



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 07:35 PM UTC

PDB ID : 7EHE / pdb_00007ehe
Title : Acetolactate Synthase from *Trichoderma harzianum*
Authors : Zang, X.; Tang, Y.; Zhou, J.
Deposited on : 2021-03-29
Resolution : 2.28 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

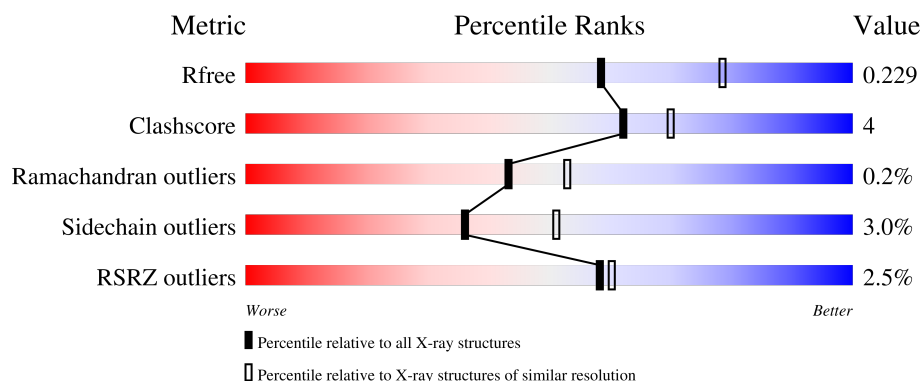
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

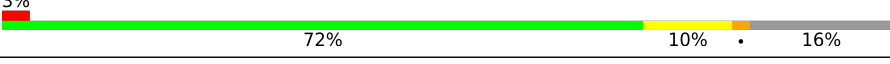
The reported resolution of this entry is 2.28 Å.

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	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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	688	 % 78% 8% 14%
1	B	688	 3% 72% 10% • 16%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9196 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	589	Total	C	N	O	S	0	0	0
			4508	2851	797	833	27			
1	B	581	Total	C	N	O	S	0	0	0
			4447	2815	784	821	27			

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	MET	-	initiating methionine	UNP A0A2N1LPC4
A	3	HIS	-	expression tag	UNP A0A2N1LPC4
A	4	HIS	-	expression tag	UNP A0A2N1LPC4
A	5	HIS	-	expression tag	UNP A0A2N1LPC4
A	6	HIS	-	expression tag	UNP A0A2N1LPC4
A	7	HIS	-	expression tag	UNP A0A2N1LPC4
A	8	HIS	-	expression tag	UNP A0A2N1LPC4
A	9	SER	-	expression tag	UNP A0A2N1LPC4
A	10	SER	-	expression tag	UNP A0A2N1LPC4
A	11	GLY	-	expression tag	UNP A0A2N1LPC4
A	12	LEU	-	expression tag	UNP A0A2N1LPC4
A	13	VAL	-	expression tag	UNP A0A2N1LPC4
A	14	PRO	-	expression tag	UNP A0A2N1LPC4
A	15	ARG	-	expression tag	UNP A0A2N1LPC4
A	16	GLY	-	expression tag	UNP A0A2N1LPC4
A	17	SER	-	expression tag	UNP A0A2N1LPC4
A	18	GLY	-	expression tag	UNP A0A2N1LPC4
A	19	MET	-	expression tag	UNP A0A2N1LPC4
A	20	LYS	-	expression tag	UNP A0A2N1LPC4
A	21	GLU	-	expression tag	UNP A0A2N1LPC4
A	22	THR	-	expression tag	UNP A0A2N1LPC4
A	23	ALA	-	expression tag	UNP A0A2N1LPC4
A	24	ALA	-	expression tag	UNP A0A2N1LPC4
A	25	ALA	-	expression tag	UNP A0A2N1LPC4
A	26	LYS	-	expression tag	UNP A0A2N1LPC4

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	PHE	-	expression tag	UNP A0A2N1LPC4
A	28	GLU	-	expression tag	UNP A0A2N1LPC4
A	29	ARG	-	expression tag	UNP A0A2N1LPC4
A	30	GLN	-	expression tag	UNP A0A2N1LPC4
A	31	HIS	-	expression tag	UNP A0A2N1LPC4
A	32	MET	-	expression tag	UNP A0A2N1LPC4
A	33	ASP	-	expression tag	UNP A0A2N1LPC4
A	34	SER	-	expression tag	UNP A0A2N1LPC4
A	35	PRO	-	expression tag	UNP A0A2N1LPC4
A	36	ASP	-	expression tag	UNP A0A2N1LPC4
A	37	LEU	-	expression tag	UNP A0A2N1LPC4
A	38	GLY	-	expression tag	UNP A0A2N1LPC4
A	39	THR	-	expression tag	UNP A0A2N1LPC4
A	40	ASP	-	expression tag	UNP A0A2N1LPC4
A	41	ASP	-	expression tag	UNP A0A2N1LPC4
A	42	ASP	-	expression tag	UNP A0A2N1LPC4
A	43	ASP	-	expression tag	UNP A0A2N1LPC4
A	44	LYS	-	expression tag	UNP A0A2N1LPC4
A	45	ALA	-	expression tag	UNP A0A2N1LPC4
A	46	MET	-	expression tag	UNP A0A2N1LPC4
A	47	ALA	-	expression tag	UNP A0A2N1LPC4
A	48	ASP	-	expression tag	UNP A0A2N1LPC4
A	49	ILE	-	expression tag	UNP A0A2N1LPC4
A	50	GLY	-	expression tag	UNP A0A2N1LPC4
A	51	SER	-	expression tag	UNP A0A2N1LPC4
A	52	MET	-	expression tag	UNP A0A2N1LPC4
A	602	ARG	LYS	engineered mutation	UNP A0A2N1LPC4
A	615	ILE	VAL	engineered mutation	UNP A0A2N1LPC4
A	627	VAL	ILE	engineered mutation	UNP A0A2N1LPC4
B	2	MET	-	initiating methionine	UNP A0A2N1LPC4
B	3	HIS	-	expression tag	UNP A0A2N1LPC4
B	4	HIS	-	expression tag	UNP A0A2N1LPC4
B	5	HIS	-	expression tag	UNP A0A2N1LPC4
B	6	HIS	-	expression tag	UNP A0A2N1LPC4
B	7	HIS	-	expression tag	UNP A0A2N1LPC4
B	8	HIS	-	expression tag	UNP A0A2N1LPC4
B	9	SER	-	expression tag	UNP A0A2N1LPC4
B	10	SER	-	expression tag	UNP A0A2N1LPC4
B	11	GLY	-	expression tag	UNP A0A2N1LPC4
B	12	LEU	-	expression tag	UNP A0A2N1LPC4
B	13	VAL	-	expression tag	UNP A0A2N1LPC4
B	14	PRO	-	expression tag	UNP A0A2N1LPC4

Continued on next page...

