



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:28 PM UTC

PDB ID : 1T9B / pdb_00001t9b
Title : Crystal structure of yeast acetohydroxyacid synthase in complex with a sulfonylurea herbicide, chlorsulfuron
Authors : McCourt, J.A.; Pang, S.S.; Guddat, L.W.; Duggleby, R.G.
Deposited on : 2004-05-16
Resolution : 2.20 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

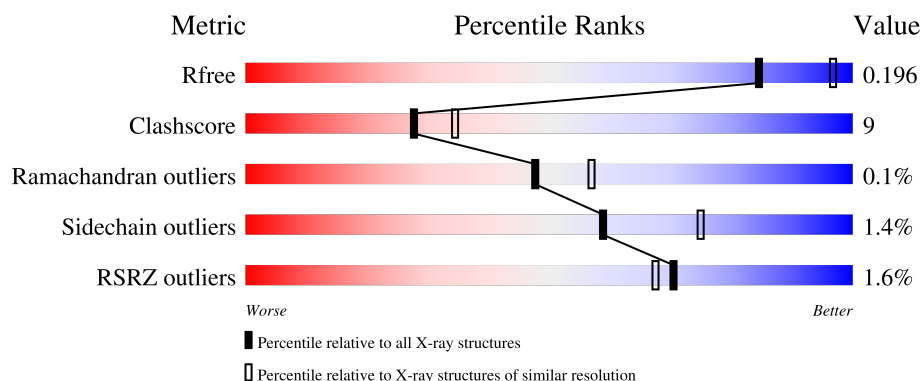
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	677	
1	B	677	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	1CS	A	695	-	X	-	-
4	1CS	B	1695	-	X	-	-
8	YF3	A	1705	X	X	-	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 10553 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 Acetolactate synthase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	583	Total	C	N	O	S	0	4	0
			4422	2798	766	837	21			
1	B	595	Total	C	N	O	S	0	9	0
			4566	2889	793	862	22			

There are 94 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	11	MET	-	cloning artifact	UNP P07342
A	12	HIS	-	cloning artifact	UNP P07342
A	13	HIS	-	cloning artifact	UNP P07342
A	14	HIS	-	cloning artifact	UNP P07342
A	15	HIS	-	cloning artifact	UNP P07342
A	16	HIS	-	cloning artifact	UNP P07342
A	17	HIS	-	cloning artifact	UNP P07342
A	18	SER	-	cloning artifact	UNP P07342
A	19	SER	-	cloning artifact	UNP P07342
A	20	GLY	-	cloning artifact	UNP P07342
A	21	LEU	-	cloning artifact	UNP P07342
A	22	VAL	-	cloning artifact	UNP P07342
A	23	PRO	-	cloning artifact	UNP P07342
A	24	ARG	-	cloning artifact	UNP P07342
A	25	GLY	-	cloning artifact	UNP P07342
A	26	SER	-	cloning artifact	UNP P07342
A	27	GLY	-	cloning artifact	UNP P07342
A	28	MET	-	cloning artifact	UNP P07342
A	29	LYS	-	cloning artifact	UNP P07342
A	30	GLU	-	cloning artifact	UNP P07342
A	31	THR	-	cloning artifact	UNP P07342
A	32	ALA	-	cloning artifact	UNP P07342
A	33	ALA	-	cloning artifact	UNP P07342
A	34	ALA	-	cloning artifact	UNP P07342
A	35	LYS	-	cloning artifact	UNP P07342

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	36	PHE	-	cloning artifact	UNP P07342
A	37	GLU	-	cloning artifact	UNP P07342
A	38	ARG	-	cloning artifact	UNP P07342
A	39	GLN	-	cloning artifact	UNP P07342
A	40	HIS	-	cloning artifact	UNP P07342
A	41	MET	-	cloning artifact	UNP P07342
A	42	ASP	-	cloning artifact	UNP P07342
A	43	SER	-	cloning artifact	UNP P07342
A	44	PRO	-	cloning artifact	UNP P07342
A	45	ASP	-	cloning artifact	UNP P07342
A	46	LEU	-	cloning artifact	UNP P07342
A	47	GLY	-	cloning artifact	UNP P07342
A	48	THR	-	cloning artifact	UNP P07342
A	49	ASP	-	cloning artifact	UNP P07342
A	50	ASP	-	cloning artifact	UNP P07342
A	51	ASP	-	cloning artifact	UNP P07342
A	52	ASP	-	cloning artifact	UNP P07342
A	53	LYS	-	cloning artifact	UNP P07342
A	54	ALA	-	cloning artifact	UNP P07342
A	55	MET	-	cloning artifact	UNP P07342
A	56	GLY	-	cloning artifact	UNP P07342
A	57	SER	-	cloning artifact	UNP P07342
B	11	MET	-	cloning artifact	UNP P07342
B	12	HIS	-	cloning artifact	UNP P07342
B	13	HIS	-	cloning artifact	UNP P07342
B	14	HIS	-	cloning artifact	UNP P07342
B	15	HIS	-	cloning artifact	UNP P07342
B	16	HIS	-	cloning artifact	UNP P07342
B	17	HIS	-	cloning artifact	UNP P07342
B	18	SER	-	cloning artifact	UNP P07342
B	19	SER	-	cloning artifact	UNP P07342
B	20	GLY	-	cloning artifact	UNP P07342
B	21	LEU	-	cloning artifact	UNP P07342
B	22	VAL	-	cloning artifact	UNP P07342
B	23	PRO	-	cloning artifact	UNP P07342
B	24	ARG	-	cloning artifact	UNP P07342
B	25	GLY	-	cloning artifact	UNP P07342
B	26	SER	-	cloning artifact	UNP P07342
B	27	GLY	-	cloning artifact	UNP P07342
B	28	MET	-	cloning artifact	UNP P07342
B	29	LYS	-	cloning artifact	UNP P07342
B	30	GLU	-	cloning artifact	UNP P07342

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	31	THR	-	cloning artifact	UNP P07342
B	32	ALA	-	cloning artifact	UNP P07342
B	33	ALA	-	cloning artifact	UNP P07342
B	34	ALA	-	cloning artifact	UNP P07342
B	35	LYS	-	cloning artifact	UNP P07342
B	36	PHE	-	cloning artifact	UNP P07342
B	37	GLU	-	cloning artifact	UNP P07342
B	38	ARG	-	cloning artifact	UNP P07342
B	39	GLN	-	cloning artifact	UNP P07342
B	40	HIS	-	cloning artifact	UNP P07342
B	41	MET	-	cloning artifact	UNP P07342
B	42	ASP	-	cloning artifact	UNP P07342
B	43	SER	-	cloning artifact	UNP P07342
B	44	PRO	-	cloning artifact	UNP P07342
B	45	ASP	-	cloning artifact	UNP P07342
B	46	LEU	-	cloning artifact	UNP P07342
B	47	GLY	-	cloning artifact	UNP P07342
B	48	THR	-	cloning artifact	UNP P07342
B	49	ASP	-	cloning artifact	UNP P07342
B	50	ASP	-	cloning artifact	UNP P07342
B	51	ASP	-	cloning artifact	UNP P07342
B	52	ASP	-	cloning artifact	UNP P07342
B	53	LYS	-	cloning artifact	UNP P07342
B	54	ALA	-	cloning artifact	UNP P07342
B	55	MET	-	cloning artifact	UNP P07342
B	56	GLY	-	cloning artifact	UNP P07342
B	57	SER	-	cloning artifact	UNP P07342

- Molecule 2 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total K 1 1	0	0
2	B	1	Total K 1 1	0	0

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

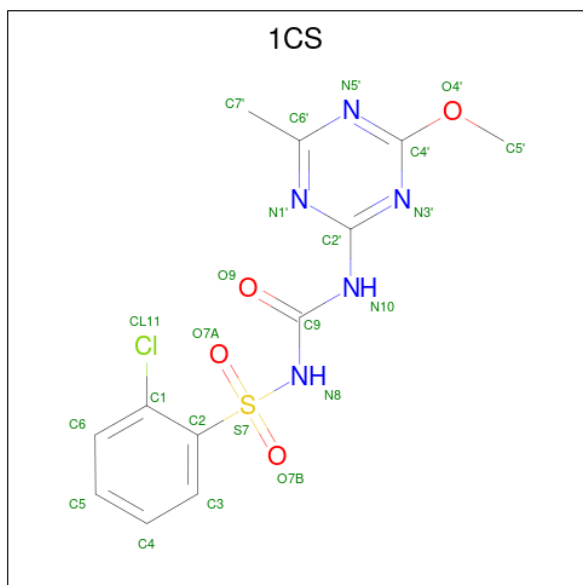
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0

Continued on next page...

Continued from previous page...

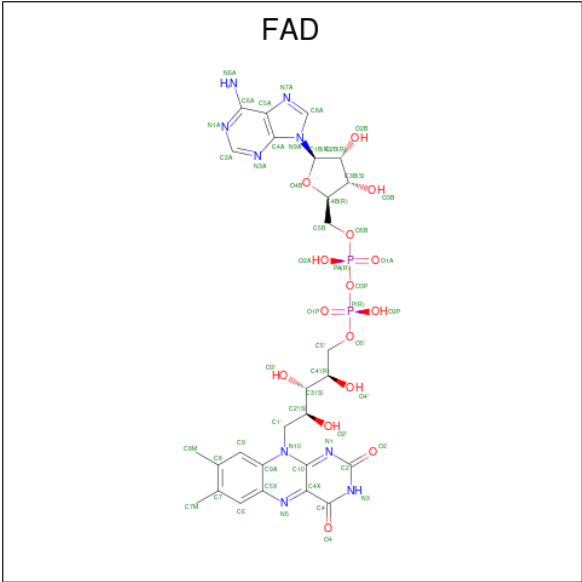
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 1-(2-CHLOROPHENYLSULFONYL)-3-(4-METHOXY-6-METHYL-L,3,5-TRIAZIN-2-YL)UREA (CCD ID: 1CS) (formula: $C_{12}H_{12}ClN_5O_4S$).



