP:CZ3	1:D:388:ARG:HB3	2.50	0.45
1:E:92:LEU:HD21	1:E:236:SER:OG	2.17	0.45
1:B:92:LEU:HD21	1:B:236:SER:OG	2.16	0.45
1:B:137:HIS:CG	1:B:138:PRO:HD2	2.51	0.45
1:B:280:GLU:HB3	5:B:698:HOH:O	2.16	0.45
1:A:220:ASP:OD1	1:A:225:TYR:OH	2.29	0.45
1:E:191:TYR:OH	1:E:389:GLU:OE2	2.29	0.45
1:F:274:HIS:ND1	3:F:502:ACO:CH3	2.73	0.45
1:B:238:HIS:ND1	2:B:501:OAA:O2	2.49	0.45
1:C:15:ARG:HD2	1:C:416:MET:HE3	1.98	0.45
1:F:282:LEU:HD23	1:F:390:TYR:HB3	1.99	0.45
1:C:2:LYS:HG3	1:C:106:ASP:OD1	2.17	0.45
1:A:179:MET:O	1:A:183:LEU:HG	2.17	0.44
1:A:287:MET:HE2	1:A:288:LEU:HA	1.99	0.44
1:B:298:LYS:HE2	1:B:355:GLU:OE1	2.17	0.44
1:C:308:THR:HG22	1:C:313:GLN:HB2	1.99	0.44
1:B:204:ASP:C	1:B:204:ASP:OD1	2.60	0.44
1:C:333:GLN:HE22	1:C:378:SER:CA	2.30	0.44
1:D:266:MET:HA	1:D:266:MET:HE2	1.99	0.44
1:D:357:ILE:N	1:D:358:PRO:CD	2.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:72:ARG:O	1:F:77:LYS:NZ	2.40	0.43
1:F:320:HIS:CB	1:F:323:LEU:HB2	2.48	0.43
1:A:29:LYS:O	1:B:437:LEU:HG	2.18	0.43
1:A:43:ARG:NH2	1:B:421:ARG:HB3	2.32	0.43
1:F:262:PHE:CZ	1:F:266:MET:HE3	2.52	0.43
1:A:297:THR:O	1:A:298:LYS:C	2.62	0.43
1:A:431:LYS:HE2	1:B:17:GLU:OE2	2.17	0.43
1:C:27:ASN:C	1:C:27:ASN:HD22	2.26	0.43
1:F:242:ASN:HB3	2:F:501:OAA:C2	2.47	0.43
1:F:297:THR:HG22	1:F:300:GLN:HE21	1.83	0.43
1:A:70:GLU:HG2	1:A:75:PRO:HD2	2.00	0.43
1:B:283:ARG:HA	1:B:286:GLN:HE21	1.84	0.43
1:F:297:THR:H	1:F:300:GLN:NE2	2.04	0.43
1:A:195:TYR:CG	1:A:389:GLU:HG2	2.54	0.43
1:A:427:THR:O	1:A:428:ARG:C	2.62	0.43
1:E:6:ARG:NH1	1:E:9:GLU:OE2	2.52	0.43
1:F:371:TRP:HB3	1:F:372:PRO:HD2	2.00	0.43
1:A:357:ILE:N	1:A:358:PRO:CD	2.82	0.42
1:C:34:THR:H	1:C:37:HIS:CD2	2.37	0.42
3:A:502:ACO:H32	1:B:165:ARG:NH2	2.34	0.42
1:B:319:GLY:HA2	1:B:369:ASN:O	2.19	0.42
1:D:91:GLY:HA2	1:D:107:VAL:HG22	2.01	0.42
1:E:253:SER:HB2	1:E:419:ILE:HA	2.00	0.42
1:A:137:HIS:CG	1:A:138:PRO:HD2	2.55	0.42
1:C:165:ARG:HA	1:C:168:HIS:CD2	2.55	0.42
1:F:29:LYS:NZ	1:F:32:ASP:OD1	2.44	0.42
1:A:327:ASP:OD1	1:A:328:PRO:HD2	2.19	0.42
3:A:502:ACO:H21	3:A:502:ACO:C7P	2.28	0.42
1:E:297:THR:OG1	1:E:299:GLU:HG2	2.20	0.42
1:F:319:GLY:HA3	3:F:502:ACO:OAP	2.20	0.42
1:C:149:MET:HG2	1:C:259:TYR:CE1	2.55	0.42
1:E:334:ARG:HA	1:E:377:HIS:NE2	2.35	0.42
1:A:320:HIS:HB3	1:A:323:LEU:HB2	2.02	0.42
1:C:413:ARG:HA	1:C:413:ARG:CZ	2.50	0.42
1:E:172:MET:HE3	1:E:413:ARG:HD3	2.02	0.42
1:D:428[A]:ARG:NH1	1:D:432:GLU:OE2	2.44	0.41
1:C:333:GLN:NE2	1:C:378:SER:HA	2.34	0.41
1:D:219:PHE:CZ	1:D:387:ILE:HG13	2.55	0.41
1:E:423:LYS:HE3	1:E:424:SER:O	2.20	0.41
1:F:421:ARG:HH11	1:F:421:ARG:HG2	1.85	0.41
1:E:183:LEU:HB2	1:E:184:PRO:HD3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:318:TYR:CE1	1:C:372:PRO:HB3	2.55	0.41
1:F:266:MET:HA	1:F:266:MET:HE2	2.01	0.41
1:F:15:ARG:HE	1:F:416:MET:HE3	1.84	0.41
1:B:315:ILE:HD13	1:B:357:ILE:HD12	2.01	0.41
1:C:45:LEU:HD21	1:E:45:LEU:CD2	2.50	0.41
1:D:421:ARG:NH2	1:F:239:GLU:OE2	2.54	0.41
1:F:244:SER:CB	1:F:274:HIS:HE2	2.33	0.41
1:F:277:ALA:O	1:F:281:VAL:HG23	2.20	0.41
1:A:94:TYR:CD1	1:A:102:PRO:HB3	2.56	0.41
1:A:47:ALA:HB1	1:B:42:MET:HE2	2.03	0.41
1:C:2:LYS:CB	5:C:614:HOH:O	2.40	0.41
1:C:433:VAL:HG13	1:C:437:LEU:HD13	2.02	0.41
1:C:123:GLN:CD	5:C:501:HOH:O	2.64	0.41
1:F:137:HIS:HA	1:F:138:PRO:HD3	1.96	0.41
1:E:86:GLU:OE2	1:E:230:LEU:HD13	2.20	0.40
1:F:23:LYS:NZ	5:F:609:HOH:O	2.45	0.40
1:F:113:GLU:HG3	1:F:117:ARG:HE	1.86	0.40
1:C:334:ARG:HA	1:C:377:HIS:NE2	2.37	0.40
1:E:122:PRO:HB3	1:E:124:TYR:CE2	2.56	0.40
1:F:428:ARG:HD3	1:F:428:ARG:C	2.46	0.40
1:A:120:ASN:CA	1:D:199:THR:HG21	2.50	0.40
1:D:314:VAL:HA	4:D:502:COA:C2A	2.51	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	431/449 (96%)	419 (97%)	12 (3%)	0	100	100
1	B	447/449 (100%)	439 (98%)	8 (2%)	0	100	100
1	C	440/449 (98%)	425 (97%)	15 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	439/449 (98%)	429 (98%)	10 (2%)	0	100	100
1	E	439/449 (98%)	429 (98%)	10 (2%)	0	100	100
1	F	439/449 (98%)	428 (98%)	11 (2%)	0	100	100
All	All	2635/2694 (98%)	2569 (98%)	66 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	368/376 (98%)	356 (97%)	12 (3%)	33	43
1	B	375/376 (100%)	360 (96%)	15 (4%)	28	36
1	C	370/376 (98%)	359 (97%)	11 (3%)	36	47
1	D	372/376 (99%)	363 (98%)	9 (2%)	43	55
1	E	369/376 (98%)	361 (98%)	8 (2%)	45	58
1	F	371/376 (99%)	355 (96%)	16 (4%)	26	33
All	All	2225/2256 (99%)	2154 (97%)	71 (3%)	34	44