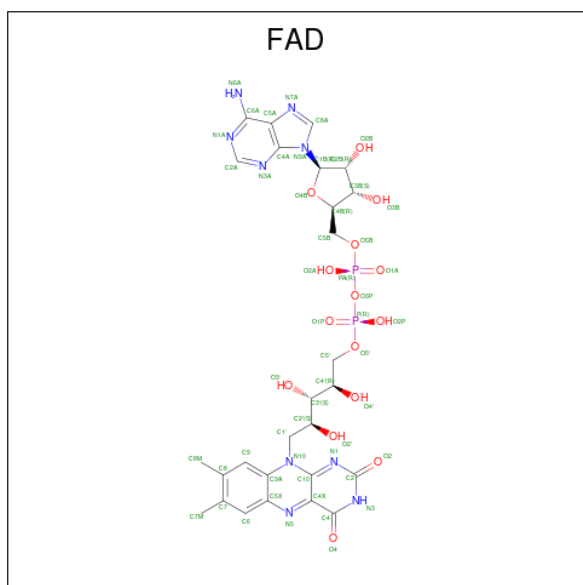
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	15	ARG	-	expression tag	UNP A0A2N1LPC4
B	16	GLY	-	expression tag	UNP A0A2N1LPC4
B	17	SER	-	expression tag	UNP A0A2N1LPC4
B	18	GLY	-	expression tag	UNP A0A2N1LPC4
B	19	MET	-	expression tag	UNP A0A2N1LPC4
B	20	LYS	-	expression tag	UNP A0A2N1LPC4
B	21	GLU	-	expression tag	UNP A0A2N1LPC4
B	22	THR	-	expression tag	UNP A0A2N1LPC4
B	23	ALA	-	expression tag	UNP A0A2N1LPC4
B	24	ALA	-	expression tag	UNP A0A2N1LPC4
B	25	ALA	-	expression tag	UNP A0A2N1LPC4
B	26	LYS	-	expression tag	UNP A0A2N1LPC4
B	27	PHE	-	expression tag	UNP A0A2N1LPC4
B	28	GLU	-	expression tag	UNP A0A2N1LPC4
B	29	ARG	-	expression tag	UNP A0A2N1LPC4
B	30	GLN	-	expression tag	UNP A0A2N1LPC4
B	31	HIS	-	expression tag	UNP A0A2N1LPC4
B	32	MET	-	expression tag	UNP A0A2N1LPC4
B	33	ASP	-	expression tag	UNP A0A2N1LPC4
B	34	SER	-	expression tag	UNP A0A2N1LPC4
B	35	PRO	-	expression tag	UNP A0A2N1LPC4
B	36	ASP	-	expression tag	UNP A0A2N1LPC4
B	37	LEU	-	expression tag	UNP A0A2N1LPC4
B	38	GLY	-	expression tag	UNP A0A2N1LPC4
B	39	THR	-	expression tag	UNP A0A2N1LPC4
B	40	ASP	-	expression tag	UNP A0A2N1LPC4
B	41	ASP	-	expression tag	UNP A0A2N1LPC4
B	42	ASP	-	expression tag	UNP A0A2N1LPC4
B	43	ASP	-	expression tag	UNP A0A2N1LPC4
B	44	LYS	-	expression tag	UNP A0A2N1LPC4
B	45	ALA	-	expression tag	UNP A0A2N1LPC4
B	46	MET	-	expression tag	UNP A0A2N1LPC4
B	47	ALA	-	expression tag	UNP A0A2N1LPC4
B	48	ASP	-	expression tag	UNP A0A2N1LPC4
B	49	ILE	-	expression tag	UNP A0A2N1LPC4
B	50	GLY	-	expression tag	UNP A0A2N1LPC4
B	51	SER	-	expression tag	UNP A0A2N1LPC4
B	52	MET	-	expression tag	UNP A0A2N1LPC4
B	602	ARG	LYS	engineered mutation	UNP A0A2N1LPC4
B	615	ILE	VAL	engineered mutation	UNP A0A2N1LPC4
B	627	VAL	ILE	engineered mutation	UNP A0A2N1LPC4

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

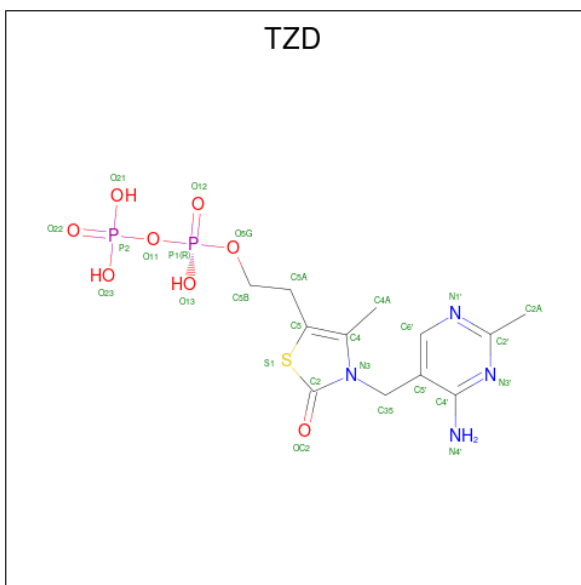
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 4 is 2-{3-[(4-AMINO-2-METHYLPYRIMIDIN-5-YL)METHYL]-4-METHYL-2-OXO-2,3-DIHYDRO-1,3-THIAZOL-5-YL}ETHYL TRIHYDROGEN DIPHOSPHATE (CCD ID: TZD) (formula: $C_{12}H_{18}N_4O_8P_2S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total 27	C 12	N 4	O 8	P 2	S 1	0	0
4	B	1	Total 27	C 12	N 4	O 8	P 2	S 1	0	0