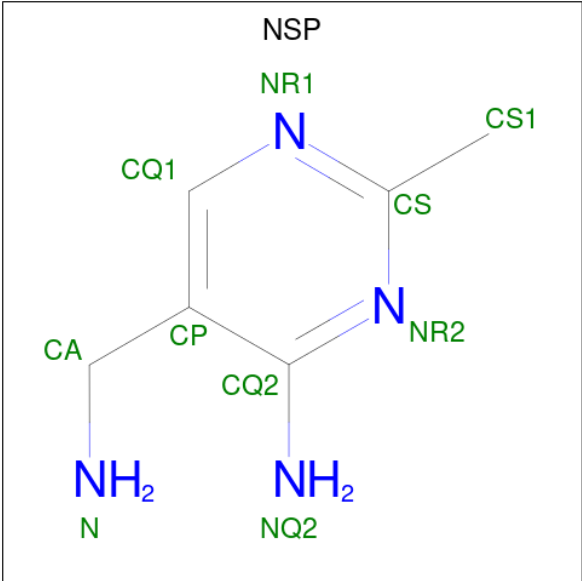
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total 23	C 12	Cl 1	N 5	O 4	S 1	0	0
4	B	1	Total 23	C 12	Cl 1	N 5	O 4	S 1	0	0

- Molecule 5 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



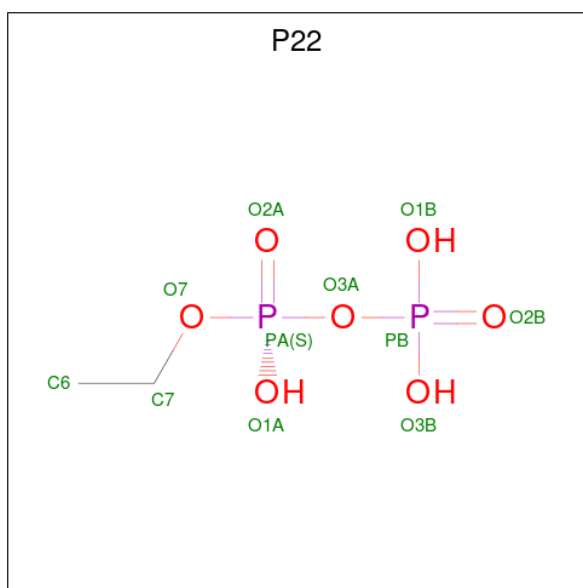
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total 53	C 27	N 9	O 15	P 2	0	0
5	B	1	Total 53	C 27	N 9	O 15	P 2	0	0

- Molecule 6 is 5-(AMINOMETHYL)-2-METHYLPYRIMIDIN-4-AMINE (CCD ID: NSP) (formula: C₆H₁₀N₄).



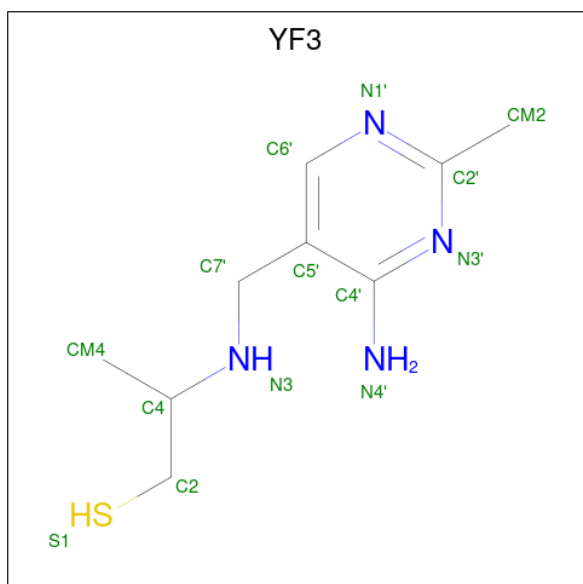
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	N	0	0
			10	6	4		

- Molecule 7 is ETHYL DIHYDROGEN DIPHOSPHATE (CCD ID: P22) (formula: $C_2H_8O_7P_2$).



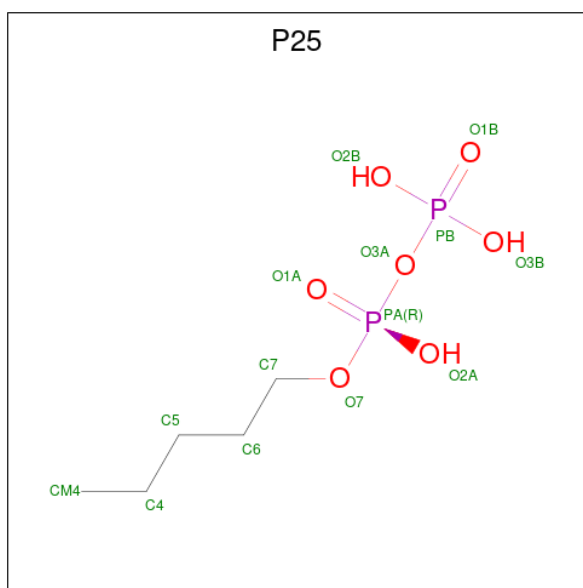
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	O	P	0	0
			11	2	7	2		

- Molecule 8 is 2-[[[4-AMINO-2-METHYLPYRIMIDIN-5-YL)METHYL]AMINO}PROPAN E-1-THIOL (CCD ID: YF3) (formula: $C_9H_{16}N_4S$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	S	0	0
			14	9	4	1		

- Molecule 9 is PENTYL TRIHYDROGEN DIPHOSPHATE (CCD ID: P25) (formula: $C_5H_{14}O_7P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	1	Total	C	O	P	0	0
			14	5	7	2		

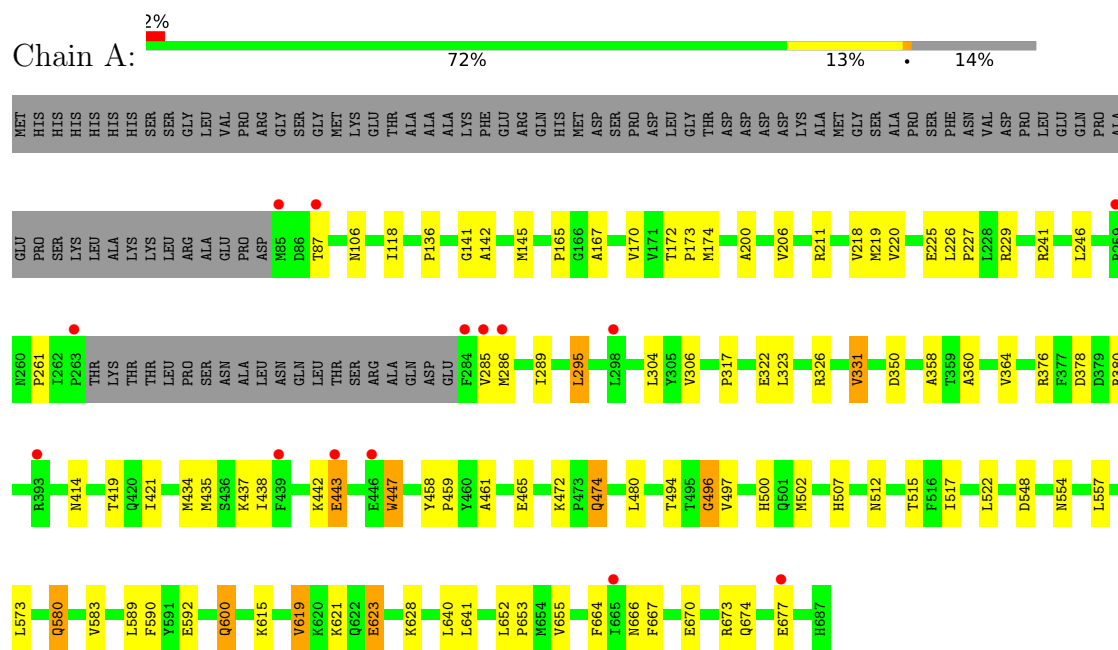
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	614	Total	O	0	0
			614	614		
10	B	746	Total	O	0	0
			746	746		

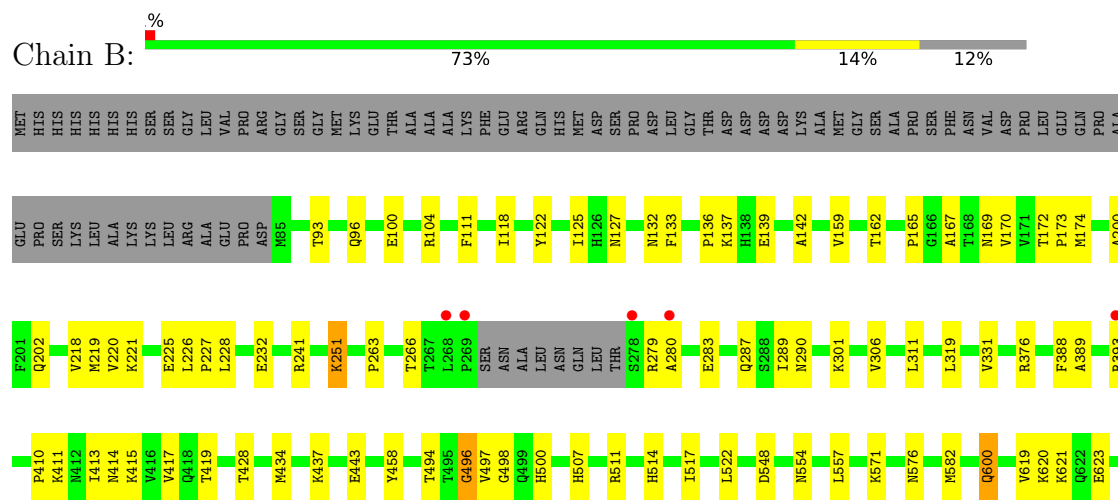
3 Residue-property plots

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: Acetolactate synthase, mitochondrial



