



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:57 PM UTC

PDB ID : 6B2M / pdb_00006b2m
Title : LarE, a sulfur transferase involved in synthesis of the cofactor for lactate racemase in complex with coenzyme A
Authors : Fellner, M.; Hausinger, R.P.; Hu, J.
Deposited on : 2017-09-20
Resolution : 2.09 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

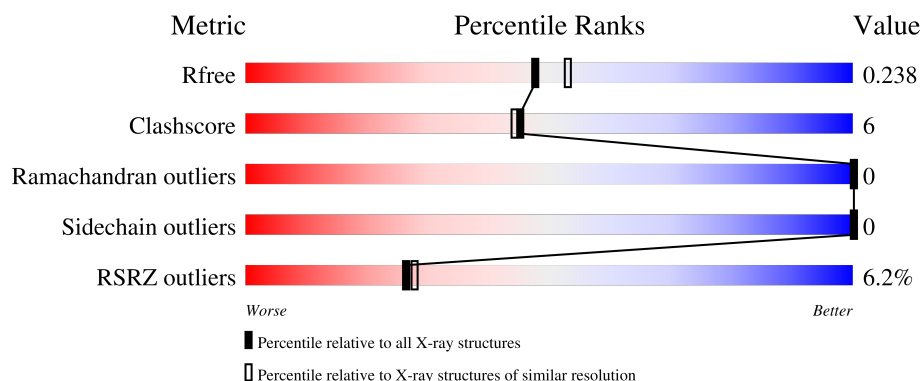
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.09 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	8172 (2.10-2.06)
Clashscore	190562	8714 (2.10-2.06)
Ramachandran outliers	187476	8641 (2.10-2.06)
Sidechain outliers	187428	8642 (2.10-2.06)
RSRZ outliers	180081	8177 (2.10-2.06)

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	286	4% 83% 11% 6%
1	B	286	2% 76% 10% 14%
1	C	286	4% 80% 9% 11%
1	D	286	18% 74% 10% 16%
1	E	286	3% 80% 12% 8%

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Mol	Chain	Length	Quality of chain
1	F	286	2% 80% 8% 12%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12554 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 ATP-utilizing enzyme of the PP-loopsuperfamily.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	268	Total	C	N	O	S	0	0	0
			2028	1278	353	390	7			
1	B	247	Total	C	N	O	S	0	0	0
			1893	1193	326	368	6			
1	C	255	Total	C	N	O	S	0	2	0
			1963	1233	346	376	8			
1	D	240	Total	C	N	O	S	0	1	0
			1807	1145	308	347	7			
1	E	263	Total	C	N	O	S	0	0	0
			2003	1265	345	386	7			
1	F	252	Total	C	N	O	S	0	1	0
			1937	1221	337	372	7			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	277	ALA	-	expression tag	UNP A0A0G9FES3
A	278	SER	-	expression tag	UNP A0A0G9FES3
A	279	TRP	-	expression tag	UNP A0A0G9FES3
A	280	SER	-	expression tag	UNP A0A0G9FES3
A	281	HIS	-	expression tag	UNP A0A0G9FES3
A	282	PRO	-	expression tag	UNP A0A0G9FES3
A	283	GLN	-	expression tag	UNP A0A0G9FES3
A	284	PHE	-	expression tag	UNP A0A0G9FES3
A	285	GLU	-	expression tag	UNP A0A0G9FES3
A	286	LYS	-	expression tag	UNP A0A0G9FES3
B	277	ALA	-	expression tag	UNP A0A0G9FES3
B	278	SER	-	expression tag	UNP A0A0G9FES3
B	279	TRP	-	expression tag	UNP A0A0G9FES3
B	280	SER	-	expression tag	UNP A0A0G9FES3
B	281	HIS	-	expression tag	UNP A0A0G9FES3
B	282	PRO	-	expression tag	UNP A0A0G9FES3
B	283	GLN	-	expression tag	UNP A0A0G9FES3

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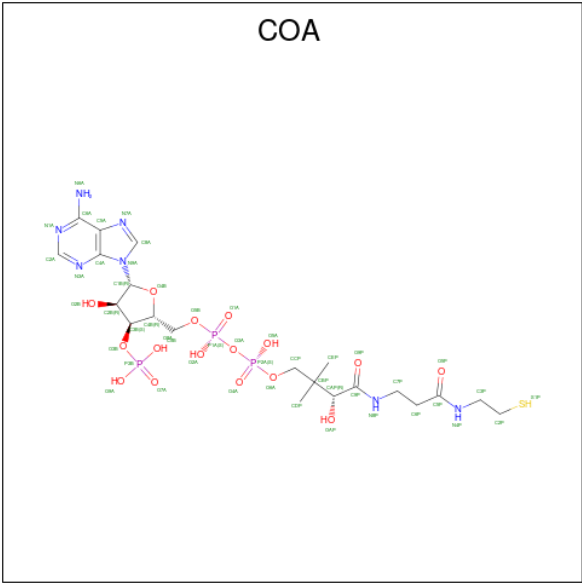
Chain	Residue	Modelled	Actual	Comment	Reference
B	284	PHE	-	expression tag	UNP A0A0G9FES3
B	285	GLU	-	expression tag	UNP A0A0G9FES3
B	286	LYS	-	expression tag	UNP A0A0G9FES3
C	277	ALA	-	expression tag	UNP A0A0G9FES3
C	278	SER	-	expression tag	UNP A0A0G9FES3
C	279	TRP	-	expression tag	UNP A0A0G9FES3
C	280	SER	-	expression tag	UNP A0A0G9FES3
C	281	HIS	-	expression tag	UNP A0A0G9FES3
C	282	PRO	-	expression tag	UNP A0A0G9FES3
C	283	GLN	-	expression tag	UNP A0A0G9FES3
C	284	PHE	-	expression tag	UNP A0A0G9FES3
C	285	GLU	-	expression tag	UNP A0A0G9FES3
C	286	LYS	-	expression tag	UNP A0A0G9FES3
D	277	ALA	-	expression tag	UNP A0A0G9FES3
D	278	SER	-	expression tag	UNP A0A0G9FES3
D	279	TRP	-	expression tag	UNP A0A0G9FES3
D	280	SER	-	expression tag	UNP A0A0G9FES3
D	281	HIS	-	expression tag	UNP A0A0G9FES3
D	282	PRO	-	expression tag	UNP A0A0G9FES3
D	283	GLN	-	expression tag	UNP A0A0G9FES3
D	284	PHE	-	expression tag	UNP A0A0G9FES3
D	285	GLU	-	expression tag	UNP A0A0G9FES3
D	286	LYS	-	expression tag	UNP A0A0G9FES3
E	277	ALA	-	expression tag	UNP A0A0G9FES3
E	278	SER	-	expression tag	UNP A0A0G9FES3
E	279	TRP	-	expression tag	UNP A0A0G9FES3
E	280	SER	-	expression tag	UNP A0A0G9FES3
E	281	HIS	-	expression tag	UNP A0A0G9FES3
E	282	PRO	-	expression tag	UNP A0A0G9FES3
E	283	GLN	-	expression tag	UNP A0A0G9FES3
E	284	PHE	-	expression tag	UNP A0A0G9FES3
E	285	GLU	-	expression tag	UNP A0A0G9FES3
E	286	LYS	-	expression tag	UNP A0A0G9FES3
F	277	ALA	-	expression tag	UNP A0A0G9FES3
F	278	SER	-	expression tag	UNP A0A0G9FES3
F	279	TRP	-	expression tag	UNP A0A0G9FES3
F	280	SER	-	expression tag	UNP A0A0G9FES3
F	281	HIS	-	expression tag	UNP A0A0G9FES3
F	282	PRO	-	expression tag	UNP A0A0G9FES3
F	283	GLN	-	expression tag	UNP A0A0G9FES3
F	284	PHE	-	expression tag	UNP A0A0G9FES3
F	285	GLU	-	expression tag	UNP A0A0G9FES3

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Chain	Residue	Modelled	Actual	Comment	Reference
F	286	LYS	-	expression tag	UNP A0A0G9FES3

- Molecule 2 is COENZYME A (CCD ID: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	B	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	C	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	D	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	E	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	F	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