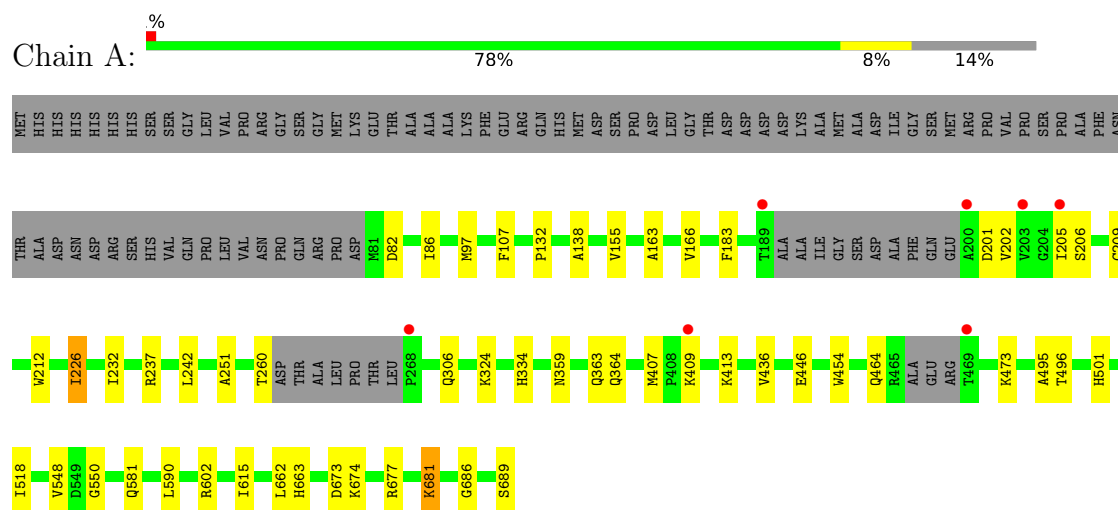
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	65	Total O 65 65	0	0
5	B	14	Total O 14 14	0	0

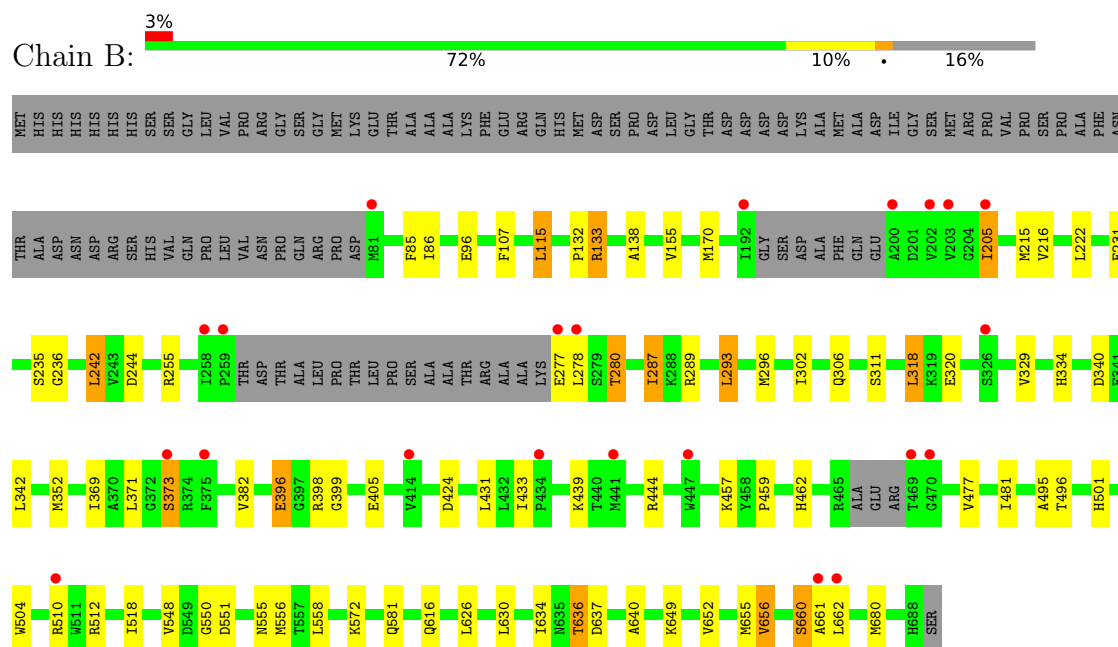
3 Residue-property plots [i](#)

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: Acetolactate synthase



• Molecule 1: Acetolactate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.10Å 88.53Å 188.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.26 – 2.28 44.26 – 2.28	Depositor EDS
% Data completeness (in resolution range)	100.0 (44.26-2.28) 100.0 (44.26-2.28)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.196 , 0.230 0.196 , 0.229	Depositor DCC
R_{free} test set	3045 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	46.3	Xtriage
Anisotropy	0.208	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9196	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.72% 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: TZD, FAD, MG

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	0.39	0/4599	0.57	0/6218
1	B	0.31	0/4537	0.53	0/6136
All	All	0.35	0/9136	0.55	0/12354

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

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	4508	0	4541	27	0
1	B	4447	0	4466	49	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	53	0	31	0	0
3	B	53	0	31	1	0
4	A	27	0	15	1	0
4	B	27	0	15	2	0
5	A	65	0	0	1	0
5	B	14	0	0	0	0
All	All	9196	0	9099	75	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 4.