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	LYS
1	A	115	THR
1	A	212	ASN
1	A	276	LEU
1	A	287	MET
1	A	298	LYS
1	A	308	THR
1	A	323	LEU
1	A	324	ARG
1	A	341	LEU

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Mol	Chain	Res	Type
1	A	412	VAL
1	A	421	ARG
1	B	17	GLU
1	B	27	ASN
1	B	105	GLU
1	B	115	THR
1	B	160	GLU
1	B	221	ASP
1	B	278	ASN
1	B	313	GLN
1	B	314	VAL
1	B	341	LEU
1	B	428	ARG
1	B	436	SER
1	B	437	LEU
1	B	439	VAL
1	B	449	GLU
1	C	27	ASN
1	C	105	GLU
1	C	123	GLN
1	C	210	SER
1	C	313	GLN
1	C	314	VAL
1	C	341	LEU
1	C	370	PRO
1	C	428	ARG
1	C	433	VAL
1	C	437	LEU
1	D	6	ARG
1	D	115	THR
1	D	118	MET
1	D	278	ASN
1	D	299	GLU
1	D	313	GLN
1	D	339	LYS
1	D	341	LEU
1	D	421	ARG
1	E	17	GLU
1	E	27	ASN
1	E	298	LYS
1	E	299	GLU
1	E	314	VAL

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Mol	Chain	Res	Type
1	E	341	LEU
1	E	437	LEU
1	E	439	VAL
1	F	17	GLU
1	F	73	GLU
1	F	105	GLU
1	F	172	MET
1	F	210	SER
1	F	278	ASN
1	F	288	LEU
1	F	301	LEU
1	F	308	THR
1	F	314	VAL
1	F	322	VAL
1	F	323	LEU
1	F	341	LEU
1	F	352	LEU
1	F	355	GLU
1	F	412	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	HIS
1	A	120	ASN
1	A	150	GLN
1	A	248	ASN
1	A	313	GLN
1	B	37	HIS
1	B	123	GLN
1	B	248	ASN
1	B	278	ASN
1	B	279	GLN
1	B	286	GLN
1	B	333	GLN
1	B	364	HIS
1	B	408	GLN
1	C	27	ASN
1	C	37	HIS
1	C	248	ASN
1	C	279	GLN
1	C	333	GLN

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Mol	Chain	Res	Type
1	C	364	HIS
1	D	37	HIS
1	D	120	ASN
1	D	150	GLN
1	D	248	ASN
1	D	278	ASN
1	D	310	ASN
1	D	364	HIS
1	E	27	ASN
1	E	37	HIS
1	E	248	ASN
1	E	286	GLN
1	E	320	HIS
1	E	333	GLN
1	E	408	GLN
1	F	278	ASN
1	F	300	GLN
1	F	333	GLN
1	F	408	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

8 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	$\# Z > 2$
2	OAA	D	501	-	8,8,8	4.19	2 (25%)	8,10,10	2.24	3 (37%)
2	OAA	F	501	-	8,8,8	8.88	2 (25%)	8,10,10	3.56	3 (37%)
3	ACO	F	502	-	51,53,53	0.73	2 (3%)	73,79,79	1.14	7 (9%)
4	COA	D	502	-	47,50,50	0.52	0	69,75,75	1.05	4 (5%)
2	OAA	A	501	-	8,8,8	5.19	2 (25%)	8,10,10	1.62	3 (37%)
2	OAA	E	501	-	8,8,8	4.85	2 (25%)	8,10,10	1.77	2 (25%)
3	ACO	A	502	-	51,53,53	0.86	3 (5%)	73,79,79	1.18	4 (5%)
2	OAA	B	501	-	8,8,8	5.08	3 (37%)	8,10,10	1.36	1 (12%)

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
2	OAA	D	501	-	-	0/8/8/8	-
2	OAA	F	501	-	-	0/8/8/8	-
3	ACO	F	502	-	-	15/51/67/67	0/3/3/3
4	COA	D	502	-	-	4/48/64/64	0/3/3/3
2	OAA	A	501	-	-	1/8/8/8	-
2	OAA	E	501	-	-	1/8/8/8	-
3	ACO	A	502	-	-	21/51/67/67	0/3/3/3
2	OAA	B	501	-	-	0/8/8/8	-

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	501	OAA	C3-C4	-24.69	1.16	1.53
2	A	501	OAA	C3-C4	-14.23	1.32	1.53
2	B	501	OAA	C3-C4	-13.86	1.32	1.53
2	E	501	OAA	C3-C4	-13.01	1.33	1.53
2	D	501	OAA	C3-C4	-10.84	1.37	1.53
2	D	501	OAA	O2-C1	-4.04	1.17	1.30
2	F	501	OAA	O5-C4	-3.58	1.20	1.30
3	A	502	ACO	P2A-O3A	3.10	1.62	1.59
3	A	502	ACO	P1A-O3A	2.87	1.62	1.59
2	E	501	OAA	O5-C4	-2.86	1.22	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	502	ACO	C-S1P	2.81	1.90	1.75
2	A	501	OAA	O5-C4	-2.76	1.23	1.30
3	A	502	ACO	P3B-O3B	2.61	1.64	1.59
2	B	501	OAA	O2-C1	-2.29	1.23	1.30
2	B	501	OAA	O5-C4	-2.23	1.24	1.30
3	F	502	ACO	P3B-O3B	2.15	1.63	1.59

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	501	OAA	O3-C3-C4	-8.88	106.99	119.67
3	A	502	ACO	C2P-S1P-C	6.40	132.21	101.42
3	F	502	ACO	C2P-S1P-C	4.05	120.90	101.42
3	F	502	ACO	P3B-O3B-C3B	-3.81	113.26	123.43
2	D	501	OAA	O4-C4-C3	-3.77	117.12	121.81
2	E	501	OAA	O3-C3-C4	-3.42	114.79	119.67
2	D	501	OAA	O5-C4-C3	3.31	122.76	113.59
4	D	502	COA	O6A-CCP-CBP	-3.25	105.33	110.55
4	D	502	COA	O3B-C3B-C2B	-3.08	100.61	111.68
2	F	501	OAA	O3-C3-C2	2.97	124.98	120.41
3	A	502	ACO	C7P-C6P-C5P	2.87	117.17	112.39
3	F	502	ACO	CDP-CBP-CCP	2.81	112.86	108.22
2	D	501	OAA	O3-C3-C2	-2.61	116.40	120.41
3	F	502	ACO	CEP-CBP-CAP	2.57	113.14	108.77
4	D	502	COA	P3B-O3B-C3B	-2.53	116.68	123.43
2	A	501	OAA	O3-C3-C2	-2.44	116.65	120.41
2	F	501	OAA	O5-C4-C3	-2.37	107.03	113.59
3	F	502	ACO	O5A-P2A-O4A	2.36	123.41	112.44
2	A	501	OAA	O4-C4-C3	-2.35	118.88	121.81
3	F	502	ACO	O6A-P2A-O4A	-2.30	99.81	108.94
2	B	501	OAA	O3-C3-C4	-2.21	116.51	119.67
2	A	501	OAA	O5-C4-C3	2.21	119.72	113.59
4	D	502	COA	CDP-CBP-CAP	2.18	112.49	108.77
3	A	502	ACO	C6P-C7P-N8P	-2.15	107.42	112.00
3	A	502	ACO	P3B-O3B-C3B	-2.08	117.88	123.43
2	E	501	OAA	O3-C3-C2	-2.05	117.26	120.41
3	F	502	ACO	C6P-C5P-N4P	2.03	120.05	116.34

There are no chirality outliers.

