



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 01:41 am BST

PDB ID : 5H73
Title : Crystal structure of human DHODH with 18F
Authors : Huang, J.; Wu, D.
Deposited on : 2016-11-16
Resolution : 1.58 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

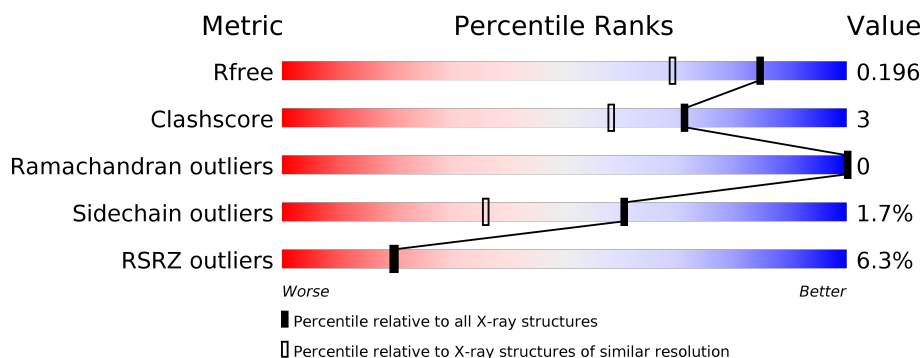
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.58 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}	130704	5534 (1.60-1.56)
Clashscore	141614	5861 (1.60-1.56)
Ramachandran outliers	138981	5708 (1.60-1.56)
Sidechain outliers	138945	5703 (1.60-1.56)
RSRZ outliers	127900	5431 (1.60-1.56)

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 on 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	390	<div> <div>6%</div> <div>80%</div> <div>12%</div> <div>7%</div> </div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3006 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.

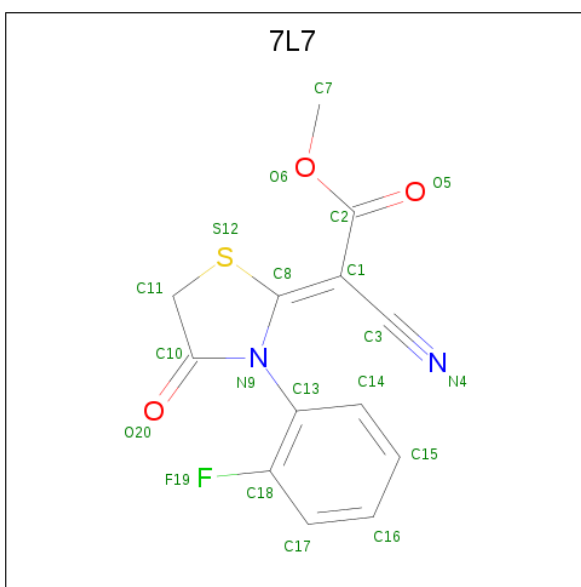
- Molecule 1 is a protein called Dihydroorotate dehydrogenase (quinone), mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	363	Total	C	N	O	S	0	0	0
			2773	1740	513	516	4			

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	MET	-	initiating methionine	UNP Q02127
A	8	GLY	-	expression tag	UNP Q02127
A	9	HIS	-	expression tag	UNP Q02127
A	10	HIS	-	expression tag	UNP Q02127
A	11	HIS	-	expression tag	UNP Q02127
A	12	HIS	-	expression tag	UNP Q02127
A	13	HIS	-	expression tag	UNP Q02127
A	14	HIS	-	expression tag	UNP Q02127
A	15	HIS	-	expression tag	UNP Q02127
A	16	HIS	-	expression tag	UNP Q02127
A	17	HIS	-	expression tag	UNP Q02127
A	18	HIS	-	expression tag	UNP Q02127
A	19	SER	-	expression tag	UNP Q02127
A	20	SER	-	expression tag	UNP Q02127
A	21	GLY	-	expression tag	UNP Q02127
A	22	HIS	-	expression tag	UNP Q02127
A	23	ILE	-	expression tag	UNP Q02127
A	24	ASP	-	expression tag	UNP Q02127
A	25	ASP	-	expression tag	UNP Q02127
A	26	ASP	-	expression tag	UNP Q02127
A	27	ASP	-	expression tag	UNP Q02127
A	28	LYS	-	expression tag	UNP Q02127
A	29	HIS	-	expression tag	UNP Q02127