All (75) 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:B:352:MET:HA	1:B:656:VAL:HG13	1.71	0.71
1:B:382:VAL:HG22	1:B:661:ALA:HA	1.79	0.66
1:B:132:PRO:HG3	1:B:138:ALA:HB2	1.78	0.64
1:B:215:MET:HA	1:B:244:ASP:HB2	1.80	0.62
1:B:396:GLU:HB3	1:B:398:ARG:HG2	1.82	0.62
1:A:237:ARG:H	1:A:407:MET:HE2	1.64	0.62
1:B:656:VAL:HG23	1:B:660:SER:HB3	1.82	0.60
1:B:342:LEU:HD21	1:B:510:ARG:HD3	1.83	0.60
1:B:340:ASP:OD2	1:B:512:ARG:NH1	2.33	0.59
1:A:132:PRO:HG3	1:A:138:ALA:HB2	1.85	0.59
4:B:703:TZD:C2	4:B:703:TZD:H4'2	2.15	0.59
1:A:581:GLN:HB3	4:A:703:TZD:H5A1	1.84	0.59
1:B:572:LYS:NZ	1:B:636:THR:HG22	2.18	0.59
1:B:302:ILE:HD13	1:B:369:ILE:HB	1.85	0.58
1:B:636:THR:HG21	1:B:640:ALA:CB	2.35	0.56
1:B:495:ALA:HA	1:B:518:ILE:O	2.05	0.55
1:B:636:THR:HG21	1:B:640:ALA:HB2	1.89	0.54
1:A:209:CYS:HB3	1:B:205:ILE:HD11	1.90	0.54
1:A:97:MET:HB3	1:A:226:ILE:HG21	1.88	0.54
1:A:82:ASP:HB2	1:A:260:THR:HG22	1.91	0.53
1:B:630:LEU:O	1:B:634:ILE:HG13	2.08	0.53
1:A:673:ASP:O	1:A:677:ARG:HG3	2.09	0.52
1:A:201:ASP:O	1:A:205:ILE:HG13	2.10	0.52
1:B:170:MET:SD	1:B:242:LEU:HD23	2.50	0.52
1:A:206:SER:HA	1:A:209:CYS:SG	2.50	0.51
1:B:504:TRP:CE2	1:B:652:VAL:HG22	2.45	0.51
1:B:302:ILE:HB	1:B:329:VAL:HG22	1.94	0.50
1:B:85:PHE:HE1	1:B:96:GLU:HG2	1.77	0.50
1:B:302:ILE:HG23	1:B:371:LEU:HD12	1.94	0.50
1:B:293:LEU:HD21	1:B:399:GLY:C	2.37	0.50
1:A:202:VAL:HG12	1:A:242:LEU:HD21	1.95	0.49
1:B:306:GLN:HB2	1:B:334:HIS:HB3	1.94	0.48
1:B:277:GLU:HB3	1:B:280:THR:HG22	1.95	0.48
1:A:681:LYS:HG2	1:A:686:GLY:HA2	1.95	0.48
1:A:464:GLN:O	1:A:473:LYS:HD2	2.14	0.47
1:B:311:SER:OG	1:B:424:ASP:OD1	2.21	0.47
1:B:302:ILE:HG21	1:B:318:LEU:HD21	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:459:PRO:HG2	1:B:462:HIS:HB2	1.96	0.47
1:A:364:GLN:HG3	1:A:454:TRP:CH2	2.50	0.47
1:B:572:LYS:HZ1	1:B:636:THR:HG22	1.79	0.47
1:B:405:GLU:OE2	3:B:702:FAD:O3B	2.28	0.46
1:A:212:TRP:CE3	1:A:232:ILE:HD12	2.50	0.46
1:B:107:PHE:O	1:B:155:VAL:HA	2.16	0.46
1:B:296:MET:SD	1:B:398:ARG:HA	2.56	0.46
1:A:496:THR:HA	1:A:548:VAL:O	2.16	0.45
1:B:496:THR:HA	1:B:548:VAL:O	2.16	0.45
1:A:495:ALA:HA	1:A:518:ILE:O	2.16	0.45
1:B:439:LYS:HG3	1:B:444:ARG:NH2	2.31	0.45
1:B:616:GLN:NE2	1:B:637:ASP:O	2.49	0.45
1:B:581:GLN:HB3	4:B:703:TZD:H5A1	1.99	0.45
1:A:107:PHE:O	1:A:155:VAL:HA	2.17	0.45
1:A:306:GLN:HB2	1:A:334:HIS:HB3	1.99	0.44
1:B:287:ILE:HD12	1:B:431:LEU:HB2	1.98	0.44
1:B:649:LYS:HB3	1:B:680:MET:HE1	2.00	0.44
1:A:251:ALA:O	5:A:801:HOH:O	2.21	0.44
1:A:409:LYS:HE2	1:A:409:LYS:HB2	1.81	0.44
1:A:363:GLN:HG3	1:A:663:HIS:HB3	2.00	0.44
1:A:183:PHE:HE1	1:A:226:ILE:HD12	1.83	0.44
1:B:133:ARG:HA	1:B:133:ARG:HD2	1.84	0.43
1:A:324:LYS:HE2	1:A:436:VAL:O	2.18	0.43
1:A:359:ASN:HB3	1:A:662:LEU:HG	2.00	0.43
1:A:602:ARG:O	1:B:133:ARG:NH2	2.30	0.43
1:B:216:VAL:HG11	1:B:222:LEU:HD13	2.01	0.43
1:B:501:HIS:CE1	1:B:550:GLY:H	2.36	0.43
1:A:501:HIS:CE1	1:A:550:GLY:H	2.37	0.42
1:B:115:LEU:HD12	1:B:115:LEU:HA	1.86	0.41
1:B:235:SER:O	1:B:236:GLY:C	2.64	0.41
1:B:555:ASN:HA	1:B:558:LEU:HD23	2.02	0.41
1:B:255:ARG:HD3	1:B:255:ARG:HA	1.78	0.41
1:B:352:MET:O	1:B:655:MET:HA	2.21	0.41
1:B:477:VAL:O	1:B:481:ILE:HG13	2.21	0.41
1:B:551:ASP:OD1	1:B:551:ASP:N	2.53	0.41
1:A:163:ALA:O	1:A:166:VAL:HG22	2.21	0.40
1:B:278:LEU:H	1:B:278:LEU:HD23	1.86	0.40
1:B:320:GLU:OE2	1:B:433:ILE:HG21	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	581/688 (84%)	574 (99%)	7 (1%)	0	100	100
1	B	573/688 (83%)	551 (96%)	20 (4%)	2 (0%)	36	44
All	All	1154/1376 (84%)	1125 (98%)	27 (2%)	2 (0%)	43	53

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	373	SER
1	B	662	LEU

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	475/556 (85%)	466 (98%)	9 (2%)	50	66
1	B	467/556 (84%)	448 (96%)	19 (4%)	27	38
All	All	942/1112 (85%)	914 (97%)	28 (3%)	36	51

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	ILE
1	A	226	ILE
1	A	413	LYS
1	A	446	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	590	LEU
1	A	615	ILE
1	A	674	LYS
1	A	681	LYS
1	A	689	SER
1	B	86	ILE
1	B	115	LEU
1	B	133	ARG
1	B	205	ILE
1	B	231	GLU
1	B	242	LEU
1	B	280	THR
1	B	287	ILE
1	B	289	ARG
1	B	293	LEU
1	B	318	LEU
1	B	373	SER
1	B	396	GLU
1	B	457	LYS
1	B	556	MET
1	B	626	LEU
1	B	636	THR
1	B	656	VAL
1	B	660	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	306	GLN
1	A	618	GLN
1	B	306	GLN
1	B	310	GLN
1	B	353	HIS
1	B	435	GLN
1	B	464	GLN
1	B	618	GLN
1	B	635	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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$
3	FAD	A	702	-	58,58,58	0.54	1 (1%)	85,89,89	0.39	0
3	FAD	B	702	-	58,58,58	0.43	0	85,89,89	0.35	0
4	TZD	B	703	2	27,28,28	4.76	9 (33%)	37,42,42	4.26	13 (35%)
4	TZD	A	703	2	27,28,28	4.51	7 (25%)	37,42,42	3.96	13 (35%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FAD	A	702	-	-	3/34/50/50	0/6/6/6
3	FAD	B	702	-	-	12/34/50/50	0/6/6/6
4	TZD	B	703	2	-	1/17/17/17	0/2/2/2
4	TZD	A	703	2	-	1/17/17/17	0/2/2/2