All (42) torsion outliers are listed below:

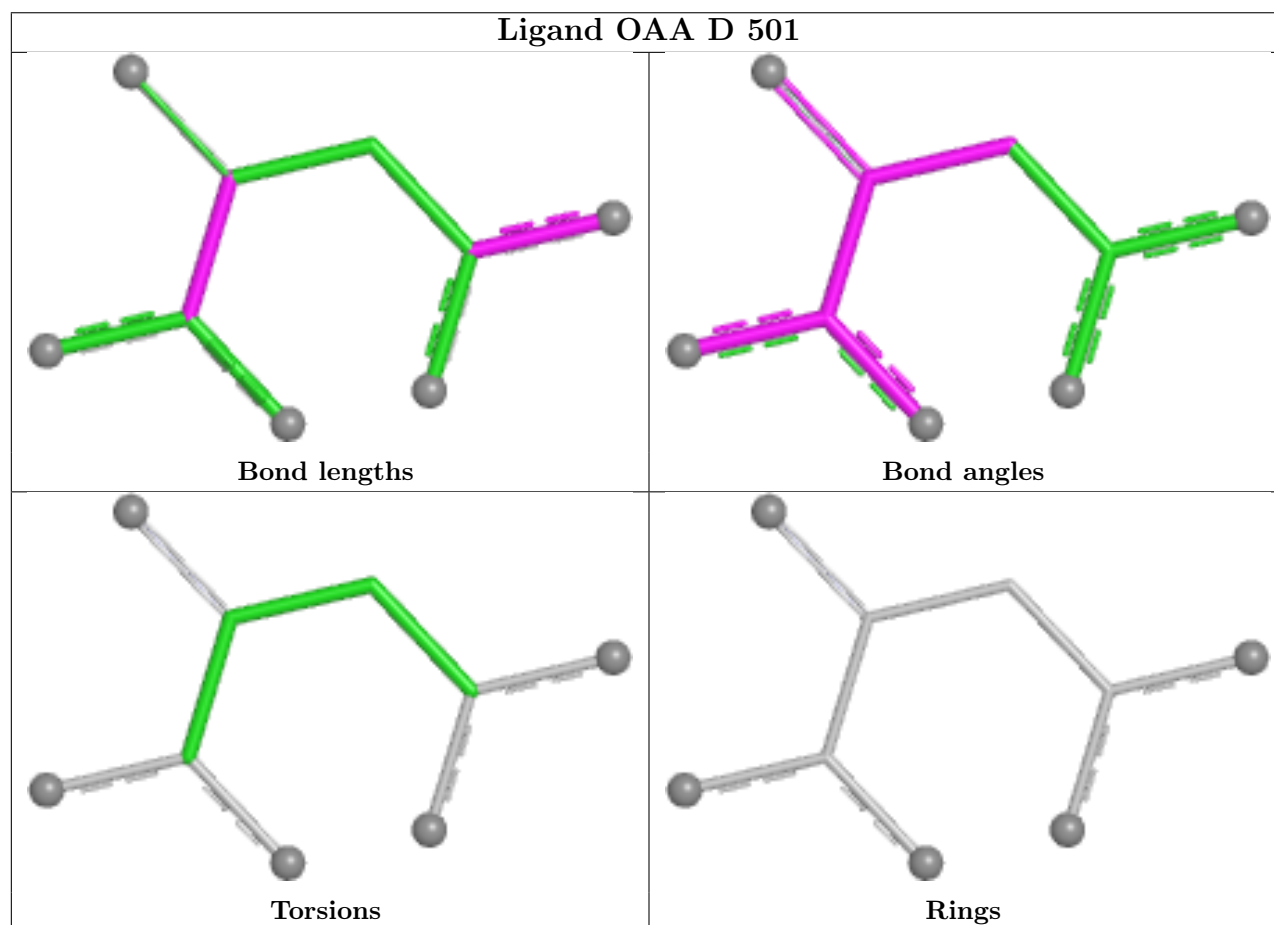
Mol	Chain	Res	Type	Atoms
3	A	502	ACO	C5B-O5B-P1A-O1A
3	A	502	ACO	C5B-O5B-P1A-O2A
3	A	502	ACO	C5B-O5B-P1A-O3A
3	A	502	ACO	CCP-O6A-P2A-O3A
3	A	502	ACO	CCP-O6A-P2A-O4A
3	A	502	ACO	CCP-O6A-P2A-O5A
3	A	502	ACO	OAP-CAP-CBP-CCP
3	A	502	ACO	C9P-CAP-CBP-CCP
3	A	502	ACO	OAP-CAP-CBP-CDP
3	A	502	ACO	C9P-CAP-CBP-CDP
3	A	502	ACO	CAP-C9P-N8P-C7P
3	A	502	ACO	C3P-C2P-S1P-C
3	F	502	ACO	CDP-CBP-CCP-O6A
3	F	502	ACO	CEP-CBP-CCP-O6A
3	F	502	ACO	CAP-CBP-CCP-O6A
3	F	502	ACO	OAP-CAP-CBP-CCP
3	F	502	ACO	C9P-CAP-CBP-CCP
3	F	502	ACO	OAP-CAP-CBP-CDP
3	F	502	ACO	C9P-CAP-CBP-CDP
3	F	502	ACO	OAP-CAP-CBP-CEP
3	F	502	ACO	C9P-CAP-CBP-CEP
3	F	502	ACO	C6P-C5P-N4P-C3P
3	F	502	ACO	O5P-C5P-N4P-C3P
3	F	502	ACO	C3P-C2P-S1P-C
3	F	502	ACO	O-C-S1P-C2P
3	F	502	ACO	CH3-C-S1P-C2P
4	D	502	COA	CCP-O6A-P2A-O4A
3	A	502	ACO	O9P-C9P-N8P-C7P
3	A	502	ACO	C6P-C5P-N4P-C3P
3	A	502	ACO	O5P-C5P-N4P-C3P
3	A	502	ACO	OAP-CAP-CBP-CEP
3	A	502	ACO	P1A-O3A-P2A-O6A
3	A	502	ACO	C3B-C4B-C5B-O5B
3	F	502	ACO	C5B-O5B-P1A-O1A
4	D	502	COA	C5B-O5B-P1A-O1A
4	D	502	COA	CCP-O6A-P2A-O3A
4	D	502	COA	CCP-O6A-P2A-O5A
2	E	501	OAA	O1-C1-C2-C3
3	A	502	ACO	O4B-C4B-C5B-O5B
3	A	502	ACO	O5P-C5P-C6P-C7P
2	A	501	OAA	C1-C2-C3-O3
3	A	502	ACO	C9P-CAP-CBP-CEP

There are no ring outliers.

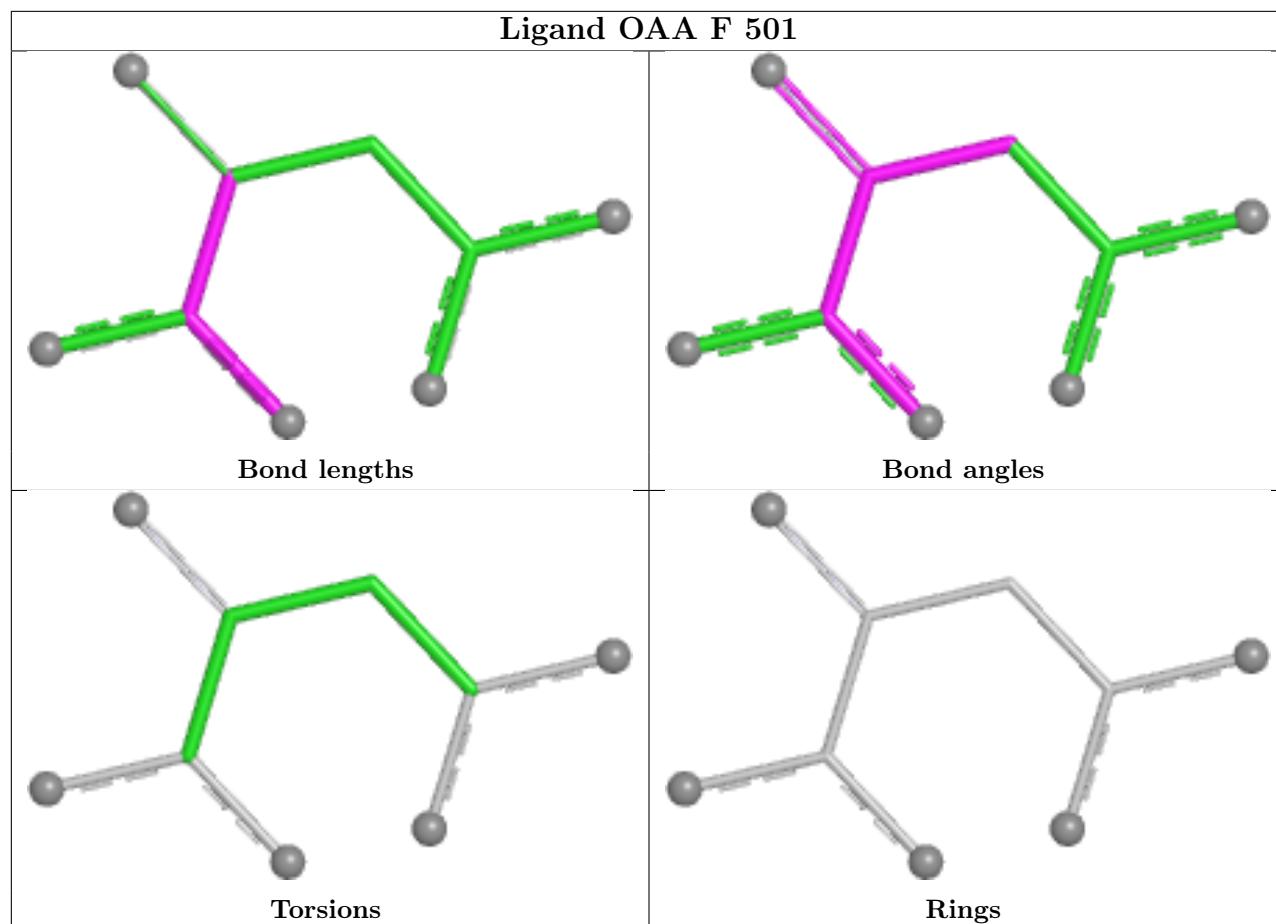
6 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	501	OAA	3	0
3	F	502	ACO	7	0
4	D	502	COA	1	0
2	E	501	OAA	1	0
3	A	502	ACO	15	0
2	B	501	OAA	1	0