- Molecule 2 is methyl (2 {Z})-2-cyano-2-[3-(2-fluorophenyl)-4-oxidanylidene-1,3-thiazolidin-2-ylidene]ethanoate (three-letter code: 7L7) (formula: C₁₃H₉FN₂O₃S).



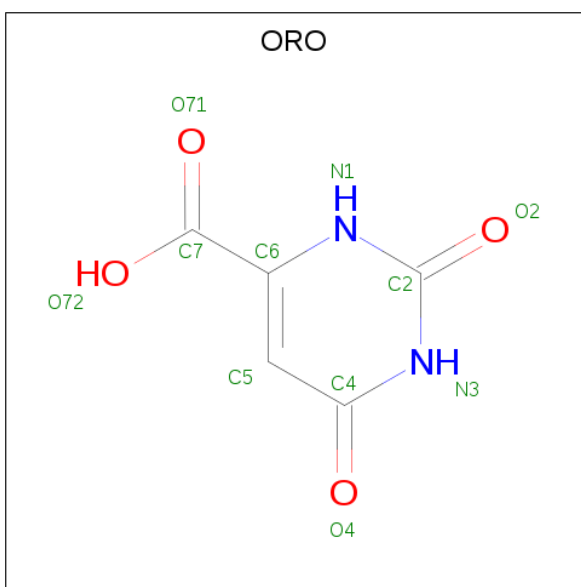
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	S	0	0
			20	13	1	2	3	1		

- Molecule 3 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 4 is OROTIC ACID (three-letter code: ORO) (formula: $C_5H_4N_2O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			11	5	2	4		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		

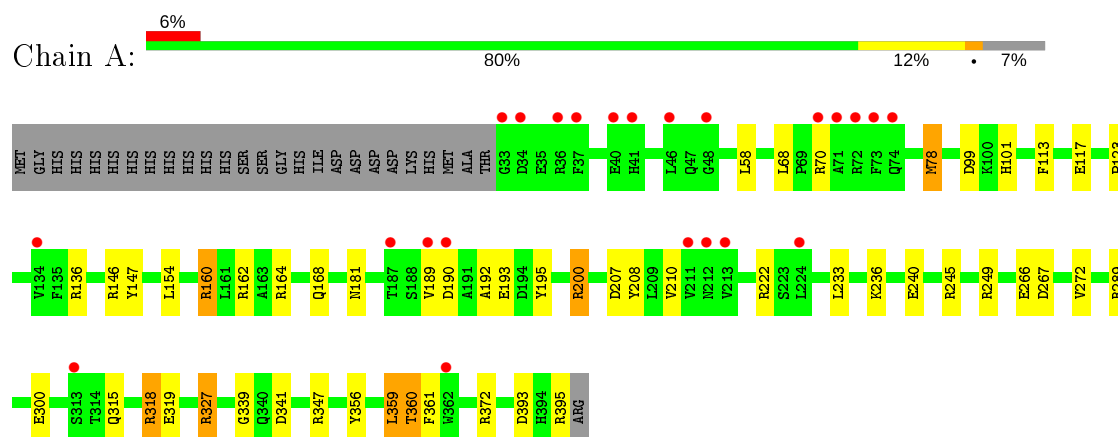
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	145	Total	O	0	0
			145	145		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Dihydroorotate dehydrogenase (quinone), mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	90.89Å 90.89Å 123.35Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.12 – 1.58 41.12 – 1.58	Depositor EDS
% Data completeness (in resolution range)	99.8 (41.12-1.58) 99.8 (41.12-1.58)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 1.58Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.170 , 0.186 0.180 , 0.196	Depositor DCC
R_{free} test set	4038 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	23.3	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 57.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3006	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.36% 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: FMN, ORO, ACT, SO4, 7L7