- Molecule 1: Acetolactate synthase, mitochondrial



K628		F632		V639		E644		L652		E670		R673		R687
L640		L641		P653		Q674								

4 Data and refinement statistics

Property	Value	Source
Space group	P 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	154.58Å 154.58Å 178.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 50.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	90.5 (50.00-2.20) 90.5 (50.00-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.58 (at 2.20Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.162 , 0.195 0.165 , 0.196	Depositor DCC
R_{free} test set	10345 reflections (10.05%)	wwPDB-VP
Wilson B-factor (Å ²)	18.3	Xtriage
Anisotropy	0.304	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 57.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10553	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.59% 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: K, FAD, NSP, YF3, P22, MG, 1CS, P25

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	0/4530	0.85	7/6152 (0.1%)
1	B	0.37	0/4696	0.89	8/6370 (0.1%)
All	All	0.35	0/9226	0.87	15/12522 (0.1%)

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	496	GLY	N-CA-C	-6.90	102.61	112.55
1	B	331	VAL	N-CA-C	6.75	117.55	108.11
1	B	306	VAL	N-CA-C	6.53	118.00	108.53
1	B	507	HIS	N-CA-C	6.30	120.96	113.28
1	A	306	VAL	N-CA-C	6.07	117.75	108.71
1	A	507	HIS	N-CA-C	5.82	120.24	113.20
1	B	376	ARG	N-CA-C	5.75	119.60	112.59
1	B	458	TYR	N-CA-C	5.65	119.25	108.97
1	A	496	GLY	N-CA-C	-5.64	102.95	112.77
1	A	331	VAL	N-CA-C	5.54	115.86	108.11
1	B	576	ASN	N-CA-C	5.28	116.85	108.67
1	A	376	ARG	N-CA-C	5.21	118.66	112.72
1	B	241	ARG	N-CA-C	-5.15	102.08	109.24
1	A	241	ARG	N-CA-C	-5.04	102.23	109.24
1	A	580	GLN	N-CA-C	-5.04	99.79	108.56

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	4422	0	4380	85	0
1	B	4566	0	4554	80	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	23	0	12	1	0
4	B	23	0	12	1	0
5	A	53	0	31	0	0
5	B	53	0	31	0	0
6	A	10	0	10	2	0
7	A	11	0	5	3	0
8	A	14	0	15	5	0
9	B	14	0	11	5	0
10	A	614	0	0	5	0
10	B	746	0	0	14	0
All	All	10553	0	9061	165	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 9.

All (165) 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:474:GLN:HE21	1:A:474:GLN:H	1.27	0.82
1:B:619:VAL:HG22	1:B:628:LYS:HG3	1.63	0.80
1:B:600:GLN:NE2	1:B:600:GLN:H	1.79	0.79
1:B:280:ALA:HA	10:B:4669:HOH:O	1.84	0.77
1:A:621:LYS:HB3	1:A:623:GLU:OE2	1.84	0.76
1:A:474:GLN:H	1:A:474:GLN:NE2	1.84	0.75
6:A:704:NSP:HN1	9:B:698:P25:H42	1.51	0.75
1:A:435:MET:HE3	1:A:435:MET:HA	1.69	0.74
1:A:623:GLU:H	1:A:623:GLU:CD	1.93	0.74
4:A:695:1CS:H5	1:B:200:ALA:HB1	1.70	0.74
6:A:704:NSP:N	9:B:698:P25:H42	2.02	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:580:GLN:HE21	1:A:600:GLN:HG3	1.54	0.73
1:A:200:ALA:HB1	4:B:1695:1CS:H5	1.71	0.73
1:B:619:VAL:HG23	1:B:641:LEU:HD11	1.71	0.73
1:A:666:ASN:ND2	1:A:667:PHE:H	1.88	0.71
1:B:600:GLN:H	1:B:600:GLN:HE21	1.39	0.71
1:B:132[A]:ASN:HD22	1:B:133:PHE:N	1.90	0.70
1:A:619:VAL:HG22	1:A:628:LYS:HG3	1.72	0.70
1:B:393:ARG:NH2	1:B:417:VAL:HG21	2.08	0.69
1:A:442:LYS:HG2	1:A:443:GLU:HG3	1.74	0.69
1:B:410:PRO:HA	10:B:4360:HOH:O	1.92	0.69
1:A:619:VAL:HG23	1:A:641:LEU:HD11	1.74	0.68
1:A:286:MET:HE2	1:A:437:LYS:HE3	1.75	0.68
1:A:167:ALA:O	1:A:170[B]:VAL:HG12	1.96	0.66
1:B:251:LYS:C	1:B:251:LYS:HD3	2.21	0.66
1:A:580:GLN:NE2	1:A:600:GLN:HG3	2.12	0.65
1:A:170[B]:VAL:HG13	1:A:174:MET:HE2	1.79	0.65
1:A:286:MET:HE3	1:A:289:ILE:HB	1.78	0.65
1:B:413:ILE:HD12	10:B:4360:HOH:O	1.97	0.64
1:B:136:PRO:HG3	1:B:142:ALA:HB2	1.80	0.63
1:B:415:LYS:HB2	10:B:4987:HOH:O	1.99	0.62
1:A:583:VAL:HG23	8:A:1705:YF3:H21	1.81	0.62
1:B:221:LYS:N	1:B:225[A]:GLU:OE1	2.29	0.62
1:A:170[A]:VAL:HG23	1:A:174:MET:HE2	1.82	0.62
1:B:127:ASN:HB3	10:B:5137:HOH:O	1.98	0.62
1:B:228:LEU:HB2	1:B:266:THR:HB	1.82	0.62
1:A:136:PRO:HG3	1:A:142:ALA:HB2	1.83	0.61
1:B:623:GLU:H	1:B:623:GLU:CD	2.09	0.61
1:A:167:ALA:O	1:A:170[A]:VAL:HG22	2.02	0.60
1:A:670:GLU:O	1:A:674:GLN:HG3	2.03	0.59
1:B:172:THR:HB	1:B:173:PRO:HD3	1.85	0.59
1:A:172:THR:HB	1:A:173:PRO:HD3	1.85	0.59
1:A:600:GLN:HB2	1:B:137:LYS:HE3	1.85	0.59
1:B:221:LYS:HE3	10:B:4432:HOH:O	2.03	0.59
1:B:226:LEU:HB3	1:B:227:PRO:HD3	1.84	0.58
1:B:104[B]:ARG:HH11	1:B:104[B]:ARG:HG3	1.68	0.58
1:B:389:ALA:O	1:B:393:ARG:HG2	2.03	0.58
1:A:358:ALA:HB3	1:A:458:TYR:HB3	1.86	0.58
1:A:326:ARG:CD	1:A:435:MET:HE2	2.35	0.56
1:A:226:LEU:HB3	1:A:227:PRO:HD3	1.86	0.56
1:A:677:GLU:HG2	10:A:4504:HOH:O	2.05	0.56
1:B:620:LYS:HE2	1:B:644:GLU:OE2	2.06	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:496:GLY:H	1:B:500:HIS:HE1	1.53	0.55
1:A:619:VAL:CG2	1:A:641:LEU:HD11	2.37	0.54
1:B:283:GLU:O	1:B:287:GLN:HG3	2.06	0.54
1:B:289:ILE:HG23	1:B:434:MET:HB2	1.89	0.54
1:B:498:GLY:C	1:B:582[B]:MET:HE2	2.32	0.54
1:B:132[A]:ASN:HD22	1:B:133:PHE:H	1.55	0.54
1:A:465:GLU:HG3	1:A:472:LYS:HG2	1.89	0.54
1:A:496:GLY:H	1:A:500:HIS:HE1	1.54	0.54
1:A:295:LEU:HD12	1:A:421:ILE:HD12	1.90	0.54
1:A:497:VAL:O	7:A:1702:P22:H62	2.07	0.53
1:B:167:ALA:O	1:B:170:VAL:HG22	2.07	0.53
1:A:87:THR:HG22	1:A:261:PRO:HG3	1.91	0.53
1:A:640:LEU:HD23	1:A:640:LEU:C	2.33	0.53
1:B:170:VAL:HG23	1:B:174:MET:HE2	1.91	0.53
1:B:411:LYS:HE3	10:B:4988:HOH:O	2.08	0.52
1:B:104[B]:ARG:HG3	1:B:104[B]:ARG:NH1	2.23	0.52
1:A:211[A]:ARG:HD2	10:A:4620:HOH:O	2.09	0.52
1:A:474:GLN:HE21	1:A:474:GLN:N	2.02	0.52
1:A:218:VAL:HG22	1:A:219:MET:N	2.25	0.52
1:A:592:GLU:HG2	10:A:4859:HOH:O	2.10	0.51
1:A:512:ASN:HB2	1:A:515:THR:HG21	1.91	0.51
1:A:289:ILE:HG23	1:A:434:MET:HB2	1.93	0.51
1:A:322:GLU:OE2	1:A:435:MET:HG2	2.10	0.51
1:A:326:ARG:HD2	1:A:435:MET:HE2	1.92	0.51
1:A:447:TRP:CE3	1:A:447:TRP:HA	2.46	0.51
1:B:413:ILE:HB	10:B:4360:HOH:O	2.09	0.51
1:B:311:LEU:O	1:B:514:HIS:HE1	1.94	0.51
1:B:220:VAL:HG13	1:B:225[A]:GLU:HG3	1.93	0.50
1:B:132[A]:ASN:ND2	1:B:133:PHE:N	2.57	0.50
1:A:165:PRO:HD3	1:B:522:LEU:HG	1.93	0.50
1:A:414:ASN:ND2	1:A:419:THR:H	2.10	0.50
1:A:522:LEU:O	1:B:202:GLN:HG2	2.12	0.50
1:B:290:ASN:OD1	1:B:437:LYS:HD3	2.12	0.50
1:B:673:ARG:HG2	10:B:4687:HOH:O	2.12	0.50
1:A:522:LEU:HG	1:B:165:PRO:HD3	1.94	0.49
1:A:304:LEU:HB2	1:A:331:VAL:HG22	1.94	0.49
1:A:447:TRP:HA	1:A:447:TRP:HE3	1.77	0.49
1:B:443:GLU:HG3	10:B:4982:HOH:O	2.14	0.48
1:B:496:GLY:N	1:B:500:HIS:HE1	2.11	0.48
1:A:480:LEU:HD22	1:A:573:LEU:HD22	1.95	0.48
1:B:670:GLU:O	1:B:674:GLN:HG3	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:295:LEU:HD12	1:A:421:ILE:CD1	2.43	0.48
1:A:326:ARG:HD3	1:A:435:MET:HE2	1.95	0.47
7:A:1702:P22:H61	8:A:1705:YF3:HM41	1.95	0.47
1:B:170:VAL:C	1:B:173:PRO:HD2	2.39	0.47
1:B:388:PHE:HD2	1:B:393:ARG:HH21	1.60	0.47
1:A:496:GLY:N	1:A:500:HIS:HE1	2.13	0.47
1:B:263:PRO:HB2	1:B:266:THR:HG23	1.96	0.47
1:B:411:LYS:HB3	1:B:411:LYS:NZ	2.29	0.46
1:A:494:THR:HG22	1:A:517:ILE:HB	1.96	0.46
7:A:1702:P22:H61	8:A:1705:YF3:H22	1.98	0.46
1:B:218:VAL:HG22	1:B:219:MET:N	2.31	0.46
1:B:494:THR:HA	1:B:517:ILE:O	2.15	0.46
1:B:319:LEU:HD12	1:B:428:THR:HG23	1.98	0.46
1:B:582[A]:MET:HB3	9:B:698:P25:H51	1.96	0.46
1:B:619:VAL:HG22	1:B:628:LYS:CG	2.39	0.46
1:B:228:LEU:O	1:B:232:GLU:HG3	2.16	0.46
1:A:666:ASN:HD22	1:A:667:PHE:H	1.64	0.45
1:A:600:GLN:H	1:A:600:GLN:CD	2.19	0.45
1:A:434:MET:HE3	1:A:438:ILE:HD11	1.98	0.45
1:A:494:THR:HA	1:A:517:ILE:O	2.16	0.45
1:B:582[B]:MET:HB3	9:B:698:P25:H51	1.98	0.45
1:A:285:VAL:O	1:A:289:ILE:HG13	2.16	0.45
1:A:378:ASP:OD2	1:A:380:ARG:HB2	2.17	0.45
1:B:571:LYS:HB3	1:B:632:PHE:CZ	2.52	0.45
1:B:100:GLU:HG3	1:B:104[B]:ARG:NH1	2.32	0.45
1:A:589:LEU:C	1:A:589:LEU:HD13	2.42	0.44
8:A:1705:YF3:H7'2	1:B:162:THR:HG21	1.99	0.44
1:B:600:GLN:HE21	1:B:600:GLN:N	2.10	0.44
1:A:323:LEU:HD13	1:A:435:MET:HE1	2.00	0.44
1:A:652:LEU:HA	1:A:653:PRO:C	2.43	0.44
1:A:666:ASN:ND2	1:A:667:PHE:N	2.63	0.44
1:B:301:LYS:HD3	10:B:4742:HOH:O	2.16	0.44
1:B:621:LYS:HB3	1:B:623:GLU:OE1	2.17	0.43
1:B:640:LEU:C	1:B:640:LEU:HD23	2.42	0.43
1:B:652:LEU:HA	1:B:653:PRO:C	2.43	0.43
1:A:206:VAL:HG21	10:A:4021:HOH:O	2.17	0.43
1:B:93:THR:OG1	1:B:96:GLN:HG3	2.18	0.43
1:B:414:ASN:ND2	1:B:419:THR:H	2.16	0.43
1:A:502:MET:HA	1:A:502:MET:HE2	2.01	0.43
1:B:496:GLY:CA	1:B:500:HIS:HE1	2.31	0.43
1:A:246:LEU:C	1:A:246:LEU:HD23	2.44	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:323:LEU:HA	1:A:435:MET:HE1	2.01	0.42
1:A:619:VAL:HG22	1:A:628:LYS:CG	2.46	0.42
1:B:111:PHE:O	1:B:159:VAL:HA	2.19	0.42
1:B:139:GLU:HB2	1:B:169:ASN:HB3	2.01	0.42
1:A:118:ILE:HG13	1:A:118:ILE:O	2.19	0.42
1:B:497:VAL:HG12	9:B:698:P25:H41	2.02	0.42
1:A:286:MET:HE3	1:A:286:MET:HA	2.02	0.42
1:A:358:ALA:HB3	1:A:458:TYR:CB	2.50	0.42
1:B:221:LYS:HB2	10:B:4910:HOH:O	2.19	0.41
1:A:589:LEU:HD12	1:A:590:PHE:CE1	2.55	0.41
1:A:360:ALA:O	1:A:364:VAL:HG23	2.20	0.41
1:A:655:VAL:HG22	1:A:664:PHE:HB3	2.01	0.41
8:A:1705:YF3:HM22	1:B:165:PRO:HB2	2.03	0.41
1:A:554:ASN:HA	1:A:557:LEU:HD23	2.02	0.41
1:A:141:GLY:O	1:A:145:MET:HG3	2.21	0.41
1:A:220:VAL:HG13	1:A:225:GLU:HG3	2.02	0.41
1:A:673:ARG:O	1:A:677:GLU:HG3	2.20	0.41
1:A:459:PRO:O	1:A:461:ALA:N	2.54	0.41
1:B:494:THR:HG22	1:B:517:ILE:HB	2.02	0.41
1:B:554:ASN:HA	1:B:557:LEU:HD23	2.03	0.41
1:B:279:ARG:HD2	10:B:4666:HOH:O	2.19	0.41
1:A:286:MET:CE	1:A:437:LYS:HE3	2.49	0.41
1:A:317:PRO:HG2	10:A:4104:HOH:O	2.19	0.41
1:B:122:TYR:HA	1:B:125:ILE:HG12	2.01	0.41
1:B:118:ILE:O	1:B:118:ILE:HG13	2.21	0.41
1:A:225:GLU:O	1:A:229:ARG:HG2	2.22	0.40
1:B:514:HIS:HD2	10:B:5035:HOH:O	2.03	0.40
1:B:571:LYS:HD2	1:B:639:VAL:CG1	2.51	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)
1:B:511:ARG:NH2	1:B:511:ARG:NH2[5_556]	2.19	0.01