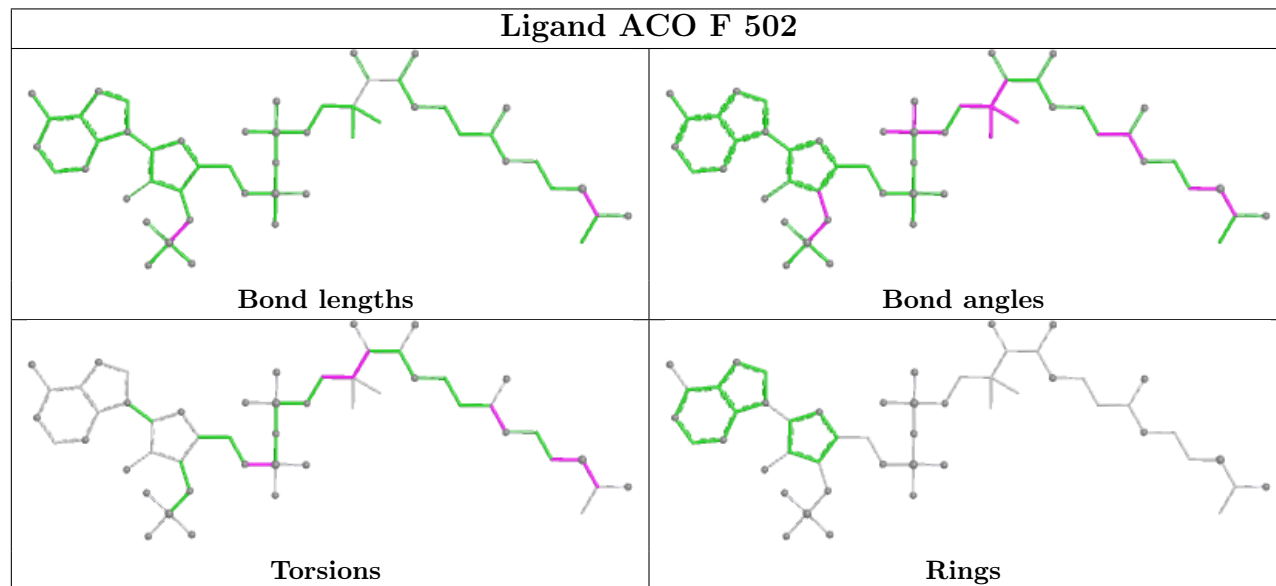
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

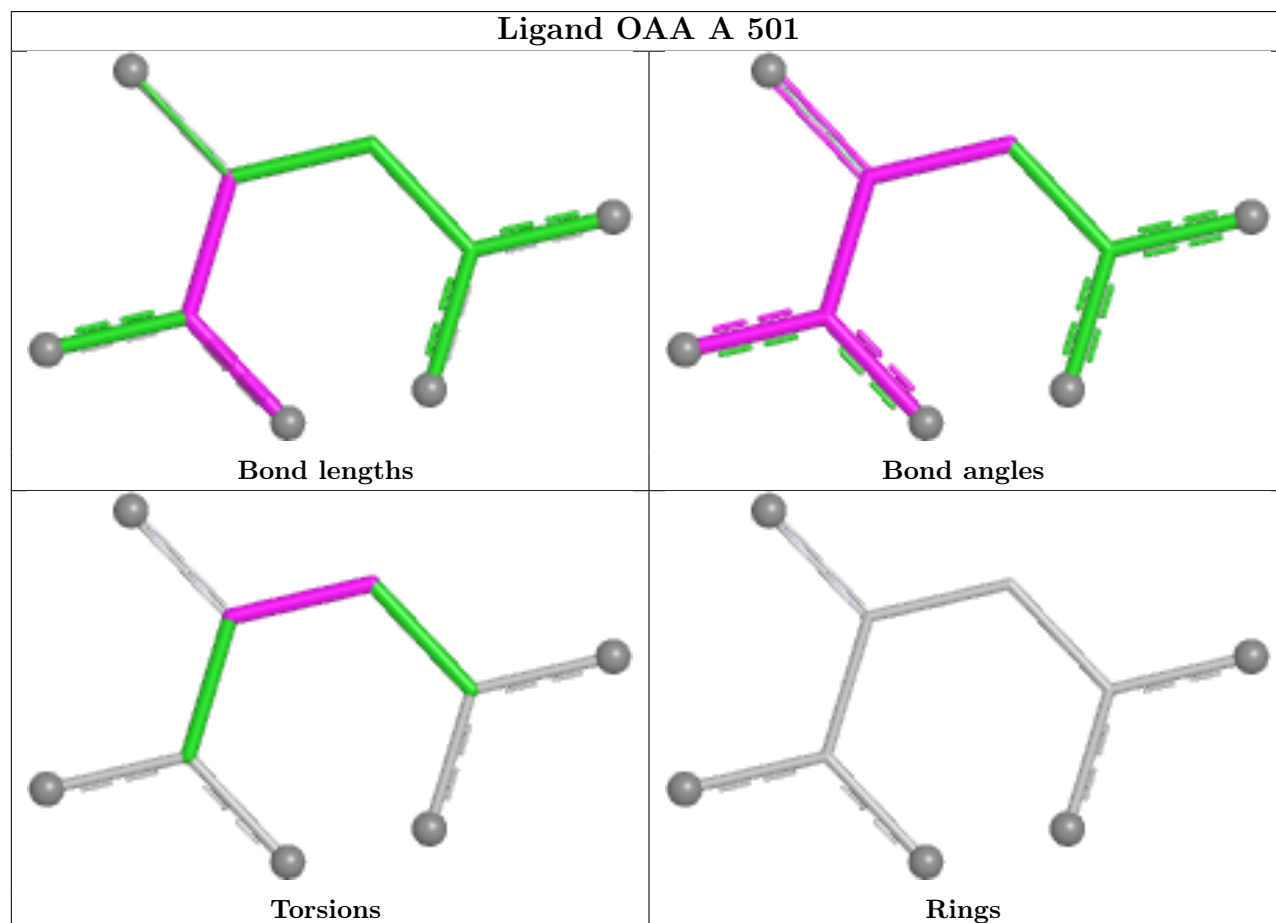
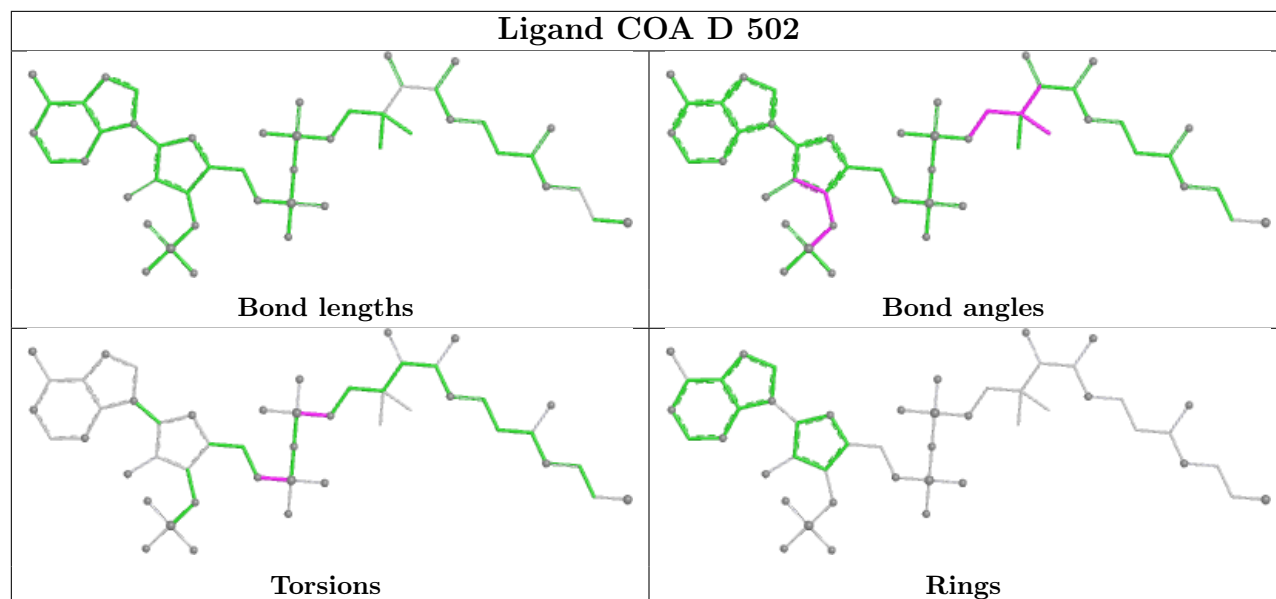