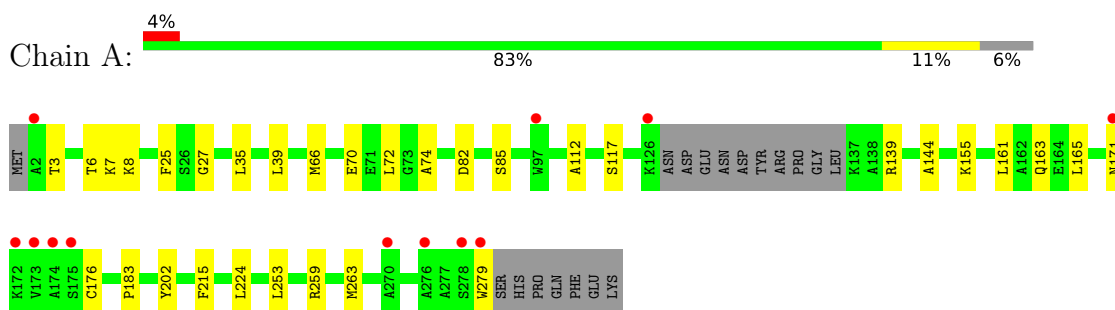
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	92	Total	O	0	0
			92	92		
4	B	124	Total	O	0	0
			124	124		
4	C	133	Total	O	0	0
			133	133		
4	D	62	Total	O	0	0
			62	62		
4	E	90	Total	O	0	0
			90	90		
4	F	104	Total	O	0	0
			104	104		

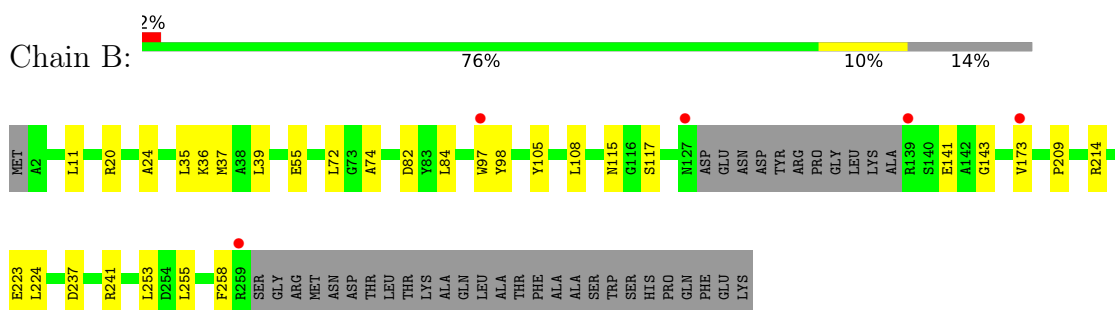
3 Residue-property plots [i](#)

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.

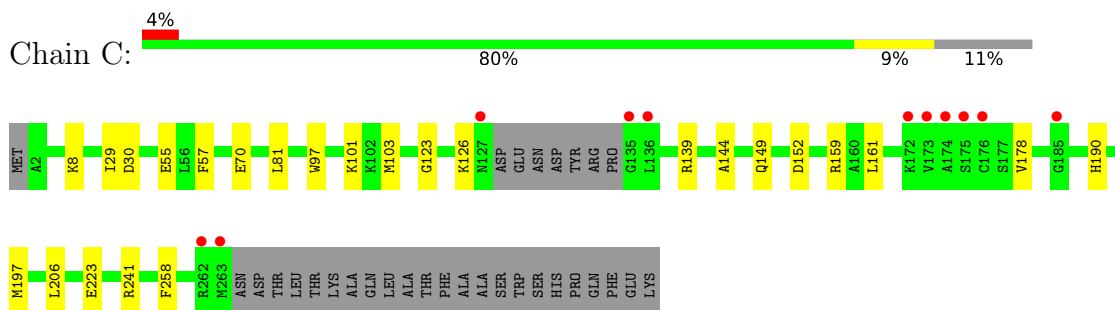
- Molecule 1: ATP-utilizing enzyme of the PP-loopsuperfamily



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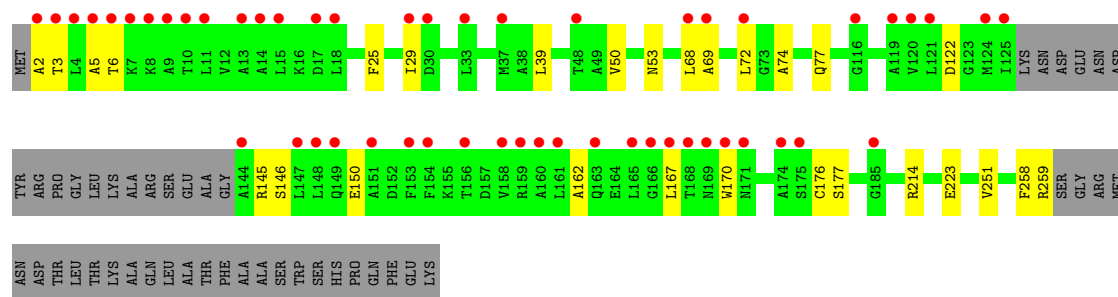


- Molecule 1: ATP-utilizing enzyme of the PP-loopsuperfamily

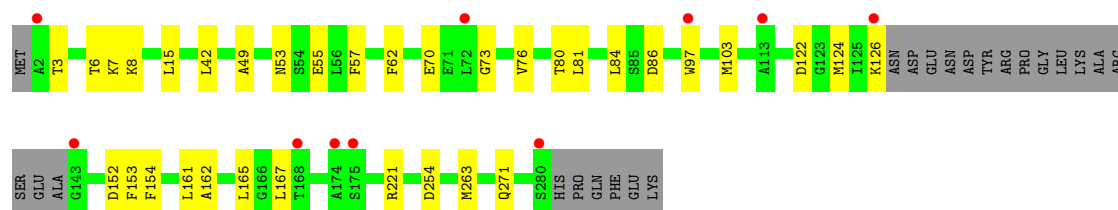
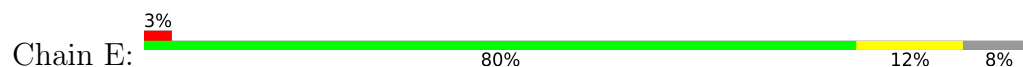


- Molecule 1: ATP-utilizing enzyme of the PP-loopsuperfamily

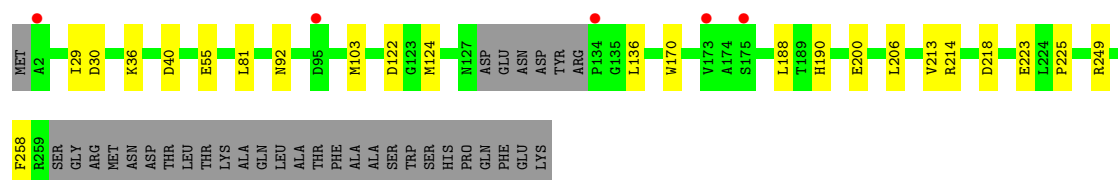
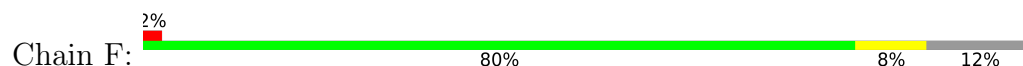




- Molecule 1: ATP-utilizing enzyme of the PP-loopsuperfamily



- Molecule 1: ATP-utilizing enzyme of the PP-loopsuperfamily



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	107.36Å 107.36Å 319.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.75 – 2.09 47.75 – 2.09	Depositor EDS
% Data completeness (in resolution range)	99.6 (47.75-2.09) 99.6 (47.75-2.09)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 2.08Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.195 , 0.234 0.199 , 0.238	Depositor DCC
R_{free} test set	5543 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	33.4	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 60.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12554	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.56% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: COA, PO4

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	0.34	0/2060	0.53	0/2797
1	B	0.36	0/1922	0.58	0/2606
1	C	0.38	0/1992	0.57	0/2696
1	D	0.30	0/1836	0.52	0/2497
1	E	0.34	0/2035	0.54	0/2761
1	F	0.35	0/1970	0.56	0/2668
All	All	0.35	0/11815	0.55	0/16025

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2028	0	1962	24	0
1	B	1893	0	1847	18	0
1	C	1963	0	1924	23	0
1	D	1807	0	1728	23	0
1	E	2003	0	1948	24	0
1	F	1937	0	1908	16	0
2	A	48	0	32	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	48	0	32	1	0
2	C	48	0	32	9	0
2	D	48	0	32	2	0
2	E	48	0	32	5	0
2	F	48	0	32	4	0
3	A	5	0	0	1	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	1	0
3	E	5	0	0	0	0
3	F	5	0	0	0	0
4	A	92	0	0	8	0
4	B	124	0	0	0	0
4	C	133	0	0	1	0
4	D	62	0	0	1	0
4	E	90	0	0	1	1
4	F	104	0	0	4	0
All	All	12554	0	11509	139	1