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	583/677 (86%)	572 (98%)	10 (2%)	1 (0%)	43	51
1	B	600/677 (89%)	588 (98%)	12 (2%)	0	100	100
All	All	1183/1354 (87%)	1160 (98%)	22 (2%)	1 (0%)	48	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	350	ASP

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	470/556 (84%)	460 (98%)	10 (2%)	47	63
1	B	492/556 (88%)	489 (99%)	3 (1%)	78	89
All	All	962/1112 (86%)	949 (99%)	13 (1%)	59	75

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	106	ASN
1	A	295	LEU
1	A	443	GLU
1	A	447	TRP
1	A	474	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	548	ASP
1	A	600	GLN
1	A	615	LYS
1	A	619	VAL
1	A	623	GLU
1	B	251	LYS
1	B	548	ASP
1	B	600	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	106	ASN
1	A	126	HIS
1	A	132	ASN
1	A	169	ASN
1	A	287	GLN
1	A	312	ASN
1	A	414	ASN
1	A	452	ASN
1	A	474	GLN
1	A	499	GLN
1	A	500	HIS
1	A	580	GLN
1	A	587	GLN
1	A	602	ASN
1	A	666	ASN
1	B	99	ASN
1	B	106	ASN
1	B	126	HIS
1	B	127	ASN
1	B	169	ASN
1	B	414	ASN
1	B	499	GLN
1	B	500	HIS
1	B	514	HIS
1	B	587	GLN
1	B	600	GLN
1	B	602	ASN
1	B	687	HIS

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 ⓘ

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 for Mogul analysis.