Ligand OAA F 501

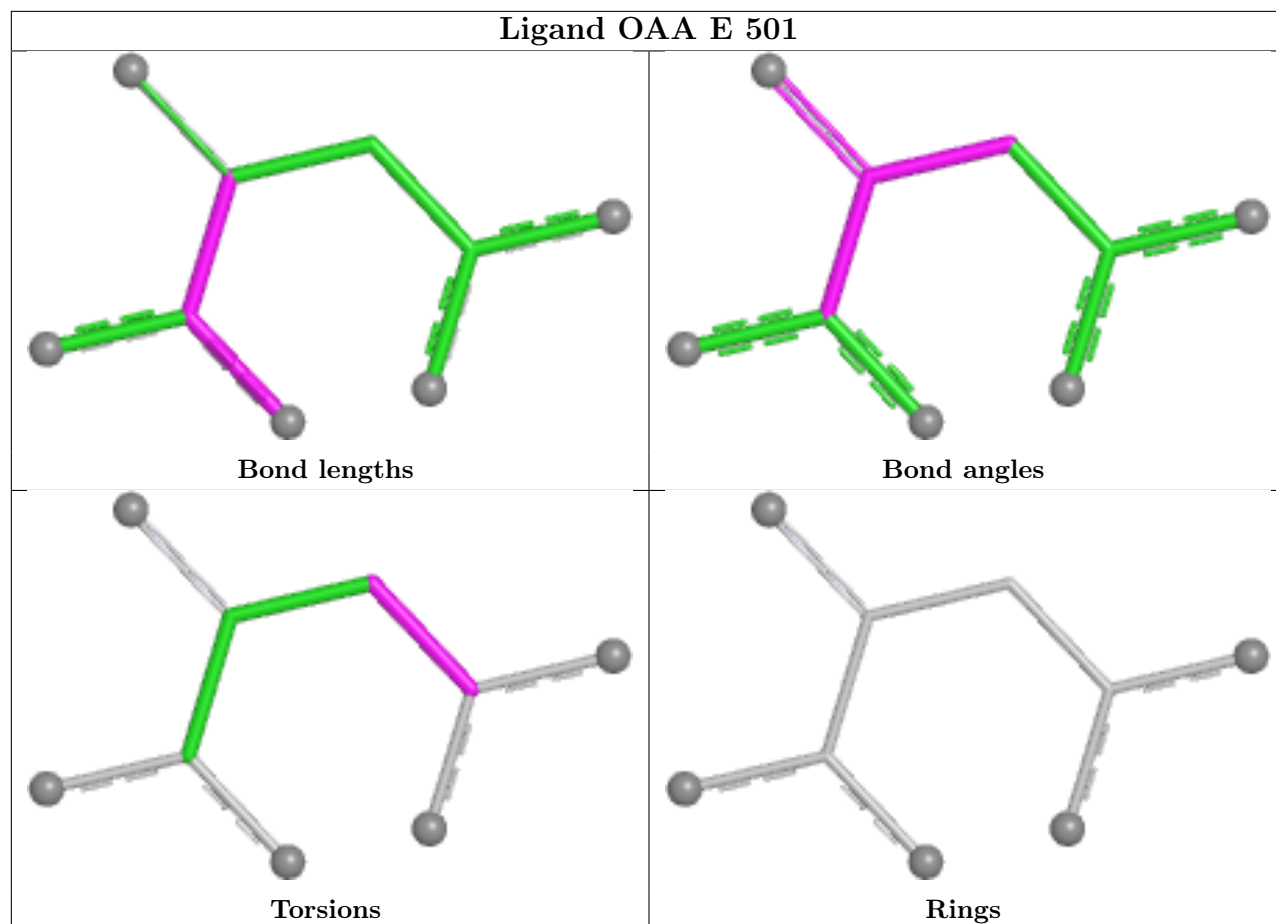


Ligand ACO F 502

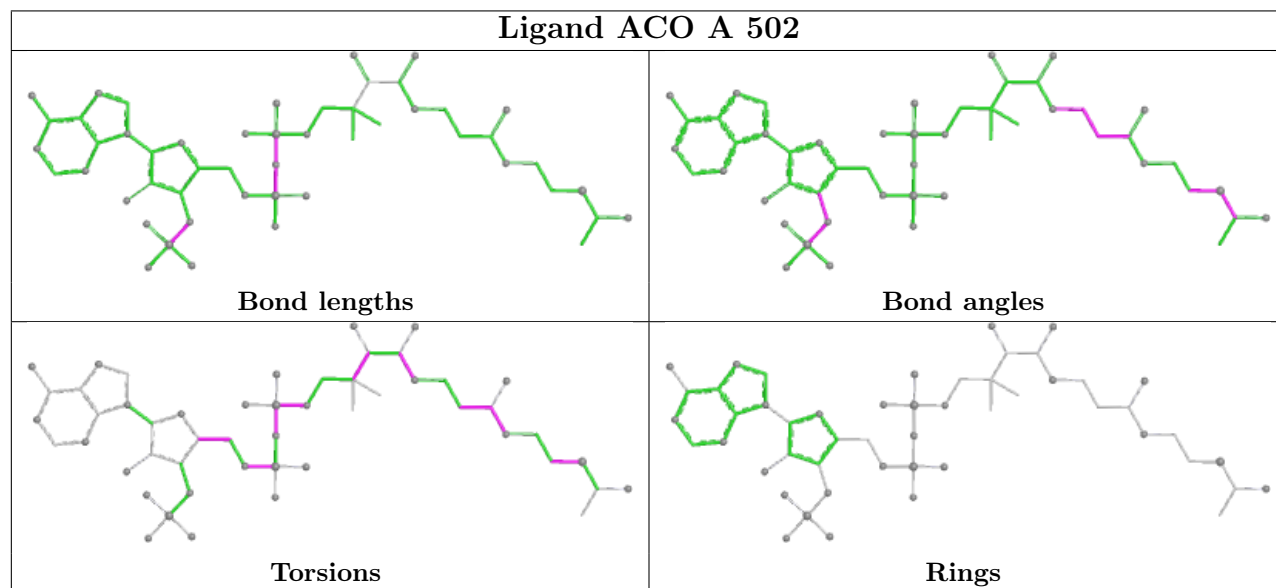


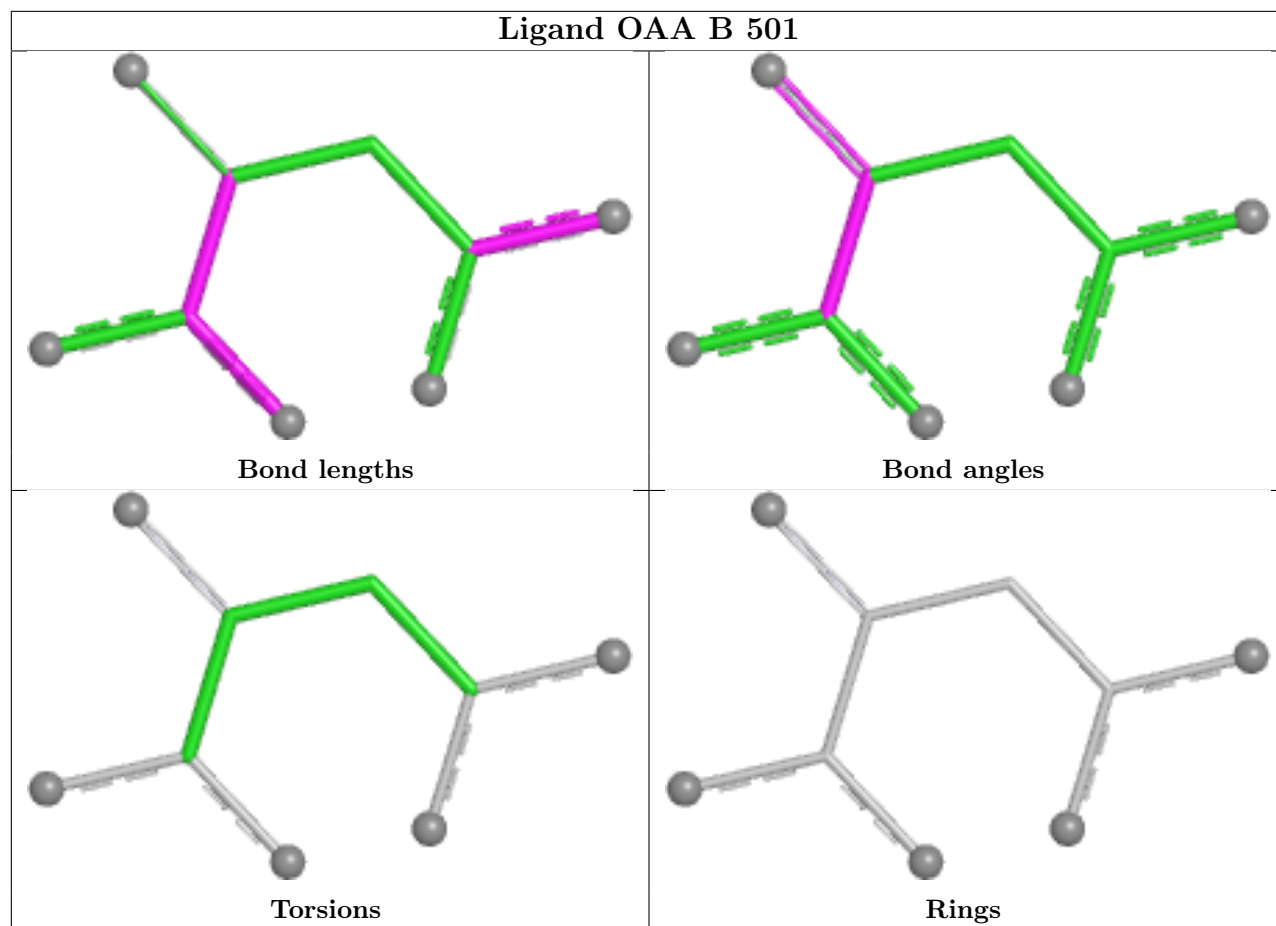


Ligand OAA E 501



Ligand ACO A 502





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	435/449 (96%)	0.05	33 (7%)	20 24	23, 39, 107, 145	0
1	B	449/449 (100%)	-0.28	6 (1%)	75 79	21, 35, 66, 133	0
1	C	442/449 (98%)	-0.07	14 (3%)	50 57	22, 36, 77, 123	0
1	D	440/449 (97%)	-0.44	0	100 100	20, 31, 55, 77	1 (0%)
1	E	441/449 (98%)	-0.33	4 (0%)	81 84	20, 32, 63, 124	0
1	F	441/449 (98%)	-0.38	1 (0%)	91 92	21, 33, 59, 78	0
All	All	2648/2694 (98%)	-0.24	58 (2%)	62 67	20, 34, 71, 145	1 (0%)

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	314	VAL	7.6
1	B	367	ALA	4.3
1	A	315	ILE	4.1
1	A	364	HIS	3.9
1	C	306	TRP	3.8
1	A	276	LEU	3.7
1	B	366	LYS	3.7
1	C	322	VAL	3.6
1	A	358	PRO	3.6
1	C	323	LEU	3.5