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	1.46	15/2819 (0.5%)	1.53	39/3810 (1.0%)

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	266	GLU	CD-OE1	16.06	1.43	1.25
1	A	266	GLU	CG-CD	11.39	1.69	1.51
1	A	266	GLU	CD-OE2	-6.95	1.18	1.25
1	A	339	GLY	N-CA	-6.88	1.35	1.46
1	A	200	ARG	CD-NE	-6.77	1.34	1.46
1	A	361	PHE	N-CA	-6.59	1.33	1.46
1	A	300	GLU	CD-OE1	-6.43	1.18	1.25
1	A	99	ASP	N-CA	6.06	1.58	1.46
1	A	160	ARG	CZ-NH1	5.91	1.40	1.33
1	A	319	GLU	CD-OE1	5.76	1.31	1.25
1	A	113	PHE	CG-CD1	5.64	1.47	1.38
1	A	147	TYR	C-O	5.63	1.34	1.23
1	A	289	ARG	CZ-NH1	5.61	1.40	1.33
1	A	360	THR	CB-CG2	-5.28	1.34	1.52
1	A	195	TYR	CE1-CZ	-5.07	1.31	1.38

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	136	ARG	NE-CZ-NH1	17.94	129.27	120.30
1	A	136	ARG	NE-CZ-NH2	-17.36	111.62	120.30
1	A	266	GLU	OE1-CD-OE2	10.99	136.49	123.30
1	A	249	ARG	NE-CZ-NH1	10.32	125.46	120.30
1	A	266	GLU	CG-CD-OE2	-9.40	99.51	118.30
1	A	117	GLU	OE1-CD-OE2	8.15	133.08	123.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	207	ASP	CB-CG-OD1	-7.82	111.27	118.30
1	A	267	ASP	CB-CG-OD1	-7.64	111.43	118.30
1	A	99	ASP	CB-CG-OD1	-7.50	111.55	118.30
1	A	190	ASP	CB-CG-OD1	7.21	124.79	118.30
1	A	113	PHE	CB-CG-CD2	7.20	125.84	120.80
1	A	359	LEU	CB-CG-CD1	7.12	123.11	111.00
1	A	245	ARG	NE-CZ-NH1	-6.96	116.82	120.30
1	A	146	ARG	NE-CZ-NH2	6.67	123.63	120.30
1	A	78	MET	CA-CB-CG	6.55	124.44	113.30
1	A	359	LEU	CA-CB-CG	6.40	130.02	115.30
1	A	393	ASP	CB-CG-OD1	6.38	124.04	118.30
1	A	136	ARG	CD-NE-CZ	6.03	132.03	123.60
1	A	160	ARG	NE-CZ-NH2	6.02	123.31	120.30
1	A	341	ASP	CB-CG-OD2	5.94	123.65	118.30
1	A	162	ARG	NE-CZ-NH1	-5.93	117.33	120.30
1	A	395	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	A	222	ARG	NE-CZ-NH2	-5.65	117.48	120.30
1	A	347	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	A	190	ASP	CB-CG-OD2	-5.59	113.27	118.30
1	A	245	ARG	NE-CZ-NH2	5.45	123.03	120.30
1	A	327	ARG	NE-CZ-NH2	5.43	123.01	120.30
1	A	164	ARG	NE-CZ-NH1	5.28	122.94	120.30
1	A	272	VAL	CG1-CB-CG2	5.18	119.18	110.90
1	A	347	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	A	70	ARG	NE-CZ-NH1	5.14	122.87	120.30
1	A	372	ARG	NE-CZ-NH2	-5.14	117.73	120.30
1	A	300	GLU	OE1-CD-OE2	5.12	129.44	123.30
1	A	68	LEU	CB-CG-CD2	-5.10	102.33	111.00
1	A	233	LEU	CB-CG-CD1	-5.10	102.34	111.00
1	A	193	GLU	OE1-CD-OE2	-5.06	117.22	123.30
1	A	359	LEU	CB-CG-CD2	5.06	119.59	111.00
1	A	208	TYR	CG-CD1-CE1	5.04	125.33	121.30
1	A	318	ARG	NE-CZ-NH1	5.01	122.80	120.30