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$
8	YF3	A	1705	-	14,14,14	2.41	5 (35%)	17,18,18	7.51	9 (52%)
4	1CS	A	695	-	24,24,24	3.38	14 (58%)	34,34,34	4.18	15 (44%)
9	P25	B	698	3	12,13,13	1.99	5 (41%)	16,18,18	3.84	2 (12%)
6	NSP	A	704	-	10,10,10	2.27	3 (30%)	13,13,13	2.74	6 (46%)
5	FAD	B	1701	-	58,58,58	2.70	26 (44%)	85,89,89	1.53	13 (15%)
7	P22	A	1702	3	9,10,10	2.31	4 (44%)	13,15,15	2.28	2 (15%)
5	FAD	A	701	-	58,58,58	2.81	26 (44%)	85,89,89	1.56	15 (17%)
4	1CS	B	1695	-	24,24,24	3.23	14 (58%)	34,34,34	4.09	15 (44%)

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
8	YF3	A	1705	-	1/1/1/2	5/6/7/7	0/1/1/1
4	1CS	A	695	-	-	6/17/17/17	0/2/2/2
9	P25	B	698	3	-	1/13/13/13	-
6	NSP	A	704	-	-	0/1/2/2	0/1/1/1
5	FAD	B	1701	-	-	1/34/50/50	0/6/6/6
7	P22	A	1702	3	-	2/10/10/10	-
5	FAD	A	701	-	-	3/34/50/50	0/6/6/6
4	1CS	B	1695	-	-	5/17/17/17	0/2/2/2

All (97) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1701	FAD	C4A-N3A	7.65	1.48	1.34
5	A	701	FAD	C4A-N3A	7.57	1.48	1.34
5	A	701	FAD	C2A-N1A	6.79	1.46	1.33
5	B	1701	FAD	C2A-N1A	6.50	1.45	1.33
5	A	701	FAD	C5A-C4A	6.23	1.50	1.39
4	A	695	1CS	C6'-N5'	6.09	1.44	1.34
5	A	701	FAD	C8A-N9A	5.78	1.47	1.37
5	B	1701	FAD	C5A-C4A	5.61	1.49	1.39
5	B	1701	FAD	C8A-N9A	5.60	1.47	1.37
5	A	701	FAD	C5A-C6A	5.51	1.56	1.41
4	A	695	1CS	C1-C2	5.43	1.47	1.40
4	B	1695	1CS	C6'-N5'	5.34	1.43	1.34
4	B	1695	1CS	C4-C3	5.25	1.47	1.38
4	A	695	1CS	C4-C3	5.24	1.47	1.38
4	B	1695	1CS	C1-C2	5.22	1.47	1.40
5	B	1701	FAD	C5A-C6A	5.14	1.55	1.41
4	A	695	1CS	C4'-N5'	5.05	1.42	1.33
4	A	695	1CS	O4'-C4'	5.00	1.45	1.33
4	A	695	1CS	C6'-N1'	4.99	1.42	1.34
4	B	1695	1CS	C4'-N5'	4.78	1.42	1.33
4	A	695	1CS	C3-C2	4.76	1.44	1.39
4	B	1695	1CS	O4'-C4'	4.71	1.44	1.33
4	B	1695	1CS	C6'-N1'	4.65	1.42	1.34
5	B	1701	FAD	C1'-C2'	-4.60	1.46	1.52
4	B	1695	1CS	C3-C2	4.56	1.44	1.39
5	A	701	FAD	C1'-C2'	-4.52	1.46	1.52
5	A	701	FAD	O4'-C4'	4.50	1.52	1.43
8	A	1705	YF3	C4-N3	-4.49	1.41	1.48
4	B	1695	1CS	C5-C4	4.48	1.48	1.38
4	A	695	1CS	C5-C4	4.44	1.48	1.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	701	FAD	C9A-C5X	4.43	1.48	1.41
5	B	1701	FAD	O4'-C4'	4.33	1.52	1.43
8	A	1705	YF3	C7'-C5'	-4.23	1.37	1.51
7	A	1702	P22	PA-O7	-4.19	1.43	1.59
5	B	1701	FAD	C9A-C5X	4.18	1.47	1.41
5	A	701	FAD	O3'-C3'	4.06	1.53	1.43
5	B	1701	FAD	O3'-C3'	3.97	1.52	1.43
8	A	1705	YF3	CM2-C2'	-3.96	1.38	1.49
5	A	701	FAD	C2A-N3A	3.93	1.40	1.33
5	A	701	FAD	C6A-N1A	3.91	1.46	1.35
5	B	1701	FAD	C6A-N1A	3.87	1.46	1.35
6	A	704	NSP	CS1-CS	-3.80	1.39	1.49
6	A	704	NSP	CA-CP	-3.69	1.38	1.51
5	A	701	FAD	C5'-C4'	-3.69	1.46	1.51
5	A	701	FAD	C4X-N5	3.58	1.38	1.30
4	A	695	1CS	C2'-N1'	3.55	1.44	1.34
5	B	1701	FAD	C5'-C4'	-3.52	1.47	1.51
5	B	1701	FAD	C2A-N3A	3.43	1.40	1.33
9	B	698	P25	PA-O7	-3.38	1.46	1.59
4	B	1695	1CS	C2'-N1'	3.38	1.44	1.34
5	B	1701	FAD	C4X-N5	3.33	1.37	1.30
5	B	1701	FAD	C10-N1	3.19	1.39	1.33
5	A	701	FAD	C10-N1	3.17	1.39	1.33
7	A	1702	P22	PA-O3A	3.15	1.62	1.59
5	B	1701	FAD	C3B-C4B	3.12	1.60	1.53
4	B	1695	1CS	C6-C1	3.00	1.44	1.38
4	A	695	1CS	C6-C1	2.96	1.44	1.38
9	B	698	P25	PA-O1A	-2.89	1.40	1.50
7	A	1702	P22	PA-O1A	-2.87	1.42	1.55
4	B	1695	1CS	C2'-N10	-2.83	1.35	1.38
9	B	698	P25	PA-O2A	-2.80	1.42	1.55
5	A	701	FAD	C1B-N9A	2.80	1.54	1.46
5	B	1701	FAD	P-O2P	-2.77	1.42	1.55
5	A	701	FAD	C6-C7	2.73	1.43	1.39
4	A	695	1CS	C2'-N10	-2.72	1.35	1.38
5	A	701	FAD	C6-C5X	2.70	1.44	1.40
9	B	698	P25	PB-O1B	-2.70	1.42	1.50
5	A	701	FAD	C3B-C4B	2.69	1.59	1.53
5	A	701	FAD	P-O2P	-2.69	1.42	1.55
5	A	701	FAD	C8-C7	2.68	1.47	1.40
5	B	1701	FAD	C8-C7	2.67	1.47	1.40
4	A	695	1CS	C4'-N3'	2.57	1.38	1.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	698	P25	PB-O2B	-2.57	1.45	1.54
5	B	1701	FAD	C6-C7	2.51	1.43	1.39
4	A	695	1CS	C2'-N3'	2.46	1.41	1.34
5	B	1701	FAD	C1B-N9A	2.44	1.53	1.46
7	A	1702	P22	O7-C7	-2.43	1.30	1.44
5	A	701	FAD	C9-C9A	2.43	1.43	1.39
4	B	1695	1CS	C4'-N3'	2.41	1.37	1.33
4	B	1695	1CS	C7'-C6'	-2.39	1.43	1.49
4	A	695	1CS	C7'-C6'	-2.34	1.43	1.49
5	B	1701	FAD	C6-C5X	2.33	1.43	1.40
6	A	704	NSP	CQ1-CP	2.33	1.42	1.37
5	A	701	FAD	C10-N10	2.32	1.42	1.37
8	A	1705	YF3	C2'-N3'	2.31	1.38	1.34
5	B	1701	FAD	C9-C9A	2.25	1.43	1.39
5	A	701	FAD	PA-O5B	-2.22	1.50	1.59
5	A	701	FAD	PA-O2A	-2.22	1.45	1.55
5	B	1701	FAD	C5A-N7A	-2.22	1.35	1.39
5	A	701	FAD	C5A-N7A	-2.22	1.35	1.39
5	B	1701	FAD	PA-O2A	-2.19	1.45	1.55
4	B	1695	1CS	C2'-N3'	2.18	1.40	1.34
5	A	701	FAD	C9-C8	2.16	1.42	1.39
5	B	1701	FAD	C10-N10	2.13	1.41	1.37
5	B	1701	FAD	PA-O5B	-2.09	1.51	1.59
8	A	1705	YF3	C4'-N3'	2.06	1.37	1.35
5	B	1701	FAD	C9-C8	2.03	1.42	1.39

All (77) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1705	YF3	C4-C2-S1	25.39	142.79	114.16
9	B	698	P25	O7-C7-C6	14.49	160.67	109.28
4	A	695	1CS	C4'-N3'-C2'	11.57	122.31	112.86
4	A	695	1CS	C1-C2-S7	11.50	131.13	123.19
4	B	1695	1CS	C4'-N3'-C2'	11.29	122.08	112.86
4	B	1695	1CS	C1-C2-S7	11.20	130.92	123.19
8	A	1705	YF3	C5'-C7'-N3	11.03	142.79	112.56
8	A	1705	YF3	CM4-C4-C2	8.84	124.14	111.62
4	A	695	1CS	O7B-S7-N8	-7.65	84.87	106.77
4	B	1695	1CS	O7B-S7-N8	-7.34	85.74	106.77
7	A	1702	P22	O7-C7-C6	6.90	151.89	110.80
4	A	695	1CS	O7B-S7-C2	-6.79	96.48	107.68
4	B	1695	1CS	O7B-S7-C2	-6.48	96.99	107.68