1	C	321	ALA	3.4
1	A	325	VAL	3.3
1	C	325	VAL	3.3
1	A	306	TRP	3.2
1	C	324	ARG	3.1
1	A	321	ALA	3.1
1	A	305	ALA	3.0
1	F	441	GLY	2.9
1	A	361	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	442	SER	2.8
1	A	370	PRO	2.8
1	A	309	LEU	2.8
1	A	316	PRO	2.8
1	A	304	PHE	2.8
1	A	360	VAL	2.8
1	A	284	TRP	2.7
1	A	319	GLY	2.7
1	C	367	ALA	2.7
1	C	363	LYS	2.6
1	A	371	TRP	2.6
1	E	365	GLY	2.6
1	A	356	VAL	2.5
1	A	352	LEU	2.5
1	A	363	LYS	2.5
1	B	17	GLU	2.5
1	A	349	ILE	2.5
1	A	357	ILE	2.4
1	A	293	GLY	2.4
1	C	441	GLY	2.4
1	C	58	ASP	2.3
1	A	318	TYR	2.3
1	C	371	TRP	2.3
1	E	367	ALA	2.3
1	E	366	LYS	2.3
1	A	296	PRO	2.3
1	A	317	GLY	2.3
1	A	362	LYS	2.3
1	C	314	VAL	2.3
1	A	312	GLY	2.2
1	E	441	GLY	2.2
1	A	350	VAL	2.2
1	A	322	VAL	2.2
1	C	369	ASN	2.2
1	A	440	ALA	2.1
1	B	158	ARG	2.1
1	A	288	LEU	2.1
1	B	449	GLU	2.0
1	B	368	LYS	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