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	2773	0	2836	18	0
2	A	20	0	0	4	0
3	A	31	0	19	0	0
4	A	11	0	3	0	0
5	A	10	0	0	0	0
6	A	16	0	12	4	0
7	A	145	0	0	0	0
All	All	3006	0	2870	20	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 3.

All (20) 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:189:VAL:O	1:A:189:VAL:HG12	1.80	0.81
1:A:101:HIS:NE2	6:A:409:ACT:H2	1.98	0.79
1:A:315:GLN:HE22	1:A:318:ARG:HE	1.33	0.76
1:A:315:GLN:NE2	6:A:408:ACT:O	2.21	0.74
1:A:58:LEU:HD22	2:A:401:7L7:N4	2.03	0.73
1:A:160:ARG:HH21	6:A:407:ACT:H2	1.64	0.63
1:A:189:VAL:CG1	1:A:189:VAL:O	2.50	0.59
1:A:315:GLN:NE2	1:A:318:ARG:HE	1.99	0.57
1:A:58:LEU:CD2	2:A:401:7L7:N4	2.67	0.57
1:A:200:ARG:NH1	1:A:240:GLU:OE1	2.37	0.57
2:A:401:7L7:O5	2:A:401:7L7:S12	2.63	0.56
1:A:200:ARG:HH11	1:A:240:GLU:CD	2.10	0.54
1:A:200:ARG:NH1	1:A:240:GLU:CD	2.62	0.52
2:A:401:7L7:C3	2:A:401:7L7:C13	2.90	0.48
1:A:123:PRO:HA	1:A:154:LEU:HG	1.98	0.46
1:A:58:LEU:C	1:A:58:LEU:HD23	2.36	0.45
1:A:168:GLN:HB3	6:A:406:ACT:H3	1.98	0.44
1:A:181:ASN:HA	1:A:210:VAL:HB	2.00	0.43
1:A:192:ALA:HB1	1:A:236:LYS:HD3	2.00	0.43
1:A:58:LEU:HD23	1:A:58:LEU:O	2.18	0.43

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	361/390 (93%)	348 (96%)	13 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	293/317 (92%)	288 (98%)	5 (2%)	60	36

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	MET
1	A	327	ARG
1	A	356	TYR
1	A	359	LEU
1	A	360	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	315	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

9 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	$\# Z > 2$
5	SO4	A	405	-	4,4,4	0.84	0	6,6,6	0.25	0
6	ACT	A	407	-	1,3,3	0.11	0	0,3,3	0.00	-
6	ACT	A	408	-	1,3,3	0.82	0	0,3,3	0.00	-
6	ACT	A	406	-	1,3,3	17.01	1 (100%)	0,3,3	0.00	-
2	7L7	A	401	-	20,21,21	2.39	6 (30%)	22,29,29	2.40	8 (36%)
4	ORO	A	403	-	6,11,11	2.51	4 (66%)	3,15,15	4.38	2 (66%)
3	FMN	A	402	-	31,33,33	3.73	12 (38%)	40,50,50	3.99	15 (37%)
5	SO4	A	404	-	4,4,4	0.67	0	6,6,6	0.86	0
6	ACT	A	409	-	1,3,3	1.22	0	0,3,3	0.00	-

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	FMN	A	402	-	-	5/18/18/18	0/3/3/3
2	7L7	A	401	-	-	0/14/29/29	0/2/2/2
4	ORO	A	403	-	-	0/0/4/4	0/1/1/1