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1695	1CS	O7A-S7-C2	6.45	118.33	107.68
4	A	695	1CS	O7A-S7-C2	6.42	118.28	107.68
8	A	1705	YF3	C7'-N3-C4	6.26	127.52	114.80
4	B	1695	1CS	O7A-S7-N8	5.82	123.44	106.77
4	A	695	1CS	O7A-S7-N8	5.71	123.13	106.77
4	A	695	1CS	C3-C2-S7	-5.36	109.81	117.51
6	A	704	NSP	CP-CA-N	5.25	142.76	114.98
4	B	1695	1CS	C2'-N10-C9	-5.19	125.00	130.34
4	B	1695	1CS	C3-C2-S7	-5.17	110.08	117.51
4	A	695	1CS	C2'-N10-C9	-5.13	125.06	130.34
5	A	701	FAD	C4A-N9A-C1B	4.92	138.13	126.63
8	A	1705	YF3	C6'-N1'-C2'	4.78	123.93	116.07
6	A	704	NSP	CQ1-NR1-CS	4.68	123.77	116.07
4	A	695	1CS	N8-C9-N10	-4.60	107.56	114.87
5	B	1701	FAD	C4A-N9A-C1B	4.60	137.39	126.63
4	B	1695	1CS	N8-C9-N10	-4.53	107.67	114.87
4	B	1695	1CS	N3'-C2'-N1'	-4.37	119.09	126.26
4	A	695	1CS	N3'-C2'-N1'	-4.34	119.15	126.26
8	A	1705	YF3	N1'-C2'-N3'	-4.33	118.33	125.53
6	A	704	NSP	NR1-CS-NR2	-4.26	118.44	125.53
4	A	695	1CS	N3'-C4'-N5'	-3.71	120.91	127.65
5	A	701	FAD	C4A-N9A-C8A	-3.64	101.91	105.74
4	B	1695	1CS	N3'-C4'-N5'	-3.63	121.06	127.65
5	B	1701	FAD	C6A-C5A-C4A	-3.48	112.42	117.18
5	A	701	FAD	C6A-C5A-C4A	-3.32	112.65	117.18
5	B	1701	FAD	N3A-C2A-N1A	-3.29	123.61	128.58
5	B	1701	FAD	C4A-N9A-C8A	-3.27	102.30	105.74
9	B	698	P25	C5-C6-C7	3.26	127.63	113.47
5	A	701	FAD	C1B-N9A-C8A	-3.23	119.92	127.09
5	A	701	FAD	O2B-C2B-C1B	3.18	121.04	110.10
5	A	701	FAD	N3A-C2A-N1A	-3.12	123.86	128.58
6	A	704	NSP	CS1-CS-NR1	3.11	120.51	117.20
8	A	1705	YF3	CM2-C2'-N1'	3.08	120.48	117.20
5	B	1701	FAD	O2B-C2B-C1B	3.08	120.71	110.10
4	B	1695	1CS	O9-C9-N10	3.07	129.09	123.64
5	B	1701	FAD	C1B-N9A-C8A	-3.07	120.29	127.09
4	A	695	1CS	O9-C9-N10	2.98	128.94	123.64
5	B	1701	FAD	C6A-C5A-N7A	2.96	137.79	132.09
5	A	701	FAD	C6A-C5A-N7A	2.92	137.72	132.09
5	B	1701	FAD	O2B-C2B-C3B	2.80	120.80	111.82
5	A	701	FAD	O2B-C2B-C3B	2.79	120.75	111.82
8	A	1705	YF3	CM2-C2'-N3'	2.71	121.18	117.13

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	704	NSP	CS1-CS-NR2	2.61	121.04	117.13
5	B	1701	FAD	O3'-C3'-C4'	-2.61	103.01	108.93
6	A	704	NSP	CP-CQ1-NR1	-2.56	119.67	123.83
5	A	701	FAD	O2-C2-N1	-2.51	117.63	121.80
5	B	1701	FAD	O2-C2-N1	-2.45	117.73	121.80
4	B	1695	1CS	C2'-N1'-C6'	2.44	118.25	114.61
5	A	701	FAD	O3'-C3'-C4'	-2.43	103.40	108.93
5	A	701	FAD	O4B-C4B-C5B	-2.42	101.57	109.33
8	A	1705	YF3	C5'-C6'-N1'	-2.42	119.89	123.83
4	A	695	1CS	C2'-N1'-C6'	2.37	118.14	114.61
4	B	1695	1CS	C7'-C6'-N1'	2.36	120.67	117.13
5	B	1701	FAD	O4B-C4B-C5B	-2.32	101.89	109.33
4	A	695	1CS	C7'-C6'-N1'	2.32	120.59	117.13
4	A	695	1CS	N1'-C6'-N5'	-2.25	121.81	125.77
4	B	1695	1CS	N1'-C6'-N5'	-2.23	121.84	125.77
7	A	1702	P22	O1B-PB-O2B	2.15	119.23	110.83
5	B	1701	FAD	O3'-C3'-C2'	-2.14	104.08	108.93
5	A	701	FAD	C1'-C2'-C3'	2.12	115.40	109.66
5	A	701	FAD	O3B-C3B-C4B	2.05	116.97	111.08
5	B	1701	FAD	O4-C4-C4X	-2.03	121.16	126.53
5	A	701	FAD	O4-C4-C4X	-2.00	121.25	126.53
5	A	701	FAD	O2'-C2'-C3'	-2.00	104.56	109.25

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
8	A	1705	YF3	C4

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	1705	YF3	C4'-C5'-C7'-N3
8	A	1705	YF3	CM4-C4-N3-C7'
8	A	1705	YF3	S1-C2-C4-N3
4	A	695	1CS	C9-N8-S7-O7A
4	B	1695	1CS	C9-N8-S7-O7A
4	A	695	1CS	C1-C2-S7-N8
4	B	1695	1CS	C1-C2-S7-N8
4	A	695	1CS	C3-C2-S7-N8
7	A	1702	P22	PA-O3A-PB-O2B
7	A	1702	P22	C6-C7-O7-PA
9	B	698	P25	PB-O3A-PA-O7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
4	B	1695	1CS	C3-C2-S7-N8
8	A	1705	YF3	C6'-C5'-C7'-N3
8	A	1705	YF3	C2-C4-N3-C7'
4	A	695	1CS	O9-C9-N10-C2'
4	B	1695	1CS	O9-C9-N10-C2'
5	A	701	FAD	O4B-C4B-C5B-O5B
5	B	1701	FAD	O4B-C4B-C5B-O5B
4	A	695	1CS	N8-C9-N10-C2'
4	B	1695	1CS	N8-C9-N10-C2'
4	A	695	1CS	C9-N8-S7-O7B
5	A	701	FAD	C2B-C1B-N9A-C8A
5	A	701	FAD	PA-O3P-P-O2P

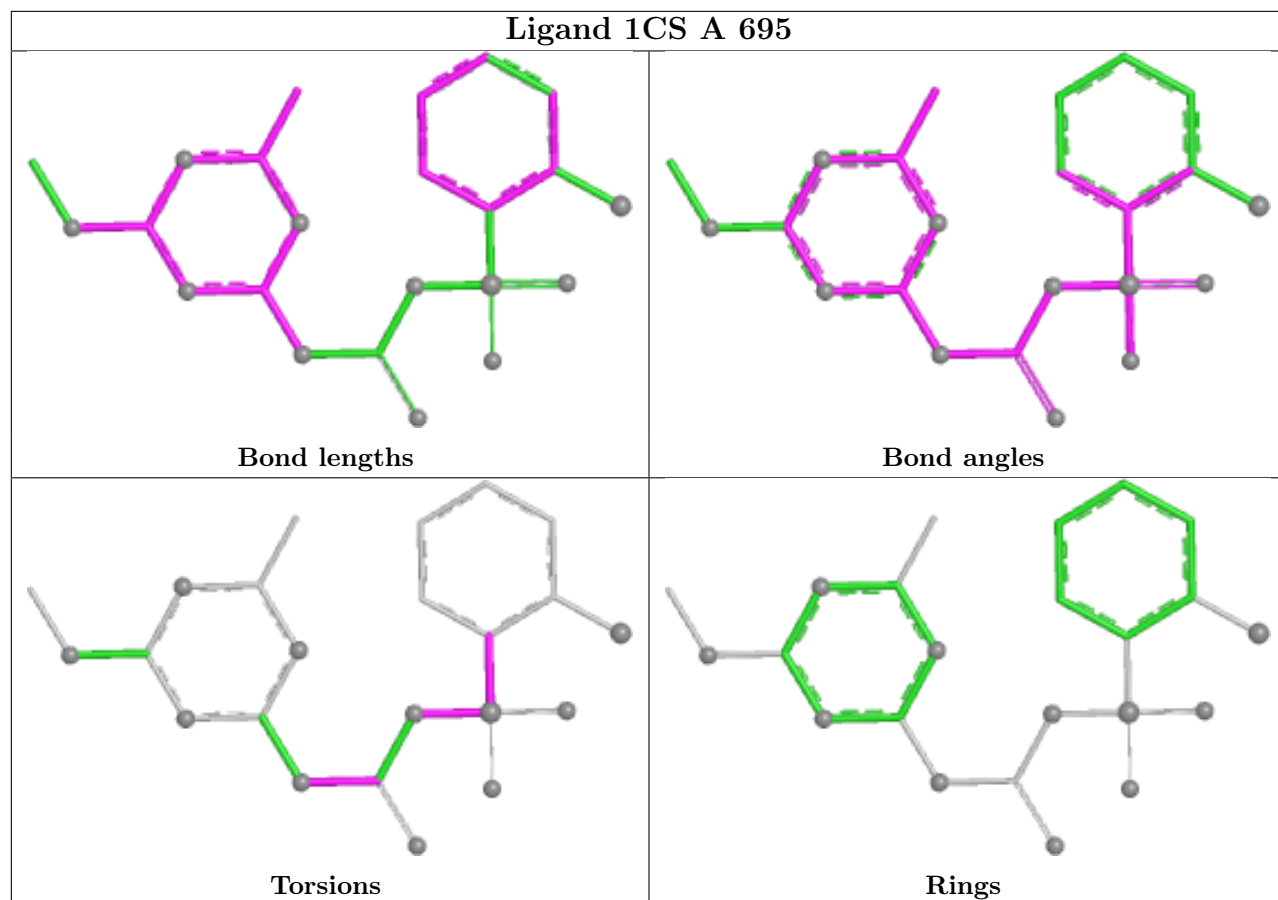
There are no ring outliers.