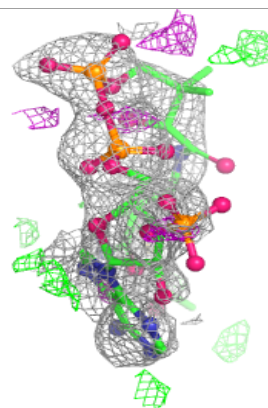
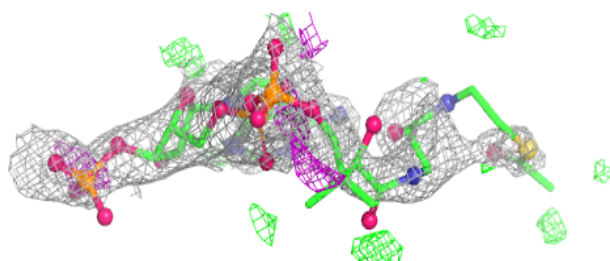
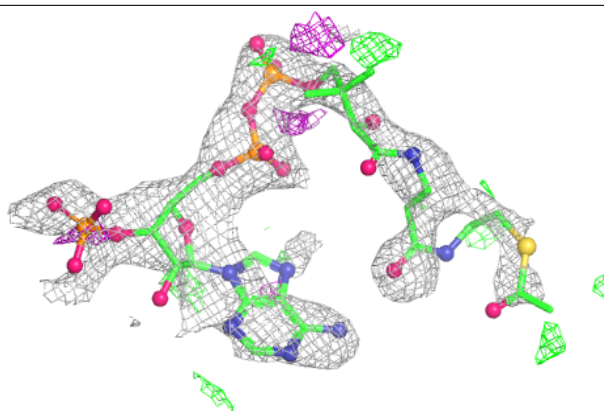
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	ACO	A	502	51/51	0.67	0.17	63,96,119,142	0
2	OAA	E	501	9/9	0.82	0.12	53,62,67,68	0
2	OAA	B	501	9/9	0.84	0.12	56,68,79,82	0
2	OAA	F	501	9/9	0.91	0.10	30,38,49,67	0
2	OAA	A	501	9/9	0.91	0.10	44,56,72,81	0
2	OAA	D	501	9/9	0.93	0.11	27,37,63,65	0
4	COA	D	502	48/48	0.93	0.08	32,45,64,80	0
3	ACO	F	502	51/51	0.97	0.07	24,30,59,90	0

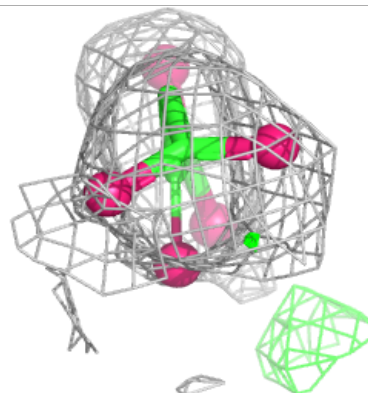
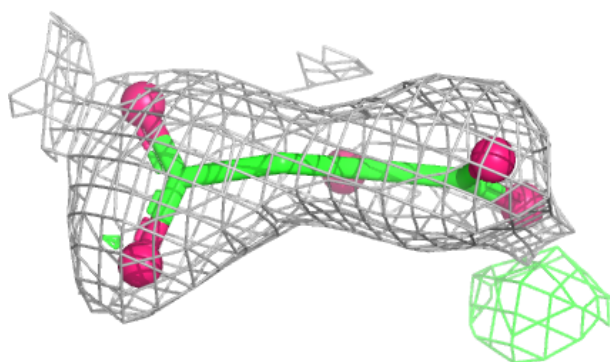
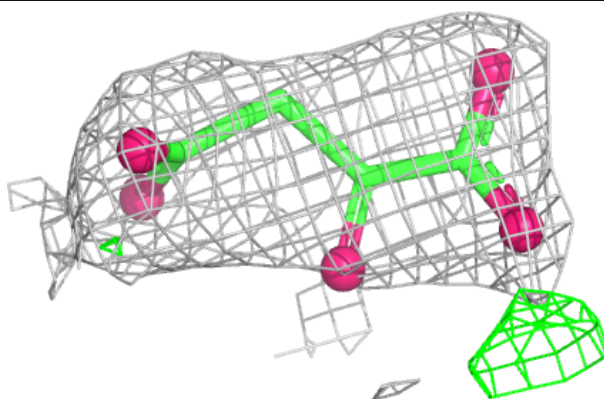
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ACO 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)

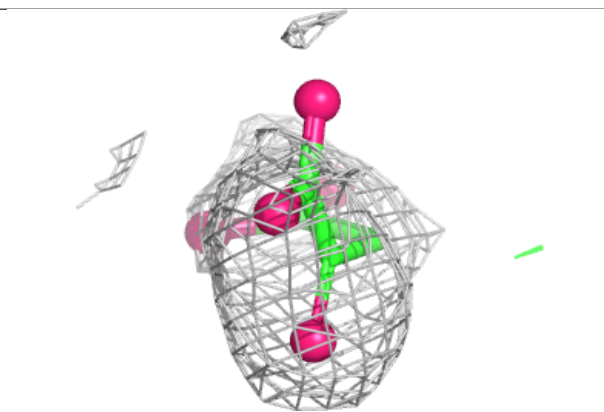
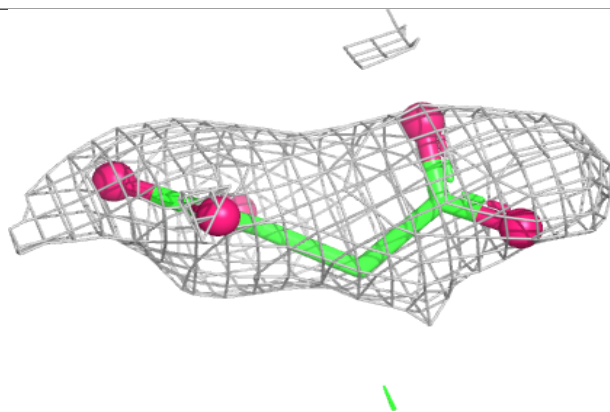
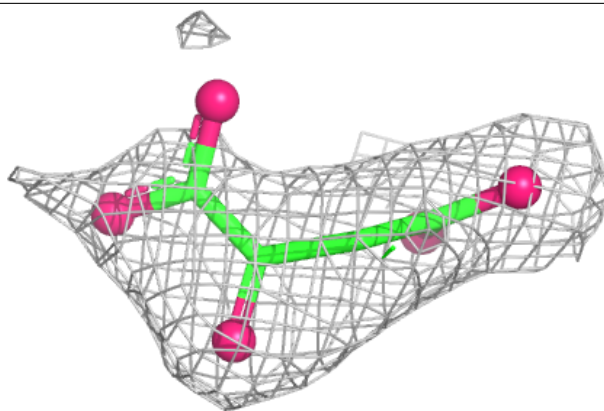
**Electron density around OAA E 501:**

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

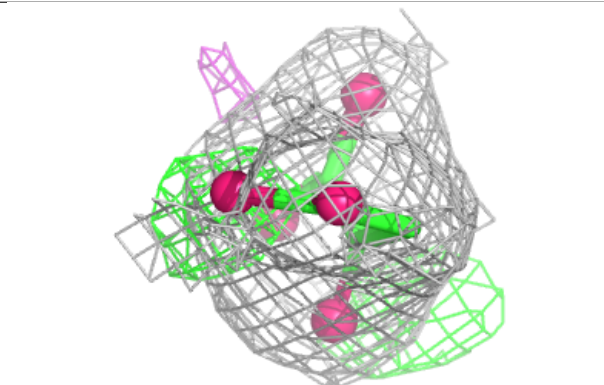
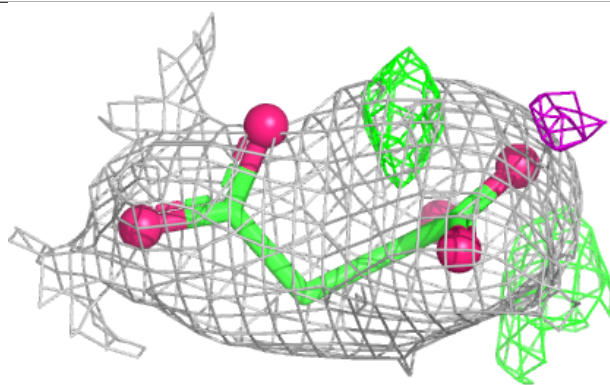
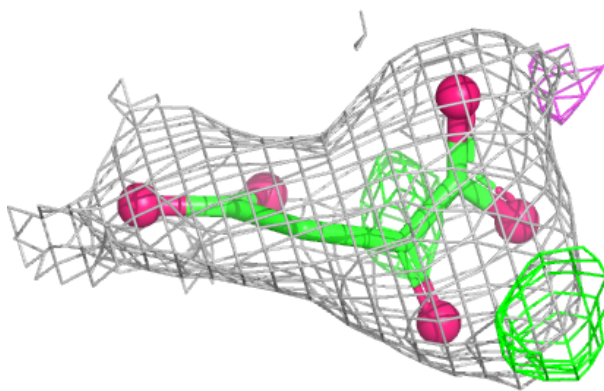