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	703	TZD	C4-N3	15.57	1.63	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	703	TZD	C4-N3	14.72	1.62	1.39
4	B	703	TZD	C2-N3	11.85	1.56	1.38
4	A	703	TZD	C2-N3	11.59	1.56	1.38
4	B	703	TZD	C5-C4	8.72	1.53	1.35
4	A	703	TZD	C5-C4	8.40	1.52	1.35
4	B	703	TZD	C2-S1	-6.84	1.69	1.77
4	A	703	TZD	C2-S1	-5.96	1.70	1.77
4	B	703	TZD	C5-S1	-5.86	1.62	1.74
4	A	703	TZD	C5-S1	-5.71	1.62	1.74
4	A	703	TZD	C4'-N4'	4.47	1.45	1.34
4	B	703	TZD	C4'-N4'	4.33	1.45	1.34
4	B	703	TZD	P1-O11	4.09	1.63	1.59
4	A	703	TZD	P1-O11	3.35	1.63	1.59
4	B	703	TZD	OC2-C2	-2.41	1.18	1.21
3	A	702	FAD	C10-N1	-2.39	1.28	1.33
4	B	703	TZD	C5'-C4'	-2.11	1.39	1.42

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	703	TZD	C5-S1-C2	23.08	102.72	91.64
4	A	703	TZD	C5-S1-C2	20.37	101.42	91.64
4	A	703	TZD	OC2-C2-N3	-5.49	118.93	125.37
4	A	703	TZD	C5'-C35-N3	-4.50	107.70	113.14
4	B	703	TZD	C5'-C35-N3	-4.03	108.26	113.14
4	B	703	TZD	C6'-N1'-C2'	3.82	122.35	116.07
4	A	703	TZD	OC2-C2-S1	3.77	130.02	125.00
4	B	703	TZD	N1'-C2'-N3'	-3.64	119.47	125.53
4	A	703	TZD	C6'-N1'-C2'	3.61	122.00	116.07
4	B	703	TZD	OC2-C2-N3	-3.47	121.30	125.37
4	A	703	TZD	N1'-C2'-N3'	-3.41	119.86	125.53
4	A	703	TZD	C5A-C5-S1	3.18	126.12	119.29
4	A	703	TZD	C2A-C2'-N1'	3.11	120.51	117.20
4	A	703	TZD	C2'-N3'-C4'	3.04	122.77	118.10
4	B	703	TZD	C2A-C2'-N3'	2.93	121.51	117.13
4	B	703	TZD	C5A-C5-S1	2.88	125.47	119.29
4	B	703	TZD	C2'-N3'-C4'	2.85	122.48	118.10
4	B	703	TZD	OC2-C2-S1	2.75	128.67	125.00
4	B	703	TZD	C5'-C6'-N1'	-2.64	119.53	123.83
4	A	703	TZD	C35-N3-C4	2.62	128.32	124.98
4	A	703	TZD	C5A-C5-C4	-2.38	122.35	128.20
4	A	703	TZD	C4-N3-C2	-2.36	105.42	112.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	703	TZD	C5'-C6'-N1'	-2.35	120.01	123.83
4	B	703	TZD	C5A-C5-C4	-2.09	123.07	128.20
4	B	703	TZD	C35-C5'-C6'	-2.07	118.33	121.30
4	B	703	TZD	C4-N3-C2	-2.04	106.36	112.39

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	702	FAD	C5'-O5'-P-O1P
3	B	702	FAD	C5'-O5'-P-O3P
3	B	702	FAD	O4'-C4'-C5'-O5'
3	B	702	FAD	C2'-C3'-C4'-O4'
3	B	702	FAD	C3'-C4'-C5'-O5'
3	B	702	FAD	O4B-C4B-C5B-O5B
3	A	702	FAD	P-O3P-PA-O5B
4	B	703	TZD	C5-C5A-C5B-O5G
3	B	702	FAD	C5B-O5B-PA-O3P
3	B	702	FAD	C5'-O5'-P-O2P
3	B	702	FAD	O3'-C3'-C4'-O4'
3	B	702	FAD	C2'-C3'-C4'-C5'
3	B	702	FAD	O3'-C3'-C4'-C5'
4	A	703	TZD	P2-O11-P1-O5G
3	A	702	FAD	C2B-C1B-N9A-C8A
3	B	702	FAD	C2B-C1B-N9A-C8A
3	A	702	FAD	O4B-C4B-C5B-O5B

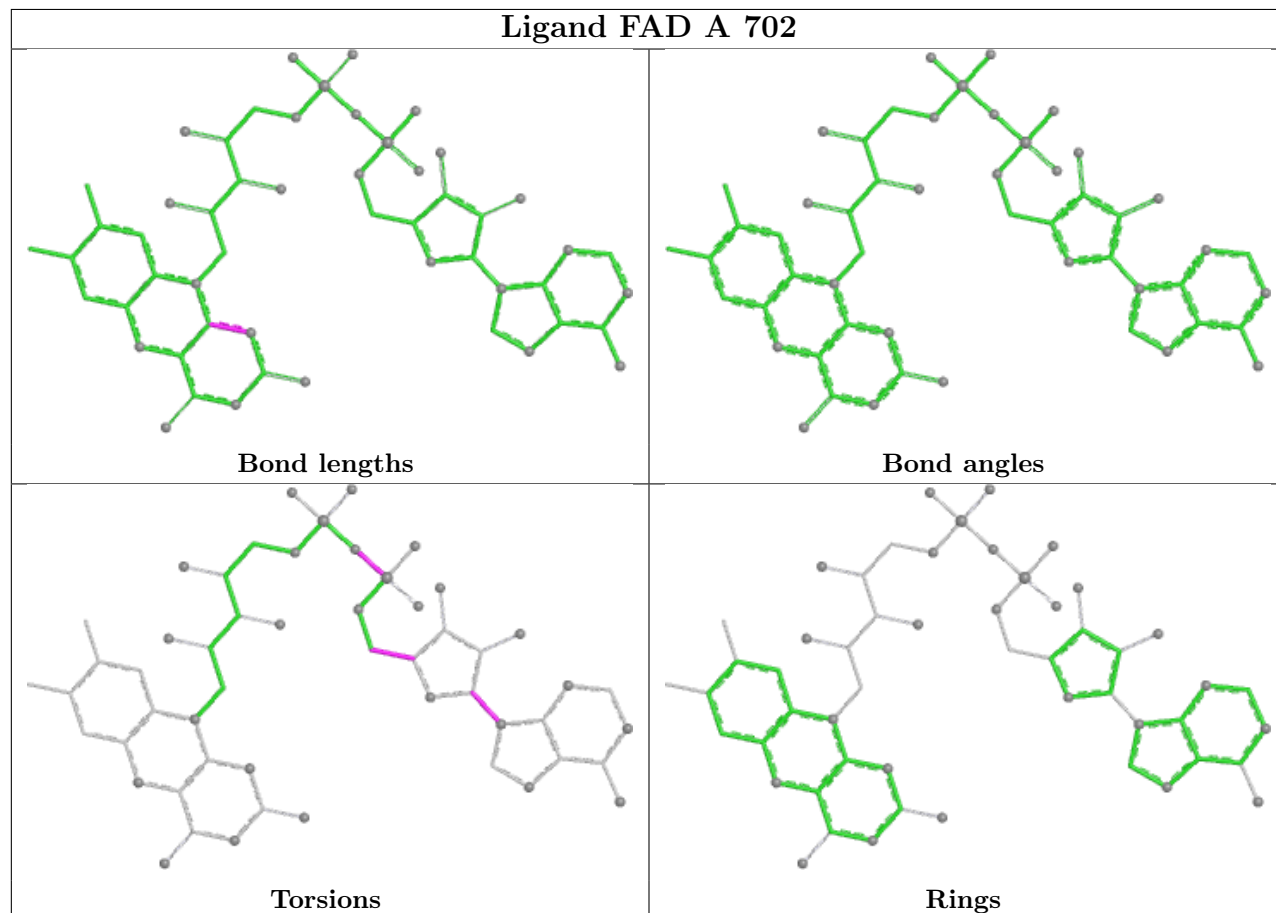
There are no ring outliers.