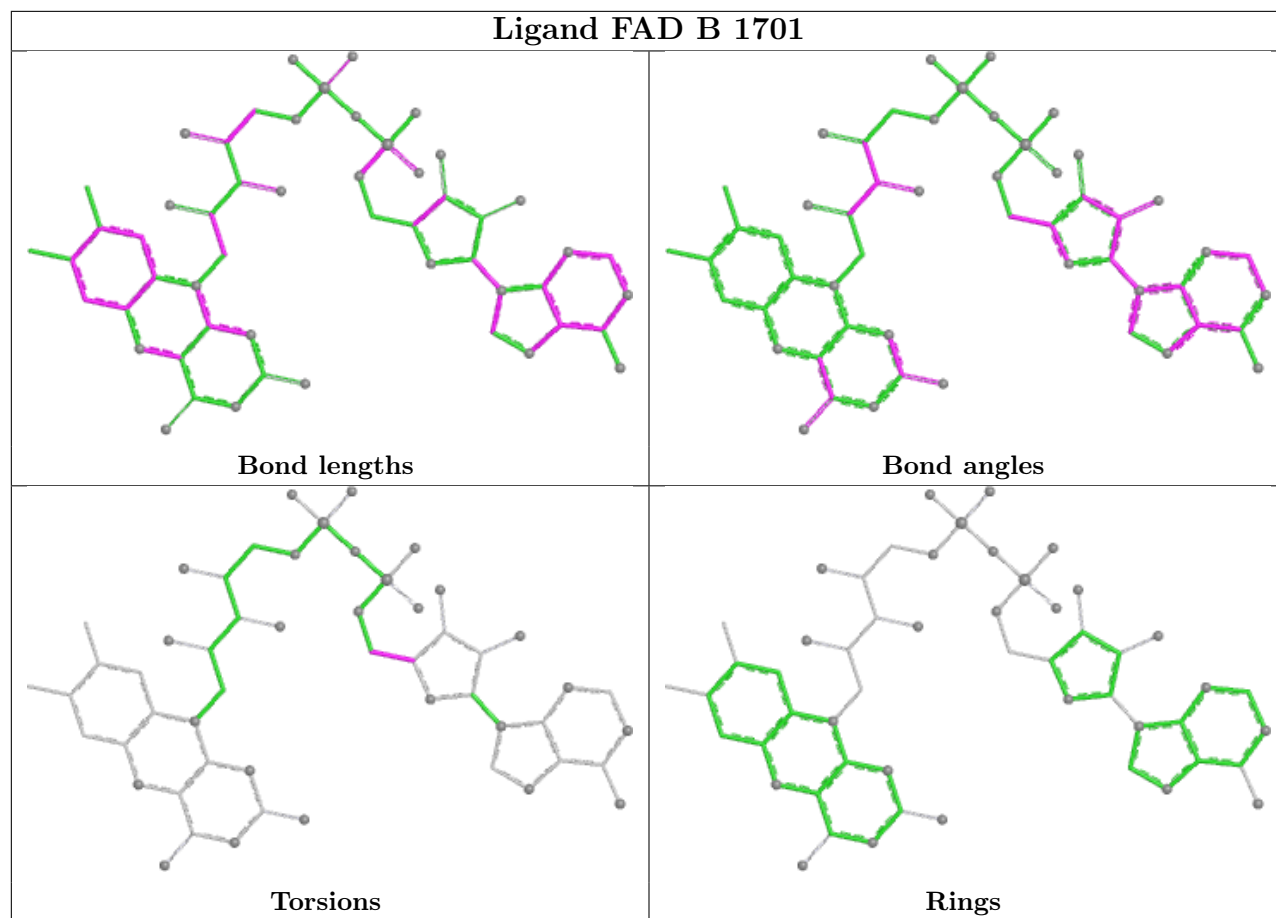
6 monomers are involved in 13 short contacts:

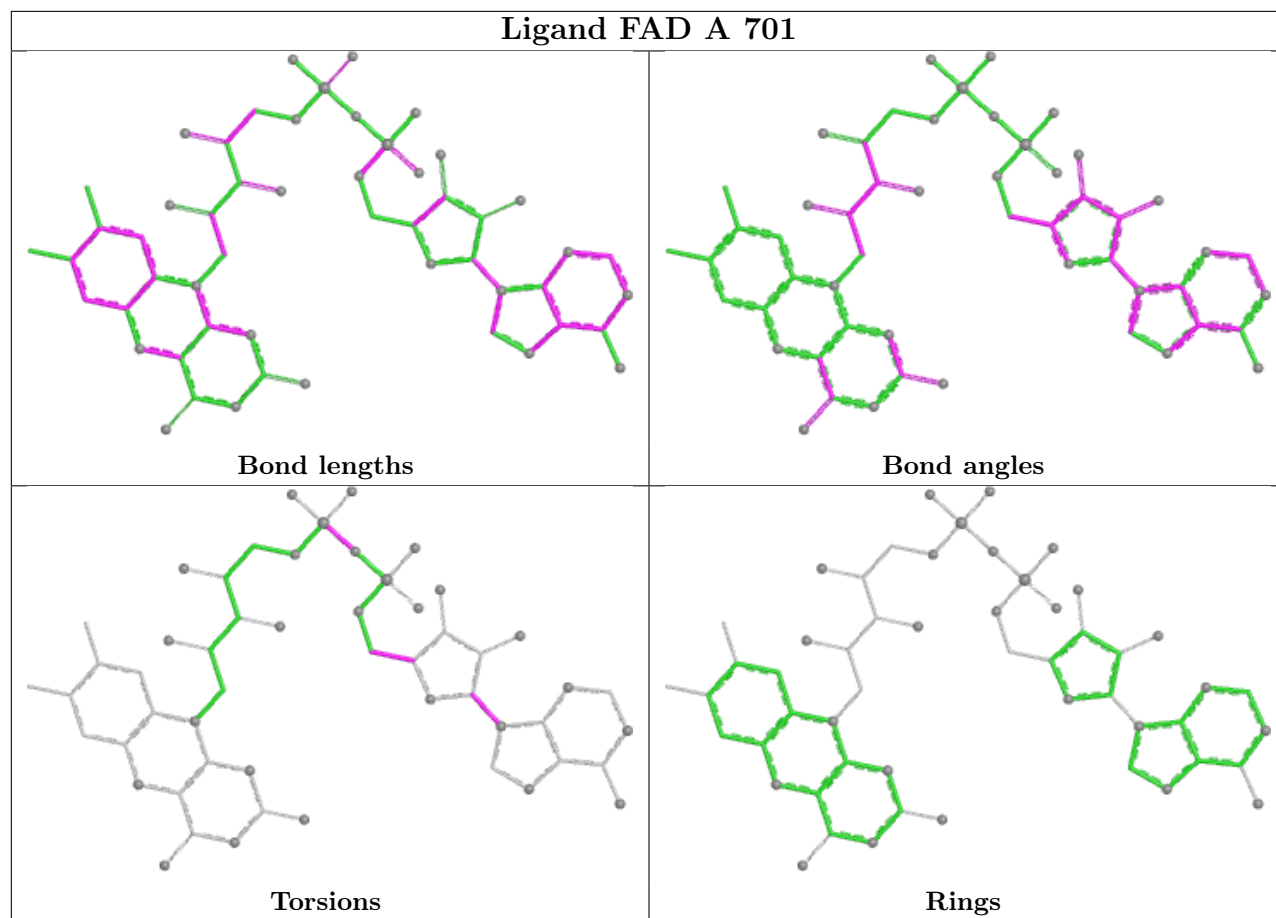
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	1705	YF3	5	0
4	A	695	1CS	1	0
9	B	698	P25	5	0
6	A	704	NSP	2	0
7	A	1702	P22	3	0
4	B	1695	1CS	1	0

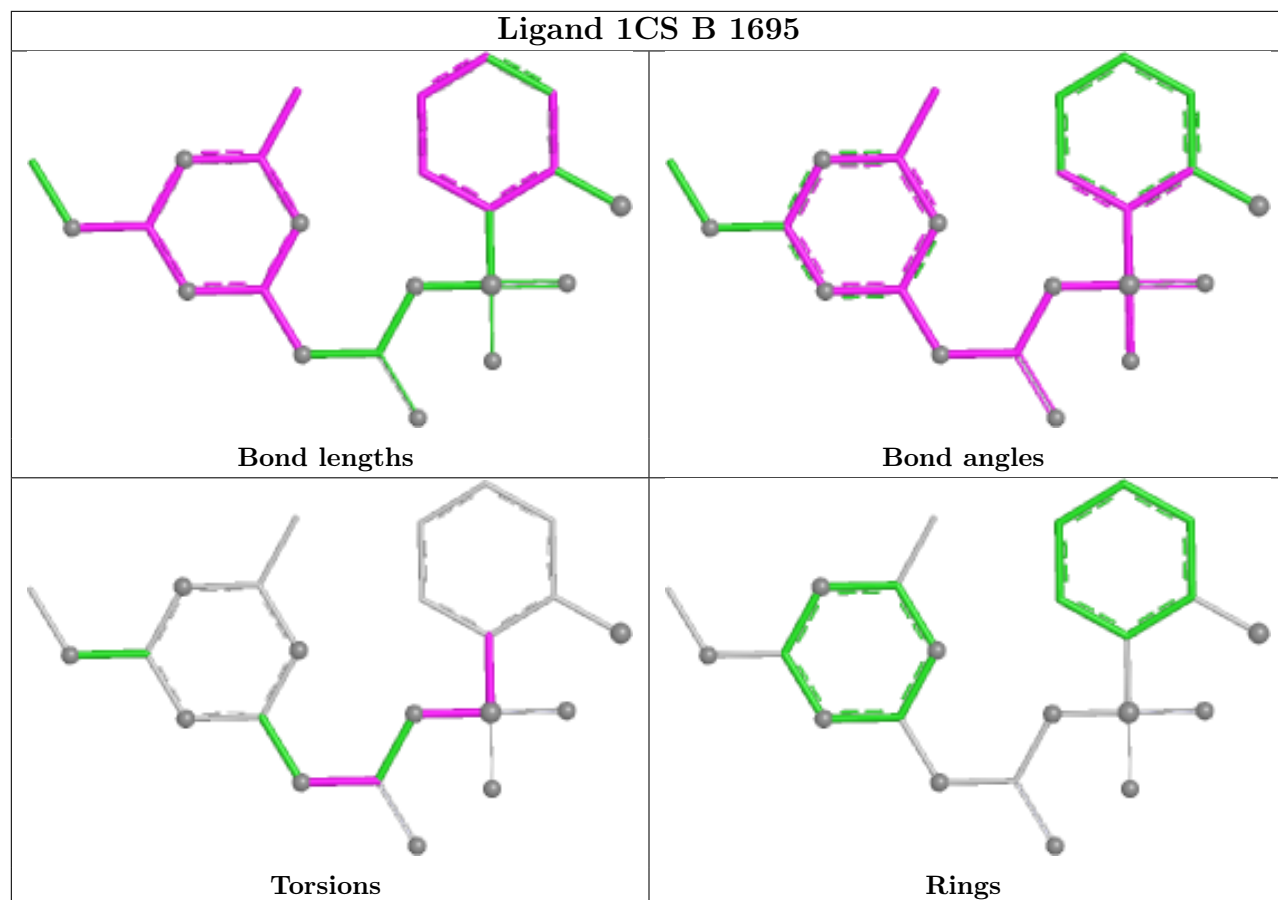
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 1CS A 695