Electron density around OAA B 501:

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

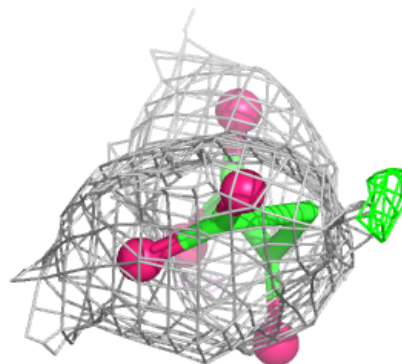
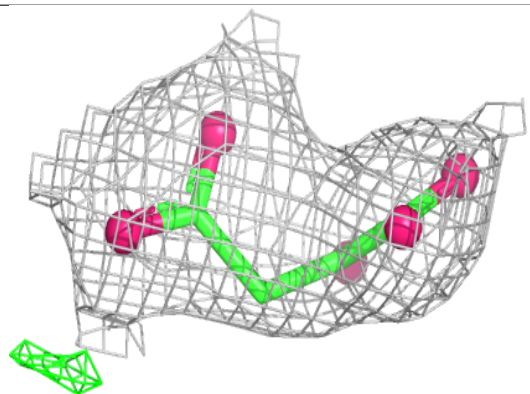
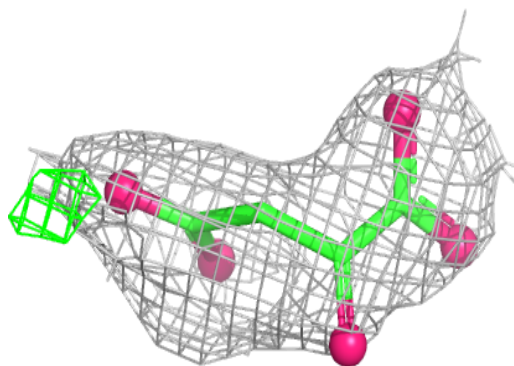
**Electron density around OAA F 501:**

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

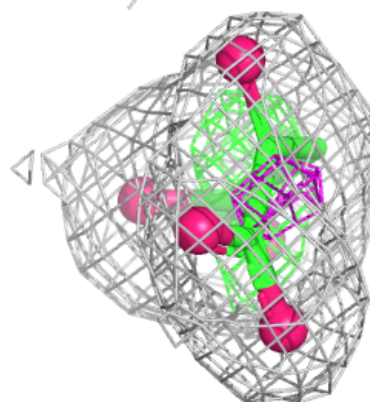
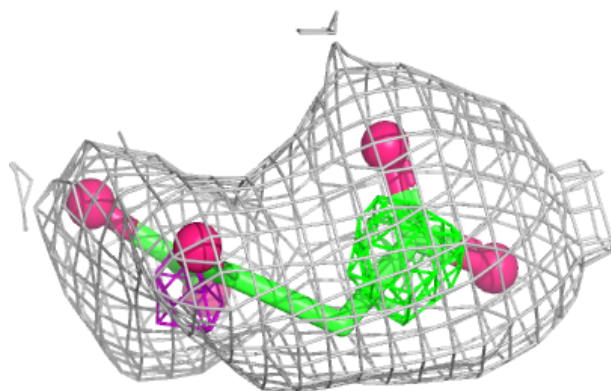
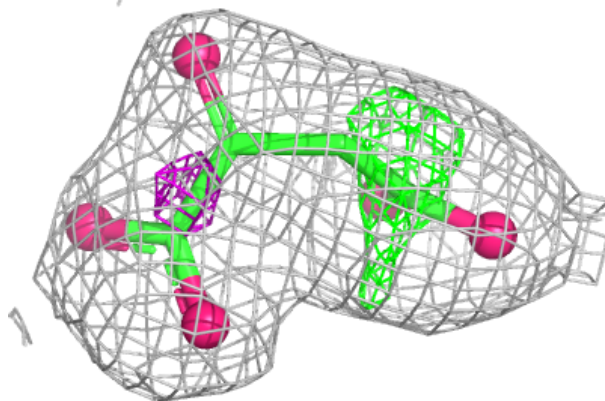


Electron density around OAA A 501:

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

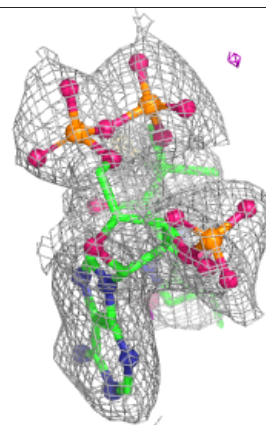
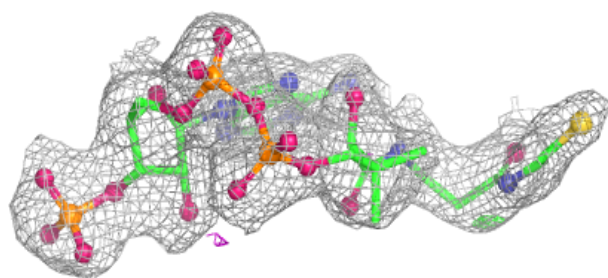
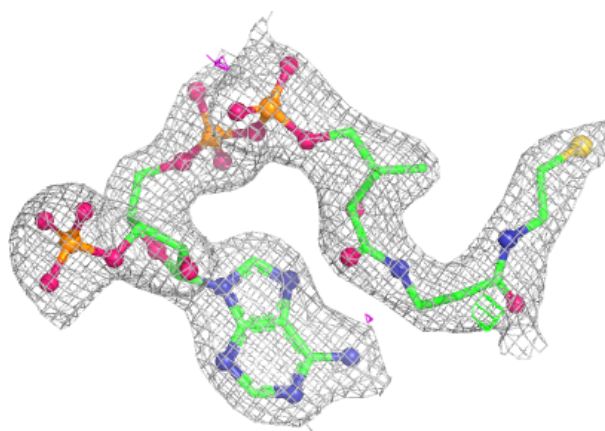
**Electron density around OAA D 501:**

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

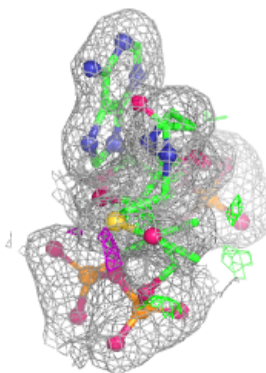
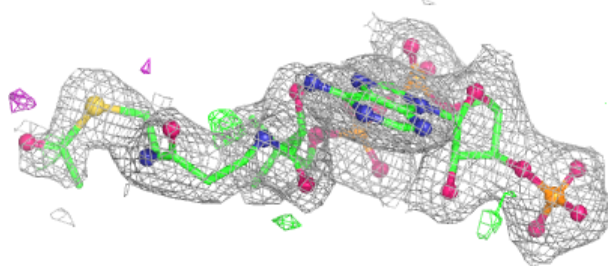
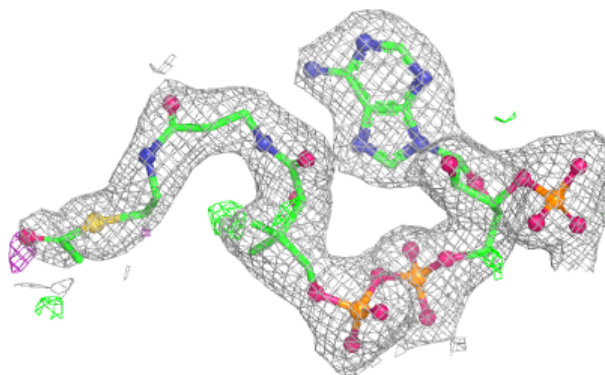


Electron density around COA D 502:

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

**Electron density around ACO F 502:**

$2mF_o-DF_c$ (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.