3 monomers are involved in 4 short contacts:

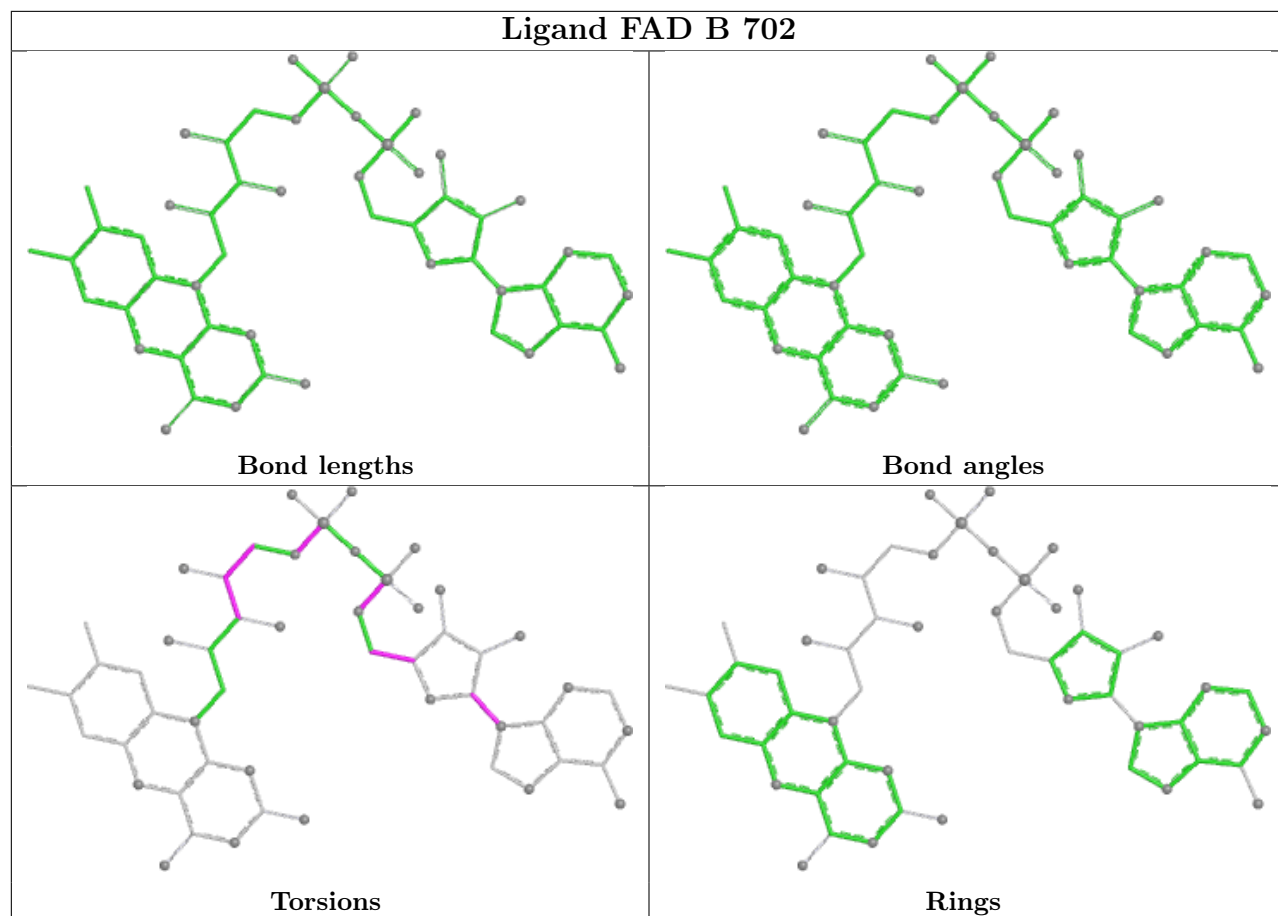
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	702	FAD	1	0
4	B	703	TZD	2	0
4	A	703	TZD	1	0