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 (139) 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)
2:C:501:COA:H32	2:C:501:COA:H62A	1.33	0.92
2:C:501:COA:H32	2:C:501:COA:N6A	1.89	0.86
2:E:501:COA:H72	2:E:501:COA:H122	1.60	0.83
1:E:55:GLU:HG3	1:E:84:LEU:HG	1.62	0.82
1:E:7:LYS:HE2	1:E:152:ASP:O	1.90	0.71
1:D:162:ALA:HA	1:D:167:LEU:HD12	1.73	0.71
1:E:3:THR:HG23	1:E:6:THR:H	1.57	0.69
2:F:501:COA:H61	2:F:501:COA:H142	1.75	0.69
2:C:501:COA:H21	2:C:501:COA:H61	1.76	0.68
2:C:501:COA:H62A	2:C:501:COA:C3P	2.05	0.68
1:A:171:ASN:OD1	4:A:601:HOH:O	2.12	0.68
1:A:139:ARG:HG3	1:A:144:ALA:HB3	1.77	0.66
1:D:68:LEU:O	1:D:72:LEU:HD12	1.96	0.66
1:D:122:ASP:OD1	1:D:146:SER:OG	2.10	0.65
1:C:126:LYS:HG3	1:C:149:GLN:HG3	1.78	0.64
1:C:70:GLU:OE1	4:C:601:HOH:O	2.15	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:TYR:OH	4:A:602:HOH:O	2.14	0.64
1:F:223:GLU:HB3	1:F:258:PHE:HA	1.80	0.63
1:C:139:ARG:HG2	1:C:144:ALA:HB3	1.81	0.62
1:D:68:LEU:HD22	1:D:170:TRP:HA	1.81	0.62
1:C:57:PHE:CD1	2:C:501:COA:H22	2.35	0.61
1:C:139:ARG:NH2	1:C:149:GLN:OE1	2.34	0.60
1:F:30:ASP:OD1	4:F:601:HOH:O	2.17	0.60
1:F:55:GLU:CD	1:F:190:HIS:HD1	2.10	0.59
1:B:35:LEU:HD23	1:B:72:LEU:HD12	1.84	0.59
1:B:20:ARG:NH2	1:B:115:ASN:O	2.32	0.59
1:C:223:GLU:HB3	1:C:258:PHE:HA	1.84	0.59
1:B:20:ARG:HG2	1:B:117:SER:HA	1.85	0.58
1:E:97:TRP:HB2	2:E:501:COA:H32	1.83	0.58
1:C:178:VAL:HB	1:C:197:MET:HE3	1.86	0.57
1:B:173:VAL:HG11	1:B:209:PRO:HB2	1.87	0.57
1:A:3:THR:HG23	1:A:6:THR:H	1.70	0.55
1:D:3:THR:HG22	1:D:6:THR:OG1	2.06	0.55
1:A:3:THR:OG1	4:A:603:HOH:O	2.15	0.55
1:A:263:MET:HE1	4:A:646:HOH:O	2.06	0.55
2:C:501:COA:H61	2:C:501:COA:C2P	2.36	0.55
2:F:501:COA:H72	2:F:501:COA:H122	1.89	0.54
1:C:97:TRP:HA	1:C:97:TRP:CE3	2.41	0.54
1:D:3:THR:OG1	1:E:73:GLY:HA2	2.07	0.54
1:D:39:LEU:HD11	1:D:74:ALA:HB2	1.90	0.54
1:D:223:GLU:HB3	1:D:258:PHE:HA	1.90	0.54
1:A:263:MET:HE3	1:C:206:LEU:HA	1.91	0.52
1:B:11:LEU:HD21	1:B:37:MET:HG3	1.92	0.51
1:E:162:ALA:HA	1:E:167:LEU:HD12	1.91	0.51
2:E:501:COA:H133	2:E:501:COA:C8A	2.40	0.51
1:C:139:ARG:HD3	1:C:144:ALA:O	2.11	0.51
1:B:255:LEU:HD12	1:D:251:VAL:HG12	1.94	0.50
1:A:66:MET:O	1:A:70:GLU:HG3	2.12	0.50
1:B:97:TRP:CG	1:B:98:TYR:N	2.80	0.50
1:D:259:ARG:NH2	3:D:502:PO4:O2	2.46	0.49
1:E:7:LYS:HB3	1:E:153:PHE:CE2	2.47	0.49
1:D:3:THR:HG23	1:D:5:ALA:N	2.27	0.49
1:E:263:MET:HE2	1:F:206:LEU:HA	1.93	0.49
2:F:501:COA:H72	2:F:501:COA:CCP	2.43	0.49
1:A:176:CYS:HB3	4:A:684:HOH:O	2.13	0.48
1:F:92:ASN:HB2	1:F:188:LEU:CD1	2.44	0.48
1:F:92:ASN:HB2	1:F:188:LEU:HD11	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:8:LYS:HD2	1:C:161:LEU:HD11	1.95	0.48
1:C:241:ARG:HD2	1:E:271:GLN:OE1	2.13	0.48
1:D:2:ALA:N	1:E:70:GLU:OE2	2.46	0.48
1:E:49:ALA:HB3	1:E:76:VAL:HG23	1.95	0.48
1:B:223:GLU:HB3	1:B:258:PHE:HA	1.95	0.48
1:A:82:ASP:OD2	1:A:85:SER:HB3	2.14	0.48
1:C:178:VAL:CG2	1:C:197:MET:HE3	2.43	0.48
1:B:24:ALA:HB2	1:B:108:LEU:HD22	1.96	0.48
1:A:155:LYS:NZ	4:A:608:HOH:O	2.43	0.47
1:A:8:LYS:HD2	1:A:161:LEU:HD11	1.97	0.47
1:A:70:GLU:OE1	4:A:604:HOH:O	2.20	0.47
1:A:163:GLN:NE2	4:A:614:HOH:O	2.48	0.47
2:D:501:COA:H72	2:D:501:COA:H121	1.96	0.47
2:E:501:COA:O6A	2:E:501:COA:H21	2.15	0.46
1:A:259:ARG:NH1	3:A:502:PO4:O2	2.43	0.46
2:B:501:COA:H121	2:B:501:COA:H72	1.98	0.46
1:C:126:LYS:HE2	1:C:152:ASP:OD1	2.16	0.46
1:D:3:THR:HG23	1:D:5:ALA:H	1.81	0.46
1:D:3:THR:CG2	1:D:6:THR:H	2.29	0.45
1:B:214:ARG:HE	1:B:223:GLU:CD	2.23	0.45
1:E:15:LEU:O	1:E:42:LEU:HD21	2.16	0.45
1:C:101:LYS:CG	2:C:501:COA:H142	2.47	0.45
1:D:176[A]:CYS:SG	1:D:177:SER:N	2.89	0.45
1:E:161:LEU:O	1:E:165:LEU:HD22	2.17	0.45
1:C:57:PHE:CG	2:C:501:COA:H22	2.52	0.44
1:F:218:ASP:HB2	1:F:249:ARG:HB3	1.98	0.44
2:A:501:COA:CCP	2:A:501:COA:H72	2.47	0.44
1:B:105:TYR:CE2	1:B:141:GLU:HG3	2.52	0.44
1:B:141:GLU:O	1:B:143:GLY:N	2.44	0.44
1:E:126:LYS:HB3	1:E:154:PHE:HA	2.00	0.44
1:B:82:ASP:OD1	1:B:82:ASP:N	2.50	0.44
1:B:237:ASP:OD1	1:B:241:ARG:NH1	2.51	0.44
1:D:25:PHE:CD2	1:D:69:ALA:HB2	2.53	0.44
1:F:200:GLU:HG2	1:F:213:VAL:HG23	2.00	0.43
1:D:25:PHE:CE2	1:D:69:ALA:HB2	2.52	0.43
1:A:35:LEU:HD23	1:A:72:LEU:HD12	2.01	0.43
1:F:36:LYS:HE3	1:F:40:ASP:OD1	2.19	0.43
1:F:122:ASP:OD2	1:F:124:MET:HG2	2.19	0.43
1:D:145:ARG:NH2	1:D:150:GLU:OE1	2.52	0.43
1:F:81:LEU:HD22	1:F:103:MET:HG2	2.00	0.43
1:A:3:THR:O	1:A:7:LYS:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:29:ILE:CD1	1:C:159:ARG:HD3	2.49	0.43
1:D:214:ARG:HE	1:D:223:GLU:CD	2.26	0.43
1:F:124:MET:HE2	1:F:136:LEU:HD21	2.00	0.43
1:B:224:LEU:HD12	1:B:253:LEU:HD11	2.01	0.43
1:C:126:LYS:HD3	1:C:152:ASP:HA	1.99	0.43
1:E:97:TRP:HB2	2:E:501:COA:C3P	2.48	0.43
1:F:214:ARG:HE	1:F:223:GLU:CD	2.27	0.43
1:E:122:ASP:OD2	1:E:124:MET:HG3	2.18	0.42
1:A:39:LEU:HD11	1:A:74:ALA:HB2	2.01	0.42
1:C:81:LEU:HD22	1:C:103:MET:HG2	2.02	0.42
2:D:501:COA:H72	2:D:501:COA:H10	1.63	0.42
1:E:81:LEU:HD22	1:E:103:MET:HG2	2.01	0.42
2:F:501:COA:O1A	4:F:602:HOH:O	2.22	0.42
1:A:25:PHE:CZ	1:A:27:GLY:HA2	2.55	0.42
2:C:501:COA:H72	2:C:501:COA:N7A	2.34	0.42
2:A:501:COA:O5A	2:A:501:COA:H21	2.20	0.42
1:C:30:ASP:HB3	1:C:123:GLY:O	2.20	0.42
1:D:53:ASN:OD1	4:D:601:HOH:O	2.22	0.42
1:F:225:PRO:HA	4:F:633:HOH:O	2.20	0.41
1:C:178:VAL:CB	1:C:197:MET:HE3	2.49	0.41
1:F:29:ILE:HD12	1:F:170:TRP:CZ2	2.55	0.41
1:A:112:ALA:HB1	1:A:117:SER:HB2	2.03	0.41
1:A:161:LEU:O	1:A:165:LEU:HG	2.21	0.41
1:A:224:LEU:HD12	1:A:253:LEU:HD11	2.03	0.41
1:E:8:LYS:HD2	1:E:161:LEU:HD11	2.01	0.41
1:E:86:ASP:HB2	1:E:103:MET:HE1	2.02	0.41
1:C:97:TRP:HA	1:C:97:TRP:HE3	1.81	0.41
1:E:53:ASN:HB2	1:E:62:PHE:CD2	2.55	0.41
1:D:50:VAL:HA	1:D:77:GLN:O	2.20	0.41
1:D:29:ILE:HD12	1:D:170:TRP:CZ2	2.55	0.41
1:B:36:LYS:HA	1:B:36:LYS:HD2	1.80	0.41
1:D:72:LEU:HA	4:F:628:HOH:O	2.20	0.41
1:E:57:PHE:O	4:E:601:HOH:O	2.22	0.41
1:E:103:MET:HE2	1:E:103:MET:HB2	1.97	0.41
1:A:183:PRO:HD3	1:A:215:PHE:O	2.21	0.41
1:B:55:GLU:HG3	1:B:84:LEU:HG	2.02	0.41
1:E:53:ASN:O	1:E:80:THR:HA	2.20	0.41
1:A:279:TRP:CD2	1:F:249:ARG:HD2	2.57	0.40
1:C:55:GLU:CD	1:C:190:HIS:HD1	2.29	0.40
1:E:221:ARG:NH1	1:E:254:ASP:OD2	2.47	0.40
1:B:39:LEU:HD11	1:B:74:ALA:HB2	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:655:HOH:O	4:E:681:HOH:O[8_555]	2.19	0.01