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 [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	583/677 (86%)	0.00	14 (2%) 59 56	10, 26, 46, 70	4 (0%)
1	B	595/677 (87%)	-0.61	5 (0%) 82 80	7, 15, 30, 60	9 (1%)
All	All	1178/1354 (87%)	-0.30	19 (1%) 70 67	7, 19, 43, 70	13 (1%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	284	PHE	5.8
1	B	268	LEU	3.7
1	A	85	MET	3.6
1	A	285	VAL	2.9
1	A	677	GLU	2.7
1	B	393	ARG	2.6
1	A	263	PRO	2.6
1	A	439	PHE	2.6
1	B	278	SER	2.5
1	A	259	ARG	2.3
1	A	298	LEU	2.2
1	A	393	ARG	2.2
1	B	269	PRO	2.2
1	A	443	GLU	2.2
1	A	665	ILE	2.1
1	A	87	THR	2.1
1	A	446	GLU	2.1
1	B	280	ALA	2.0
1	A	286	MET	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](#)

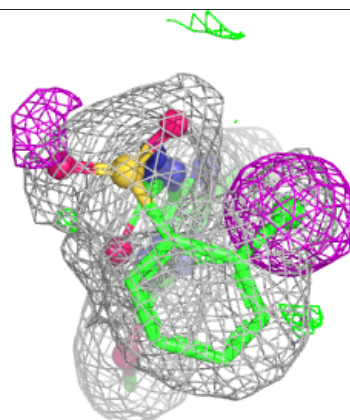
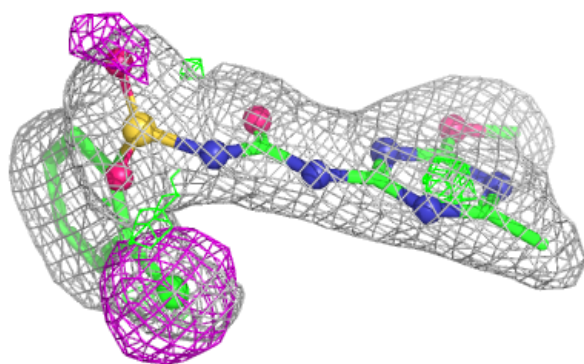
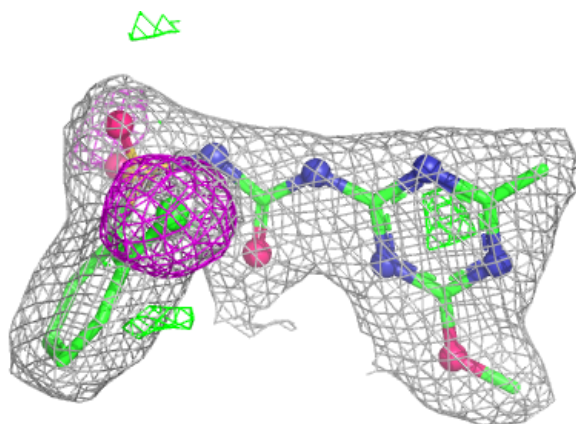
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	YF3	A	1705	14/14	0.83	0.17	23,25,43,51	0
4	1CS	B	1695	23/23	0.87	0.10	16,21,26,29	0
4	1CS	A	695	23/23	0.87	0.11	28,31,37,39	0
6	NSP	A	704	10/10	0.89	0.11	18,22,24,28	0
5	FAD	A	701	53/53	0.97	0.07	19,22,26,29	0
7	P22	A	1702	11/11	0.98	0.08	18,20,26,31	0
5	FAD	B	1701	53/53	0.98	0.05	6,9,12,15	0
9	P25	B	698	14/14	0.98	0.06	9,13,27,29	0
3	MG	B	699	1/1	0.99	0.02	10,10,10,10	0
2	K	A	1696	1/1	0.99	0.04	29,29,29,29	0
3	MG	A	1699	1/1	0.99	0.03	18,18,18,18	0
2	K	B	696	1/1	1.00	0.02	14,14,14,14	0

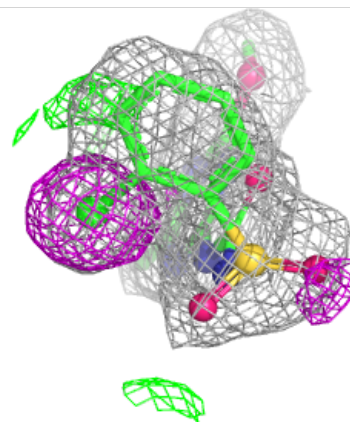
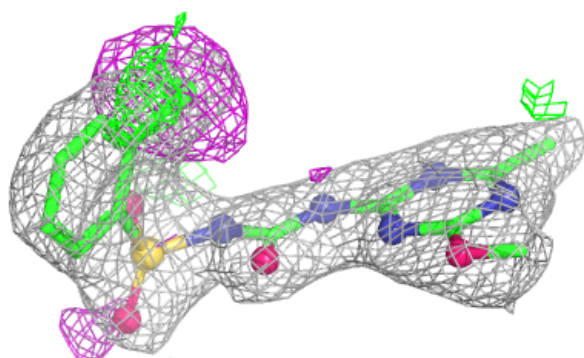
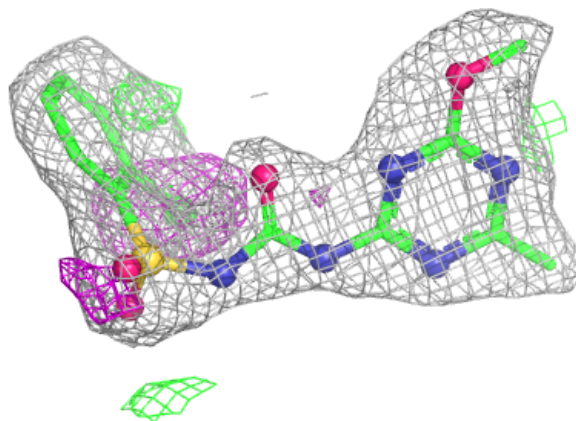
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 1CS B 1695:

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

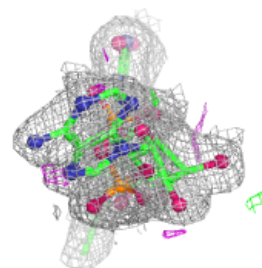
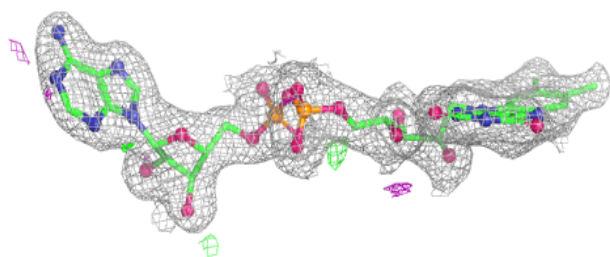
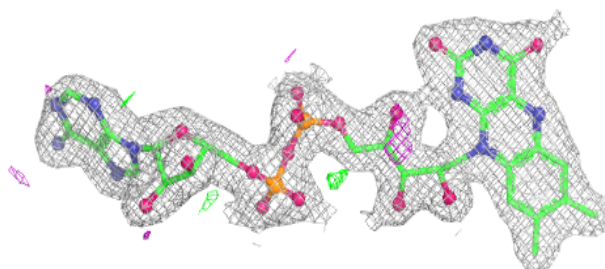
**Electron density around 1CS A 695:**

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

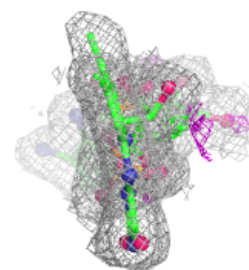
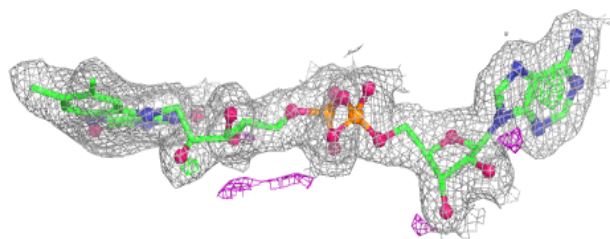
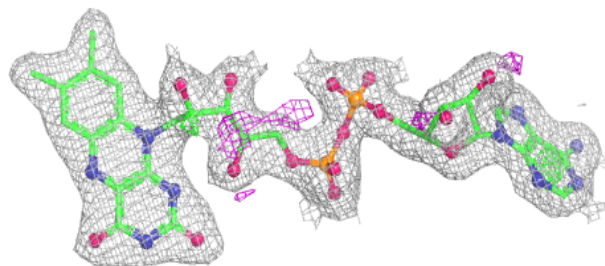


Electron density around FAD A 701:

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

**Electron density around FAD B 1701:**

$2mF_o-DF_c$ (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.