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

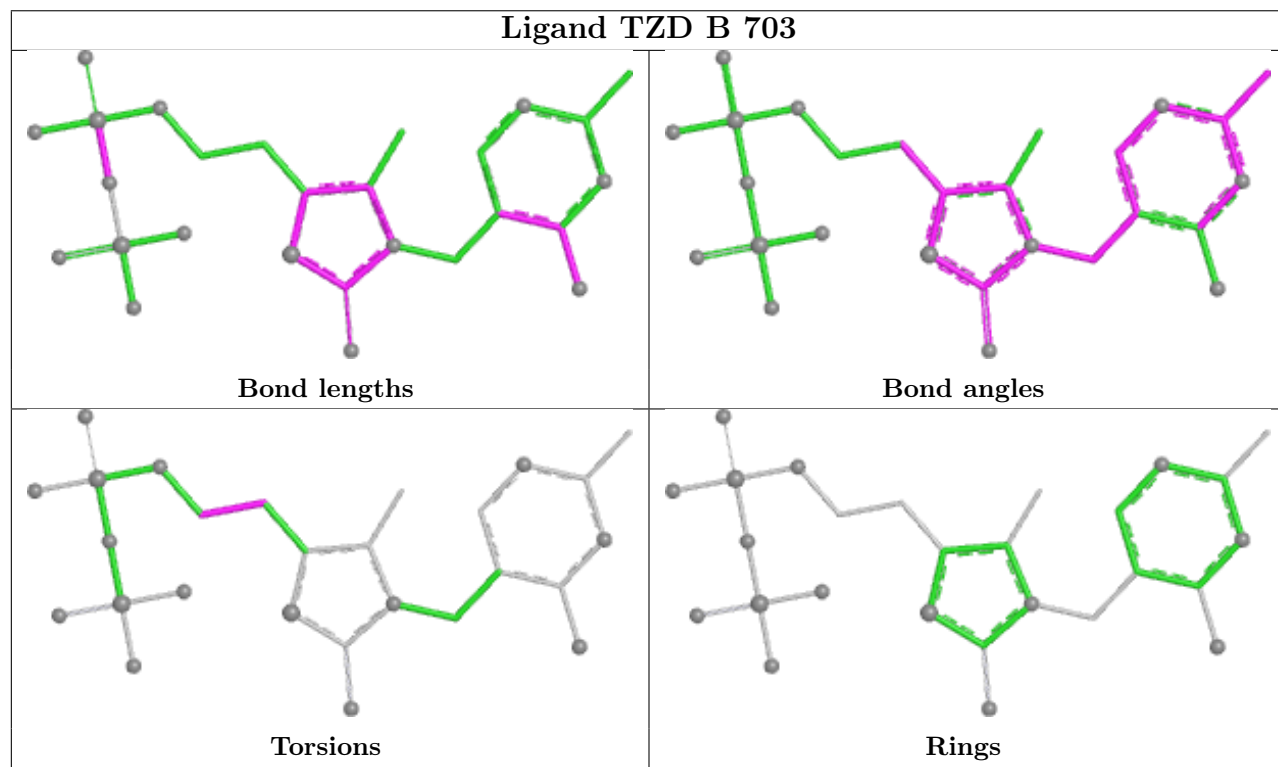
in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

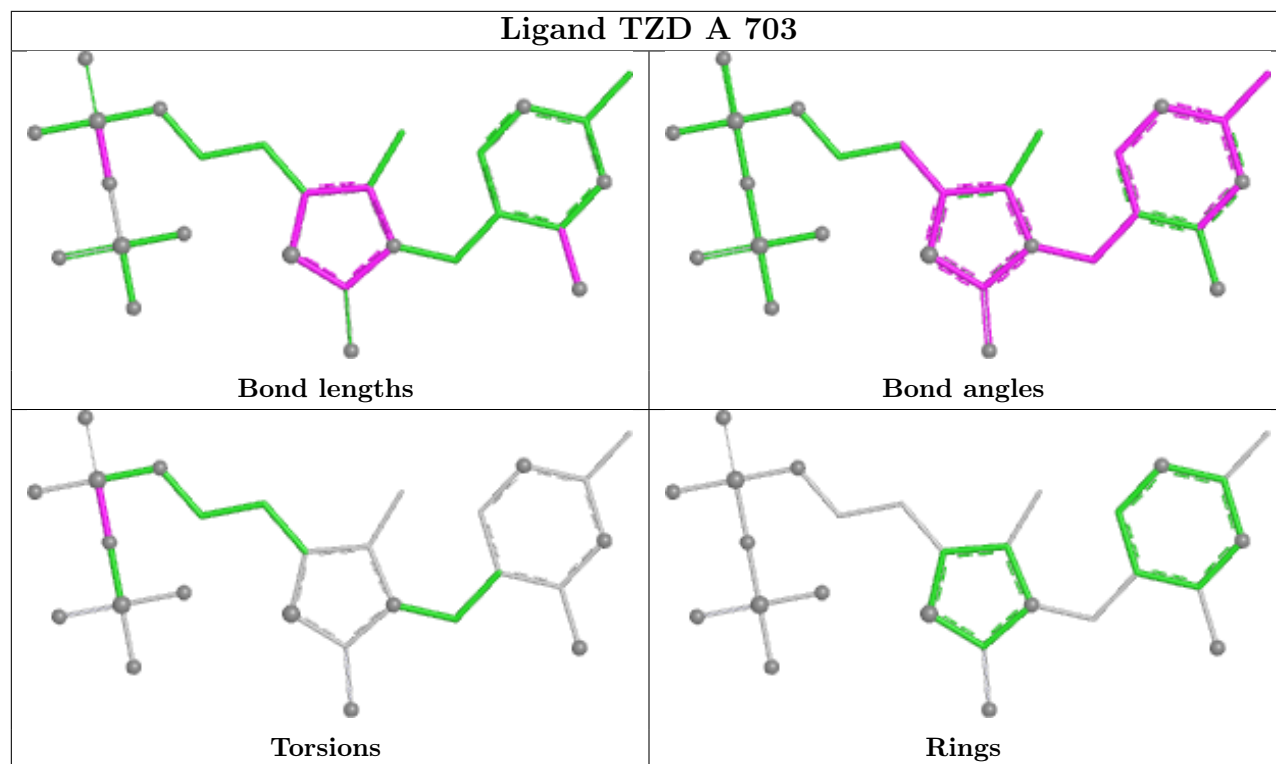


Ligand FAD B 702



Ligand TZD B 703





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	589/688 (85%)	-0.28	7 (1%) 76 78	29, 42, 61, 89	0
1	B	581/688 (84%)	0.47	22 (3%) 44 46	35, 61, 91, 106	0
All	All	1170/1376 (85%)	0.09	29 (2%) 58 60	29, 49, 87, 106	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	278	LEU	3.7
1	A	469	THR	3.4
1	B	441	MET	3.4
1	B	192	ILE	3.2
1	A	268	PRO	3.2
1	B	373	SER	2.9
1	B	205	ILE	2.8
1	B	326	SER	2.8
1	B	259	PRO	2.8
1	B	202	VAL	2.8
1	B	510	ARG	2.8
1	A	409	LYS	2.7
1	A	189	THR	2.7
1	B	277	GLU	2.6
1	B	203	VAL	2.6
1	A	203	VAL	2.5
1	A	205	ILE	2.5
1	B	469	THR	2.5
1	B	375	PHE	2.4
1	B	447	TRP	2.4
1	B	434	PRO	2.3
1	B	81	MET	2.3
1	B	661	ALA	2.3
1	B	258	ILE	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	414	VAL	2.1
1	B	470	GLY	2.1
1	A	200	ALA	2.1
1	B	200	ALA	2.1
1	B	662	LEU	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](#)