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	264/286 (92%)	257 (97%)	7 (3%)	0	100	100
1	B	243/286 (85%)	235 (97%)	8 (3%)	0	100	100
1	C	253/286 (88%)	244 (96%)	9 (4%)	0	100	100
1	D	237/286 (83%)	232 (98%)	5 (2%)	0	100	100
1	E	259/286 (91%)	252 (97%)	7 (3%)	0	100	100
1	F	249/286 (87%)	244 (98%)	5 (2%)	0	100	100
All	All	1505/1716 (88%)	1464 (97%)	41 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	205/236 (87%)	205 (100%)	0	100	100
1	B	197/236 (84%)	197 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	203/236 (86%)	203 (100%)	0	100	100
1	D	181/236 (77%)	181 (100%)	0	100	100
1	E	205/236 (87%)	205 (100%)	0	100	100
1	F	202/236 (86%)	202 (100%)	0	100	100
All	All	1193/1416 (84%)	1193 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	88	HIS
1	A	91	ASN
1	B	75	ASN
1	C	88	HIS
1	E	77	GLN
1	E	88	HIS
1	F	46	ASN
1	F	88	HIS
1	F	109	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

12 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	PO4	C	502	-	4,4,4	0.78	0	6,6,6	0.62	0
3	PO4	B	502	-	4,4,4	0.82	0	6,6,6	0.44	0
2	COA	F	501	-	47,50,50	0.52	0	69,75,75	1.09	4 (5%)
3	PO4	E	502	-	4,4,4	1.03	0	6,6,6	0.65	0
3	PO4	A	502	-	4,4,4	0.85	0	6,6,6	0.52	0
3	PO4	D	502	-	4,4,4	0.97	0	6,6,6	0.43	0
2	COA	C	501	-	47,50,50	0.75	1 (2%)	69,75,75	0.96	3 (4%)
2	COA	D	501	-	47,50,50	0.46	1 (2%)	69,75,75	0.48	0
2	COA	B	501	-	47,50,50	0.91	1 (2%)	69,75,75	0.56	0
3	PO4	F	502	-	4,4,4	1.20	0	6,6,6	0.67	0
2	COA	E	501	-	47,50,50	0.41	0	69,75,75	0.55	0
2	COA	A	501	-	47,50,50	0.56	1 (2%)	69,75,75	0.56	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
2	COA	F	501	-	-	17/48/64/64	0/3/3/3
2	COA	C	501	-	-	19/48/64/64	0/3/3/3
2	COA	D	501	-	-	17/48/64/64	0/3/3/3
2	COA	B	501	-	-	22/48/64/64	0/3/3/3
2	COA	E	501	-	-	21/48/64/64	0/3/3/3
2	COA	A	501	-	-	27/48/64/64	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	COA	P1A-O3A	-5.07	1.54	1.59
2	C	501	COA	P1A-O3A	-4.35	1.54	1.59
2	A	501	COA	P1A-O3A	-2.30	1.57	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	501	COA	P1A-O3A	2.05	1.61	1.59

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	501	COA	O6A-CCP-CBP	6.46	120.94	110.55
2	C	501	COA	C3P-N4P-C5P	5.48	133.03	122.82
2	F	501	COA	C7P-N8P-C9P	2.96	127.86	122.55
2	C	501	COA	C6P-C5P-N4P	2.59	121.05	116.34
2	F	501	COA	CAP-C9P-N8P	2.32	120.89	116.48
2	C	501	COA	O5P-C5P-C6P	-2.11	118.19	122.02
2	F	501	COA	O2B-C2B-C3B	2.06	116.96	111.19

There are no chirality outliers.

All (123) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	COA	C5B-O5B-P1A-O1A
2	A	501	COA	C5B-O5B-P1A-O2A
2	A	501	COA	C5B-O5B-P1A-O3A
2	A	501	COA	CCP-O6A-P2A-O5A
2	A	501	COA	OAP-CAP-CBP-CCP
2	A	501	COA	C9P-CAP-CBP-CCP
2	A	501	COA	OAP-CAP-CBP-CDP
2	A	501	COA	C9P-CAP-CBP-CDP
2	A	501	COA	OAP-CAP-CBP-CEP
2	A	501	COA	C9P-CAP-CBP-CEP
2	A	501	COA	CAP-C9P-N8P-C7P
2	A	501	COA	C5P-C6P-C7P-N8P
2	B	501	COA	C5B-O5B-P1A-O1A
2	B	501	COA	C5B-O5B-P1A-O2A
2	B	501	COA	C5B-O5B-P1A-O3A
2	B	501	COA	CDP-CBP-CCP-O6A
2	B	501	COA	CEP-CBP-CCP-O6A
2	B	501	COA	CAP-CBP-CCP-O6A
2	B	501	COA	OAP-CAP-CBP-CCP
2	B	501	COA	C9P-CAP-CBP-CCP
2	B	501	COA	OAP-CAP-CBP-CDP
2	B	501	COA	C9P-CAP-CBP-CDP
2	B	501	COA	OAP-CAP-CBP-CEP
2	B	501	COA	C9P-CAP-CBP-CEP
2	B	501	COA	CAP-C9P-N8P-C7P

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Mol	Chain	Res	Type	Atoms
2	B	501	COA	S1P-C2P-C3P-N4P
2	C	501	COA	C5B-O5B-P1A-O2A
2	C	501	COA	CCP-O6A-P2A-O3A
2	C	501	COA	CDP-CBP-CCP-O6A
2	C	501	COA	CEP-CBP-CCP-O6A
2	C	501	COA	CAP-CBP-CCP-O6A
2	C	501	COA	O9P-C9P-CAP-OAP
2	C	501	COA	N8P-C9P-CAP-OAP
2	C	501	COA	CAP-C9P-N8P-C7P
2	C	501	COA	C2P-C3P-N4P-C5P
2	D	501	COA	C5B-O5B-P1A-O1A
2	D	501	COA	C5B-O5B-P1A-O2A
2	D	501	COA	C5B-O5B-P1A-O3A
2	D	501	COA	CDP-CBP-CCP-O6A
2	D	501	COA	CEP-CBP-CCP-O6A
2	D	501	COA	CAP-CBP-CCP-O6A
2	D	501	COA	OAP-CAP-CBP-CCP
2	D	501	COA	C9P-CAP-CBP-CCP
2	D	501	COA	OAP-CAP-CBP-CDP
2	D	501	COA	C9P-CAP-CBP-CDP
2	D	501	COA	OAP-CAP-CBP-CEP
2	D	501	COA	C9P-CAP-CBP-CEP
2	D	501	COA	CAP-C9P-N8P-C7P
2	D	501	COA	S1P-C2P-C3P-N4P
2	E	501	COA	CEP-CBP-CCP-O6A
2	E	501	COA	CAP-CBP-CCP-O6A
2	E	501	COA	OAP-CAP-CBP-CCP
2	E	501	COA	C9P-CAP-CBP-CCP
2	E	501	COA	OAP-CAP-CBP-CDP
2	E	501	COA	C9P-CAP-CBP-CDP
2	E	501	COA	OAP-CAP-CBP-CEP
2	E	501	COA	C9P-CAP-CBP-CEP
2	E	501	COA	CAP-C9P-N8P-C7P
2	E	501	COA	S1P-C2P-C3P-N4P
2	F	501	COA	CCP-O6A-P2A-O3A
2	F	501	COA	CDP-CBP-CCP-O6A
2	F	501	COA	CAP-CBP-CCP-O6A
2	F	501	COA	OAP-CAP-CBP-CCP
2	F	501	COA	C9P-CAP-CBP-CCP
2	F	501	COA	OAP-CAP-CBP-CDP
2	F	501	COA	C9P-CAP-CBP-CDP
2	F	501	COA	OAP-CAP-CBP-CEP

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Mol	Chain	Res	Type	Atoms
2	F	501	COA	C9P-CAP-CBP-CEP
2	F	501	COA	O9P-C9P-CAP-CBP
2	F	501	COA	N8P-C9P-CAP-CBP
2	F	501	COA	CAP-C9P-N8P-C7P
2	F	501	COA	S1P-C2P-C3P-N4P
2	C	501	COA	C6P-C5P-N4P-C3P
2	A	501	COA	O9P-C9P-N8P-C7P
2	B	501	COA	O9P-C9P-N8P-C7P
2	C	501	COA	O9P-C9P-N8P-C7P
2	D	501	COA	O9P-C9P-N8P-C7P
2	E	501	COA	O9P-C9P-N8P-C7P
2	F	501	COA	O9P-C9P-N8P-C7P
2	A	501	COA	O4B-C4B-C5B-O5B
2	C	501	COA	O5P-C5P-N4P-C3P
2	B	501	COA	O5P-C5P-C6P-C7P
2	B	501	COA	N4P-C5P-C6P-C7P
2	C	501	COA	O9P-C9P-CAP-CBP
2	C	501	COA	N8P-C9P-CAP-CBP
2	F	501	COA	N8P-C9P-CAP-OAP
2	B	501	COA	C5P-C6P-C7P-N8P
2	A	501	COA	O5P-C5P-C6P-C7P
2	E	501	COA	N4P-C5P-C6P-C7P
2	E	501	COA	C3B-C4B-C5B-O5B
2	B	501	COA	P1A-O3A-P2A-O4A
2	A	501	COA	CDP-CBP-CCP-O6A
2	E	501	COA	CDP-CBP-CCP-O6A
2	F	501	COA	CEP-CBP-CCP-O6A
2	A	501	COA	C2P-C3P-N4P-C5P
2	A	501	COA	S1P-C2P-C3P-N4P
2	C	501	COA	S1P-C2P-C3P-N4P
2	A	501	COA	CCP-O6A-P2A-O3A
2	A	501	COA	CCP-O6A-P2A-O4A
2	C	501	COA	C5B-O5B-P1A-O1A
2	D	501	COA	CCP-O6A-P2A-O4A
2	E	501	COA	CCP-O6A-P2A-O3A
2	E	501	COA	CCP-O6A-P2A-O4A
2	E	501	COA	CCP-O6A-P2A-O5A
2	E	501	COA	O5P-C5P-C6P-C7P
2	F	501	COA	P2A-O3A-P1A-O2A
2	A	501	COA	C3B-C4B-C5B-O5B
2	A	501	COA	N4P-C5P-C6P-C7P
2	C	501	COA	O4B-C4B-C5B-O5B

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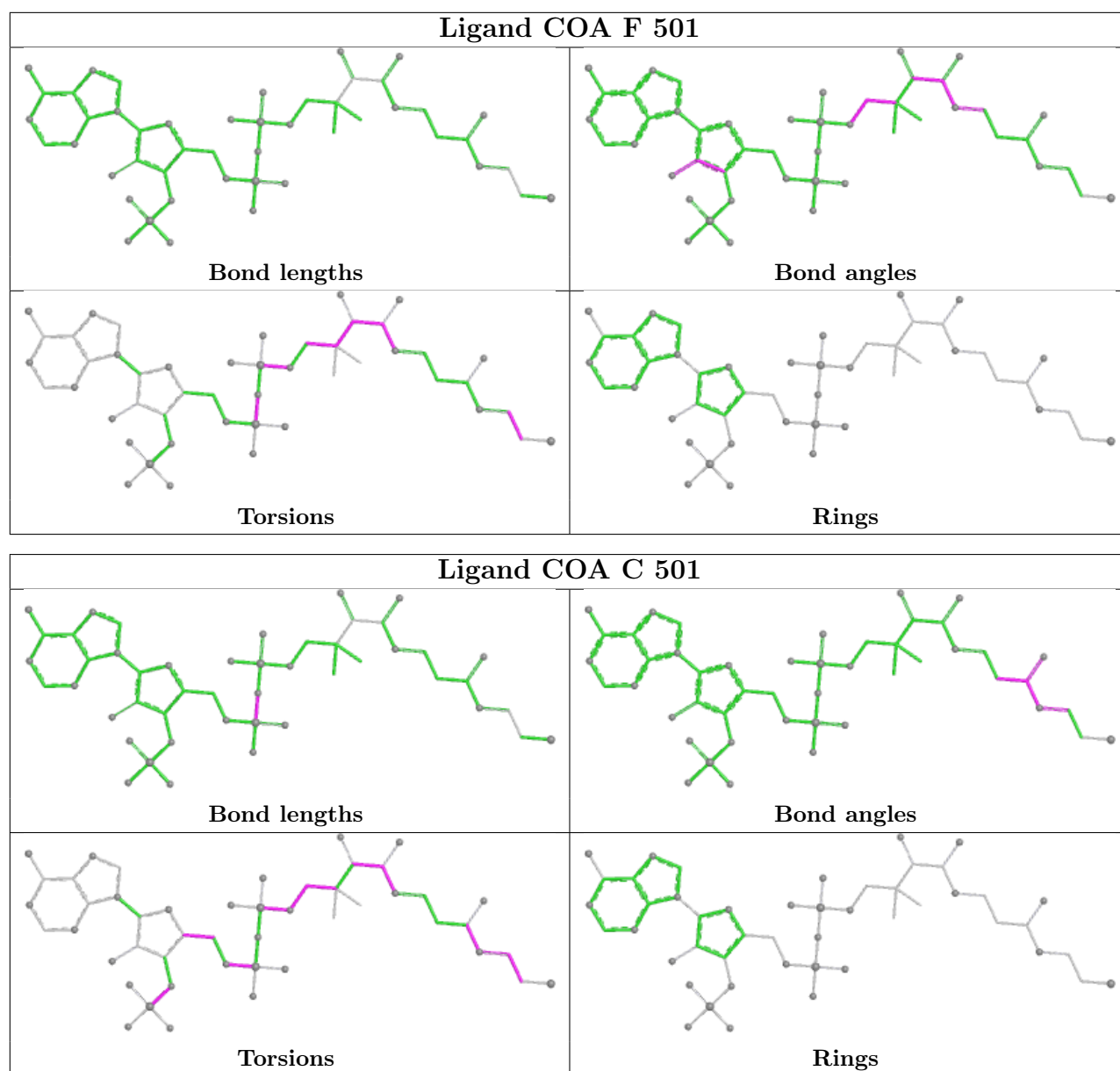
Mol	Chain	Res	Type	Atoms
2	A	501	COA	CBP-CCP-O6A-P2A
2	B	501	COA	CBP-CCP-O6A-P2A
2	C	501	COA	CBP-CCP-O6A-P2A
2	A	501	COA	CEP-CBP-CCP-O6A
2	A	501	COA	C3B-O3B-P3B-O7A
2	B	501	COA	C3B-O3B-P3B-O7A
2	C	501	COA	C3B-O3B-P3B-O7A
2	E	501	COA	C3B-O3B-P3B-O7A
2	A	501	COA	N8P-C9P-CAP-OAP
2	D	501	COA	N8P-C9P-CAP-OAP
2	E	501	COA	N8P-C9P-CAP-OAP
2	A	501	COA	CAP-CBP-CCP-O6A
2	B	501	COA	P1A-O3A-P2A-O5A
2	E	501	COA	P2A-O3A-P1A-O2A