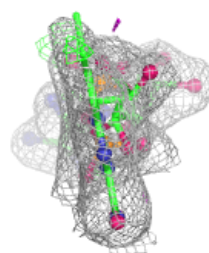
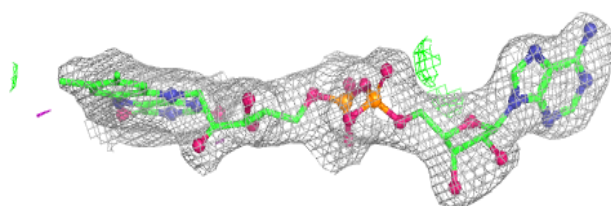
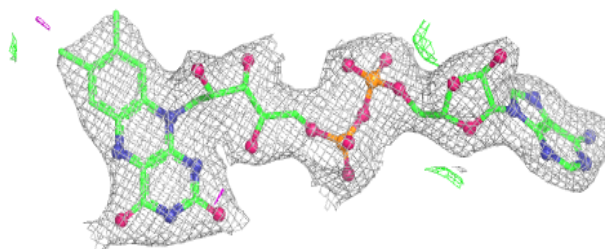
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	FAD	B	702	53/53	0.95	0.09	46,57,67,70	0
4	TZD	B	703	27/27	0.96	0.07	38,43,48,50	0
4	TZD	A	703	27/27	0.98	0.06	28,33,36,39	0
3	FAD	A	702	53/53	0.98	0.06	29,34,42,48	0
2	MG	B	701	1/1	0.99	0.10	31,31,31,31	0
2	MG	A	701	1/1	1.00	0.11	18,18,18,18	0

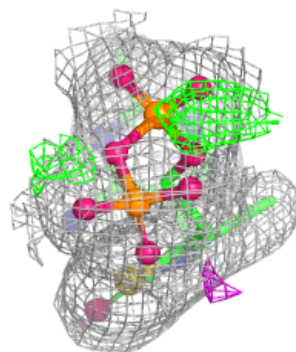
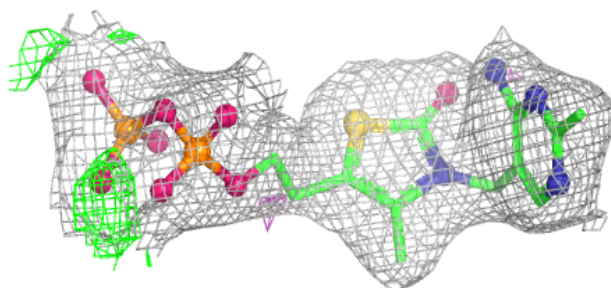
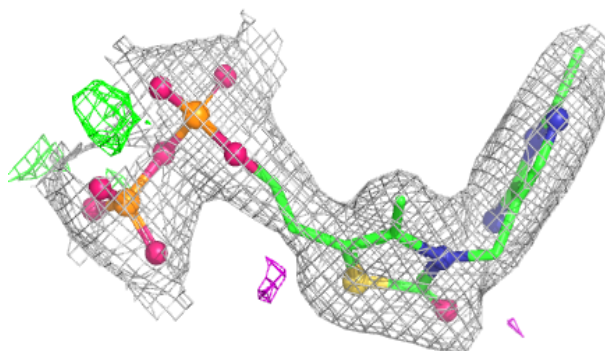
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FAD B 702:

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

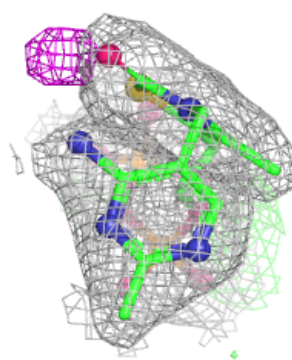
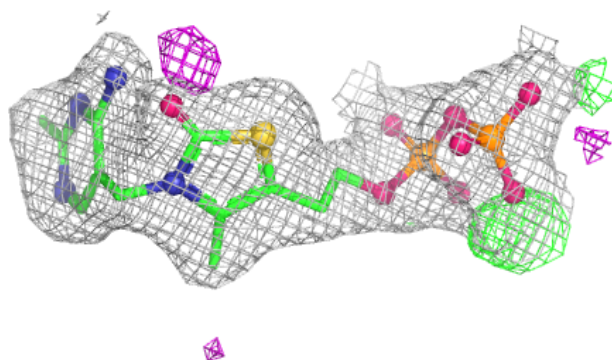
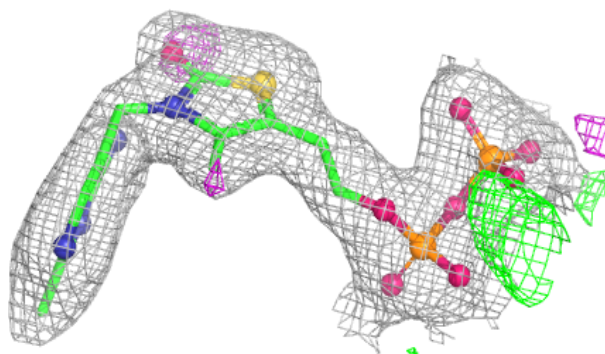
**Electron density around TZD B 703:**

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

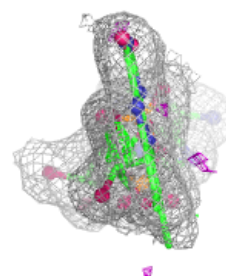
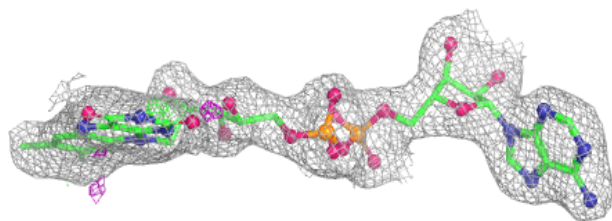
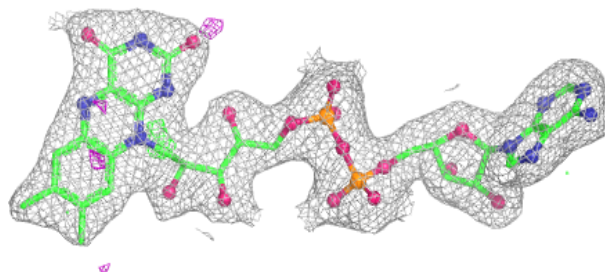


Electron density around TZD A 703:

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

**Electron density around FAD A 702:**

$2mF_o-DF_c$ (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.