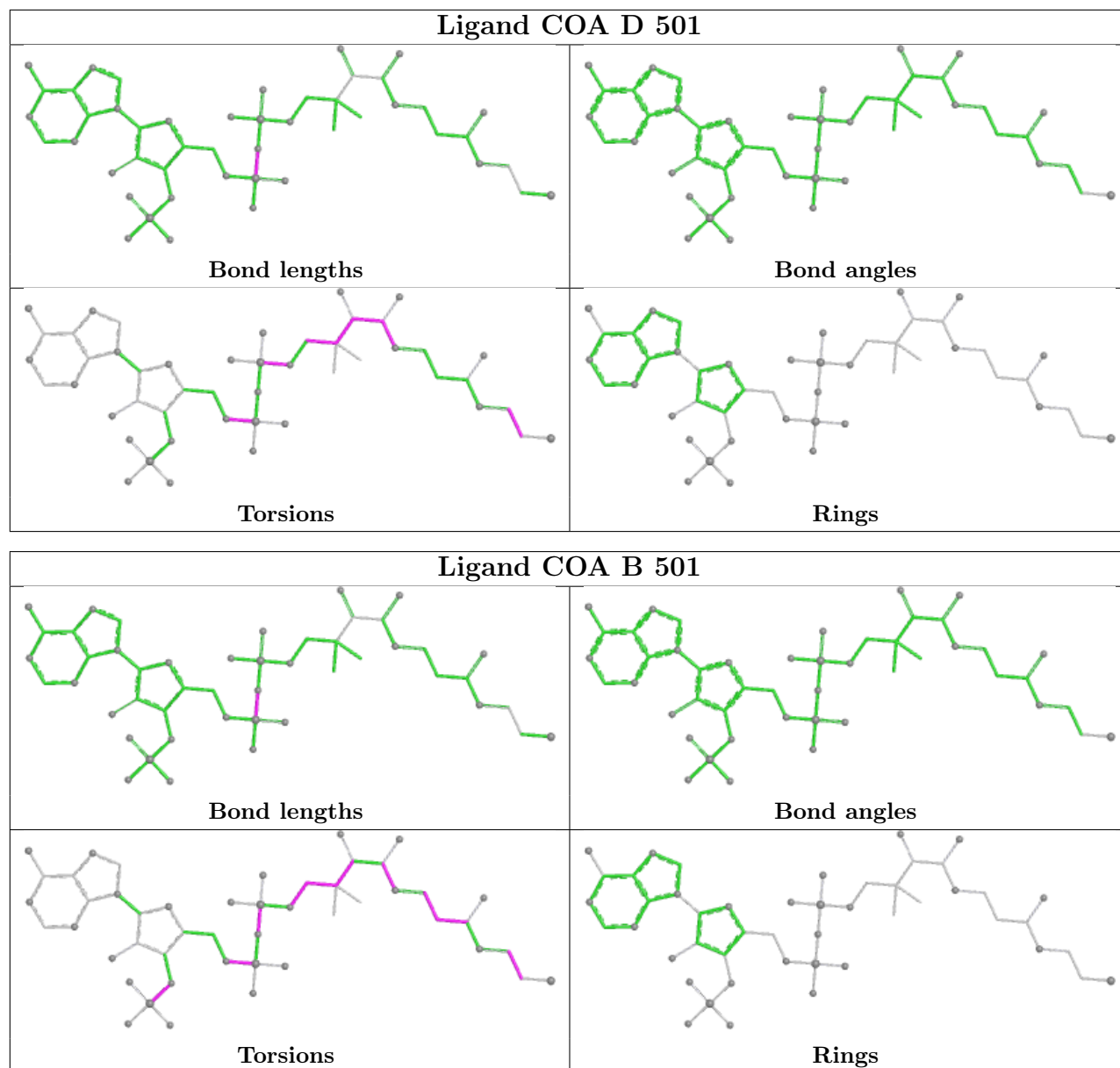
There are no ring outliers.

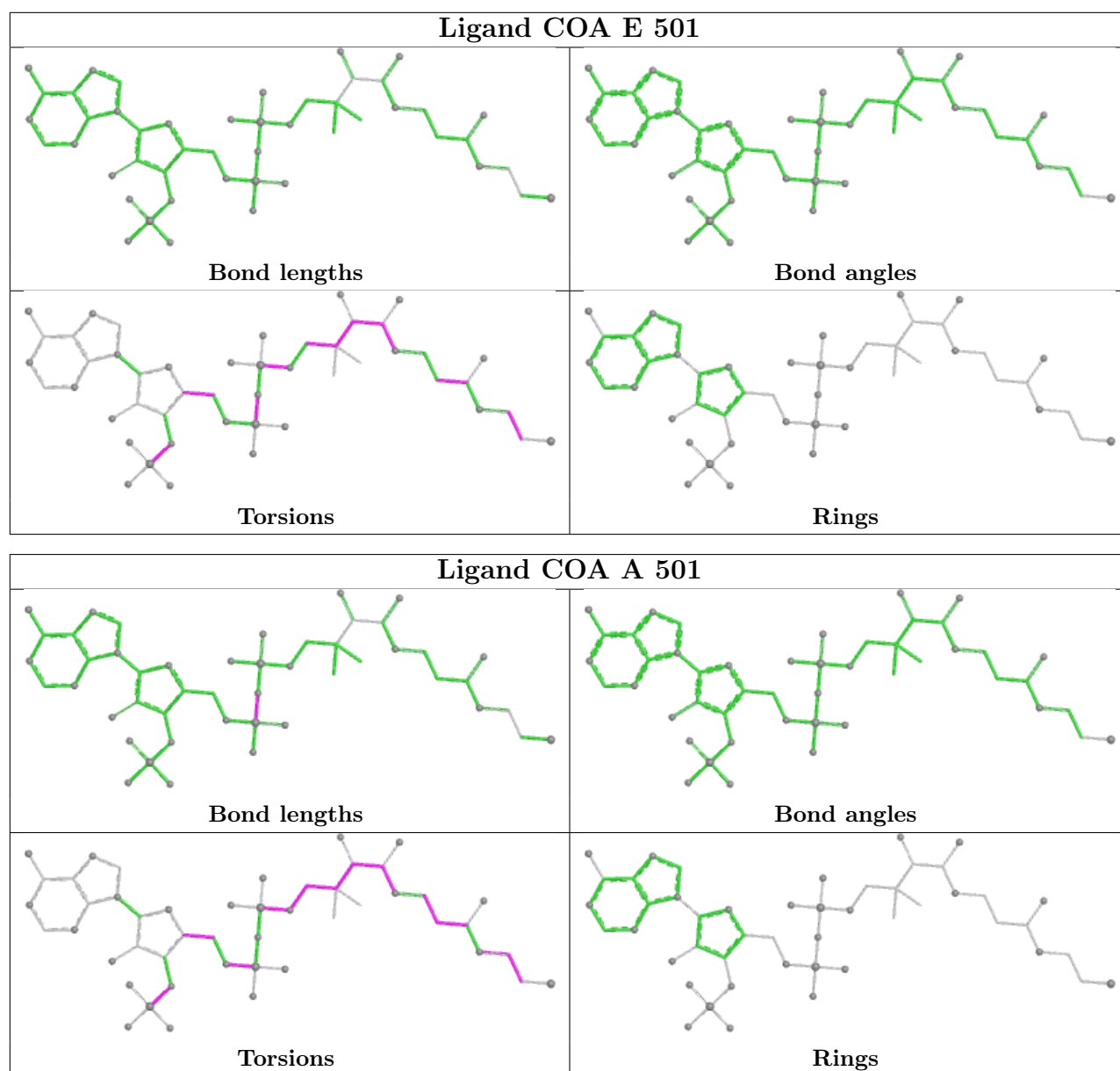
8 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	501	COA	4	0
3	A	502	PO4	1	0
3	D	502	PO4	1	0
2	C	501	COA	9	0
2	D	501	COA	2	0
2	B	501	COA	1	0
2	E	501	COA	5	0
2	A	501	COA	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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 [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	268/286 (93%)	0.12	12 (4%) 38 40	23, 40, 61, 75	0
1	B	247/286 (86%)	-0.05	5 (2%) 65 67	22, 37, 54, 79	0
1	C	255/286 (89%)	-0.05	11 (4%) 40 41	17, 35, 62, 87	2 (0%)
1	D	240/286 (83%)	0.79	52 (21%) 2 2	24, 55, 91, 138	1 (0%)
1	E	263/286 (91%)	0.36	10 (3%) 44 46	23, 48, 73, 89	0
1	F	252/286 (88%)	-0.06	5 (1%) 65 67	23, 38, 59, 86	1 (0%)
All	All	1525/1716 (88%)	0.18	95 (6%) 26 28	17, 40, 74, 138	4 (0%)

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	2	ALA	5.0
1	E	97	TRP	4.8
1	C	135	GLY	4.2
1	D	160	ALA	4.0
1	D	4	LEU	4.0
1	A	279	TRP	3.8
1	C	175	SER	3.8
1	D	125	ILE	3.7
1	D	14	ALA	3.7
1	D	3	THR	3.6
1	C	185	GLY	3.6
1	D	153	PHE	3.4
1	C	173	VAL	3.4
1	D	174	ALA	3.4
1	F	2	ALA	3.4
1	D	120	VAL	3.4
1	D	170	TRP	3.3
1	C	174	ALA	3.3
1	D	151	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	18	LEU	3.2
1	C	262	ARG	3.2
1	D	5	ALA	3.1
1	B	259	ARG	3.1
1	F	134	PRO	3.1
1	D	17	ASP	3.1
1	B	97	TRP	3.0
1	D	163	GLN	3.0
1	B	127	ASN	3.0
1	D	159	ARG	3.0
1	D	147	LEU	3.0
1	D	169	ASN	3.0
1	D	29	ILE	2.8
1	D	154	PHE	2.8
1	C	263	MET	2.8
1	D	148	LEU	2.8
1	D	6	THR	2.8
1	E	175	SER	2.7
1	E	280	SER	2.7
1	A	174	ALA	2.7
1	D	161	LEU	2.6
1	A	172	LYS	2.6
1	A	97	TRP	2.6
1	C	127	ASN	2.6
1	D	13	ALA	2.6
1	E	174	ALA	2.6
1	D	158	VAL	2.5
1	F	173	VAL	2.5
1	D	167	LEU	2.5
1	C	172	LYS	2.5
1	D	7	LYS	2.5
1	D	30	ASP	2.4
1	D	175	SER	2.4
1	E	168	THR	2.4
1	D	144	ALA	2.4
1	E	143	GLY	2.4
1	A	2	ALA	2.4
1	D	37	MET	2.4
1	D	10	THR	2.4
1	D	165	LEU	2.3
1	D	171	ASN	2.3
1	E	72	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	185	GLY	2.3
1	D	15	LEU	2.3
1	A	175	SER	2.3
1	D	69	ALA	2.3
1	D	121	LEU	2.3
1	D	166	GLY	2.3
1	A	173	VAL	2.3
1	C	176[A]	CYS	2.3
1	C	136	LEU	2.3
1	A	171	ASN	2.2
1	D	68	LEU	2.2
1	D	156	THR	2.2
1	D	11	LEU	2.2
1	D	33	LEU	2.2
1	A	126	LYS	2.2
1	D	9	ALA	2.2
1	A	278	SER	2.2
1	D	124	MET	2.2
1	F	95	ASP	2.2
1	D	116	GLY	2.1
1	B	139	ARG	2.1
1	D	149	GLN	2.1
1	E	2	ALA	2.1
1	E	126	LYS	2.1
1	A	276	ALA	2.1
1	E	113	ALA	2.1
1	D	72	LEU	2.1
1	F	175	SER	2.1
1	D	8	LYS	2.1
1	A	270	ALA	2.1
1	D	119	ALA	2.1
1	D	48	THR	2.0
1	D	168	THR	2.0
1	B	173	VAL	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 [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

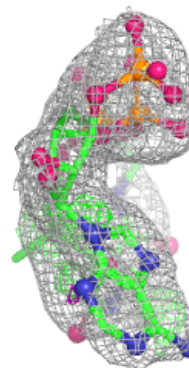
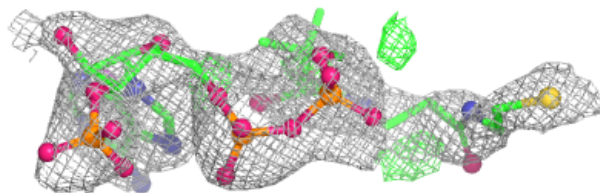
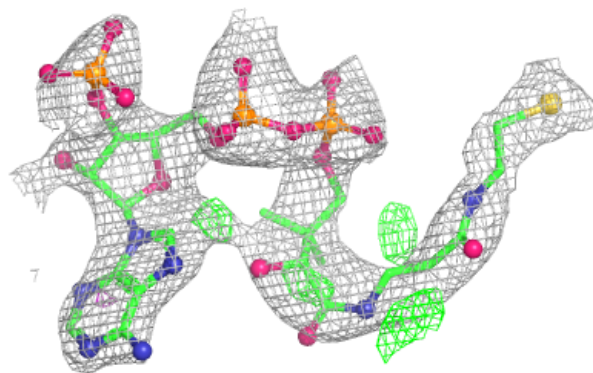
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	COA	D	501	48/48	0.84	0.16	46,74,86,89	48
2	COA	E	501	48/48	0.88	0.16	38,86,95,102	48
2	COA	F	501	48/48	0.90	0.12	22,43,73,77	0
2	COA	B	501	48/48	0.91	0.14	29,52,86,90	48
2	COA	A	501	48/48	0.91	0.13	27,52,81,89	48
2	COA	C	501	48/48	0.93	0.13	22,55,100,101	0
3	PO4	C	502	5/5	0.97	0.06	36,38,43,44	0
3	PO4	B	502	5/5	0.98	0.04	33,33,36,38	0
3	PO4	A	502	5/5	0.98	0.05	34,37,41,47	0
3	PO4	D	502	5/5	0.98	0.04	32,36,39,43	0
3	PO4	E	502	5/5	0.98	0.05	33,35,40,43	0
3	PO4	F	502	5/5	0.98	0.05	33,37,40,41	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.

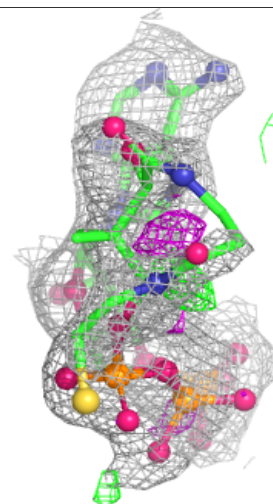
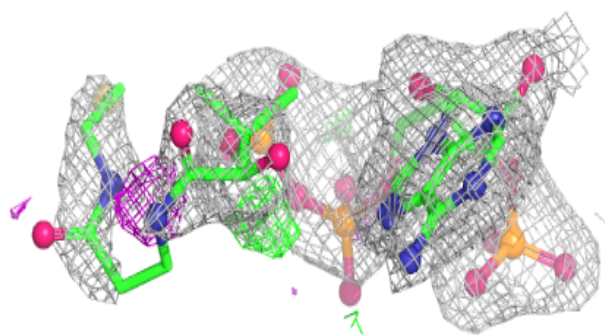
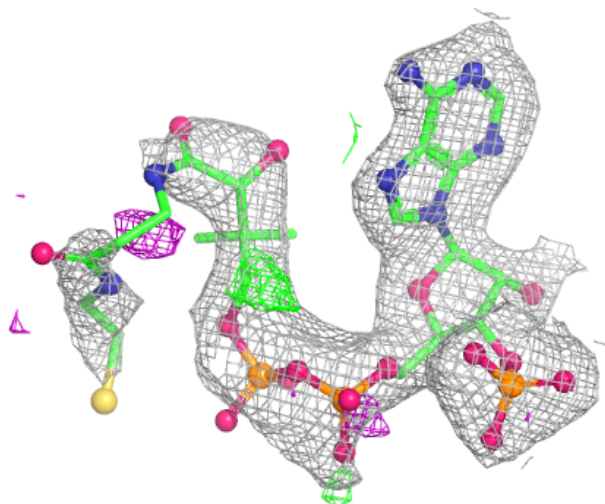
Electron density around COA D 501:

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



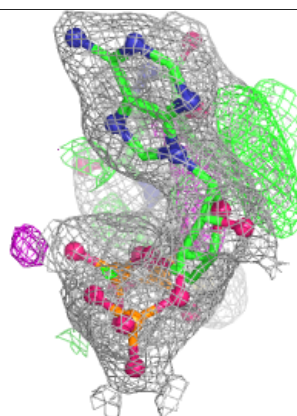
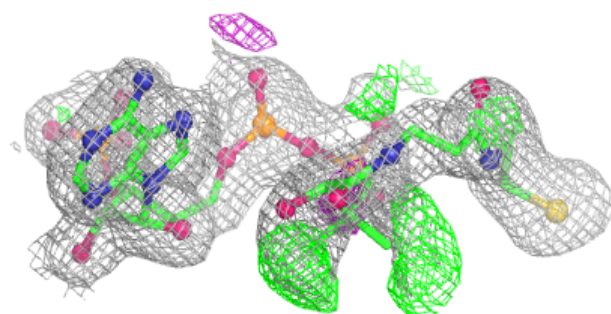
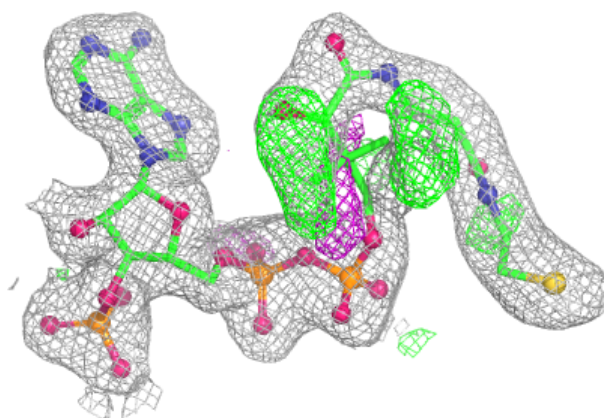
Electron density around COA E 501:

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



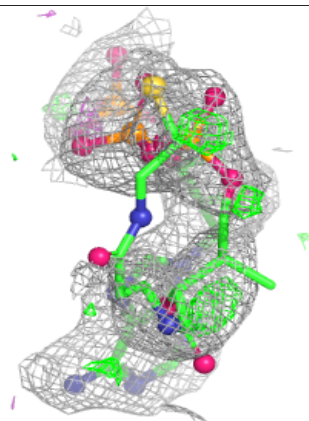
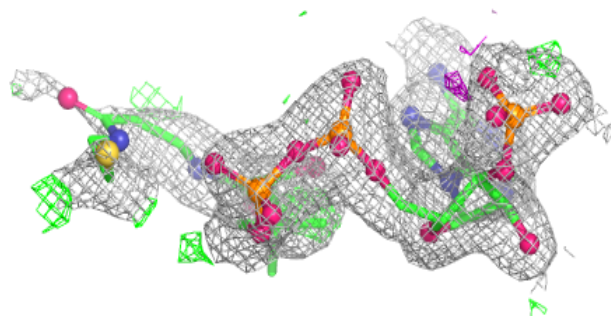
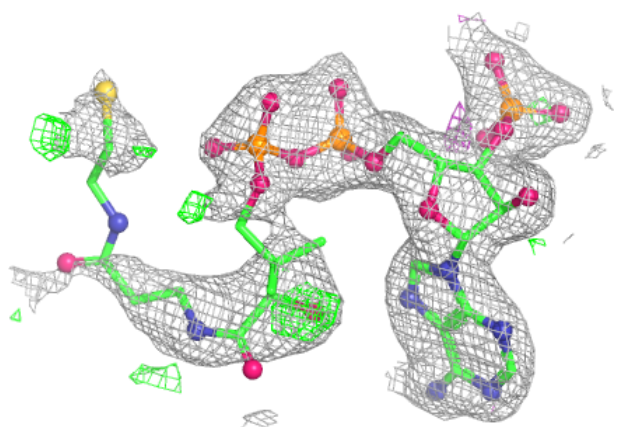
Electron density around COA F 501:

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



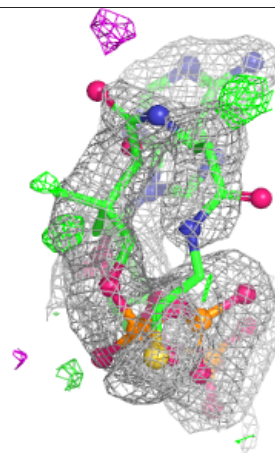
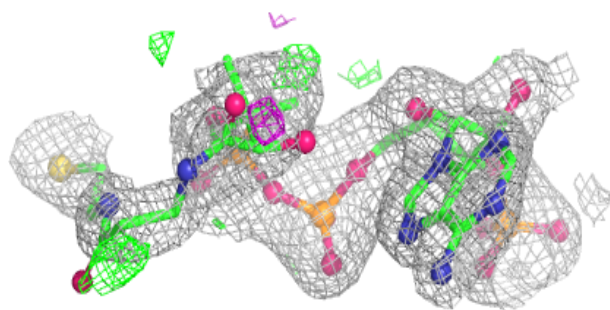
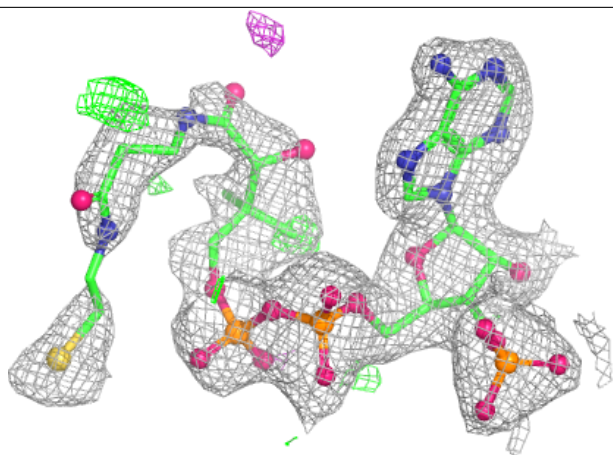
Electron density around COA B 501:

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



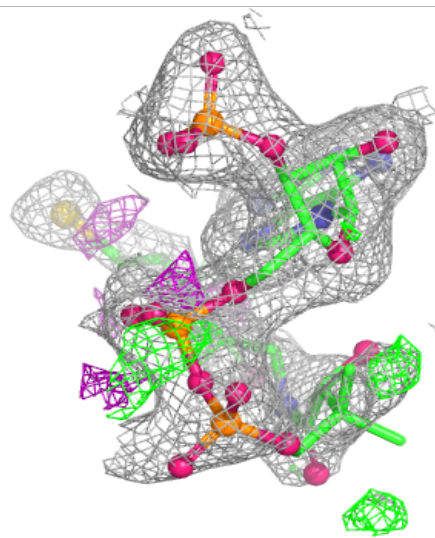
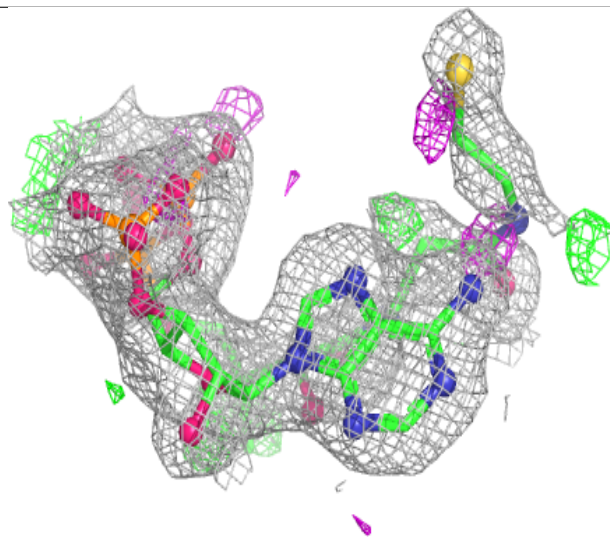
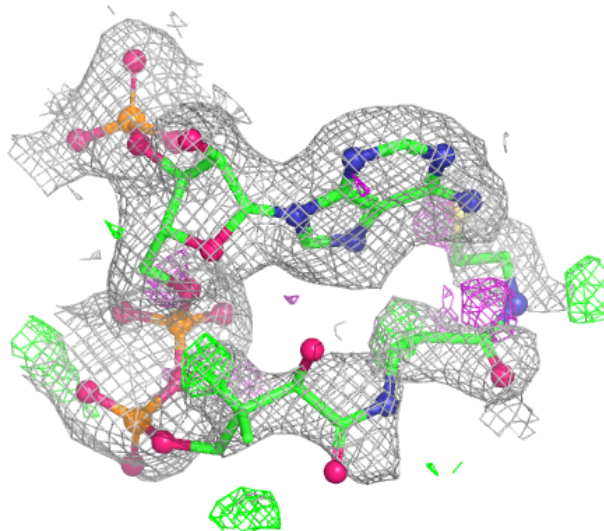
Electron density around COA A 501:

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



Electron density around COA C 501:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.