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	406	ACT	CH3-C	17.01	1.70	1.48
3	A	402	FMN	C4A-C10	15.66	1.54	1.38
2	A	401	7L7	C3-C1	-7.46	1.28	1.43
3	A	402	FMN	O4-C4	5.57	1.38	1.24
3	A	402	FMN	C6-C5A	-5.02	1.34	1.41
2	A	401	7L7	O6-C2	4.95	1.44	1.33
3	A	402	FMN	C2-N1	-4.74	1.28	1.38
3	A	402	FMN	C9A-C5A	4.68	1.51	1.42
3	A	402	FMN	C2-N3	4.00	1.46	1.38
3	A	402	FMN	C5'-C4'	3.83	1.57	1.51
4	A	403	ORO	C2-N3	-3.36	1.31	1.38
3	A	402	FMN	C4-N3	-3.35	1.27	1.33
4	A	403	ORO	C6-N1	3.05	1.39	1.34
3	A	402	FMN	C1'-N10	3.02	1.51	1.48
4	A	403	ORO	C5-C6	-2.71	1.33	1.40
4	A	403	ORO	C4-N3	2.57	1.37	1.33
3	A	402	FMN	C10-N1	-2.49	1.30	1.33
2	A	401	7L7	C11-S12	-2.33	1.76	1.80
3	A	402	FMN	C4A-N5	2.29	1.36	1.33
2	A	401	7L7	C17-C18	2.17	1.42	1.37
2	A	401	7L7	C16-C15	2.15	1.43	1.38
3	A	402	FMN	C8-C7	2.05	1.46	1.40
2	A	401	7L7	C3-N4	2.00	1.18	1.14

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	FMN	C4-C4A-C10	-16.37	109.12	119.95
3	A	402	FMN	C4-C4A-N5	10.33	130.41	118.60
3	A	402	FMN	C4A-N5-C5A	7.11	123.87	116.77
4	A	403	ORO	C5-C4-N3	-6.79	116.16	124.08
3	A	402	FMN	C4-N3-C2	6.49	120.62	115.14
2	A	401	7L7	C13-N9-C10	-6.35	115.32	122.67
3	A	402	FMN	C4A-C10-N10	-5.96	114.18	120.30
3	A	402	FMN	C6-C5A-N5	5.69	125.32	119.05
2	A	401	7L7	C11-C10-N9	4.15	113.66	111.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	7L7	O6-C2-C1	3.80	118.57	111.41
3	A	402	FMN	C9A-C5A-N5	-3.78	116.44	122.36
3	A	402	FMN	C9-C9A-C5A	-3.31	114.23	119.88
3	A	402	FMN	C1'-N10-C10	-3.13	115.61	118.41
4	A	403	ORO	C5-C6-N1	2.98	125.89	122.35
2	A	401	7L7	C10-C11-S12	-2.82	103.03	107.59
3	A	402	FMN	C4A-C4-N3	2.74	127.18	123.43
3	A	402	FMN	O4'-C4'-C3'	2.64	115.51	109.10
3	A	402	FMN	C8-C9-C9A	2.60	127.27	119.19
3	A	402	FMN	C7-C6-C5A	2.60	124.90	121.22
2	A	401	7L7	C13-N9-C8	2.59	128.48	124.79
3	A	402	FMN	C9-C8-C7	-2.49	115.72	119.91
3	A	402	FMN	C9A-N10-C10	2.46	125.13	121.91
2	A	401	7L7	C14-C13-C18	2.35	121.99	117.30
2	A	401	7L7	O20-C10-N9	2.27	126.04	124.01
2	A	401	7L7	C7-O6-C2	2.25	120.11	115.86

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	FMN	C2'-C3'-C4'-O4'
3	A	402	FMN	O3'-C3'-C4'-O4'
3	A	402	FMN	C4'-C5'-O5'-P
3	A	402	FMN	O3'-C3'-C4'-C5'
3	A	402	FMN	C5'-O5'-P-O1P

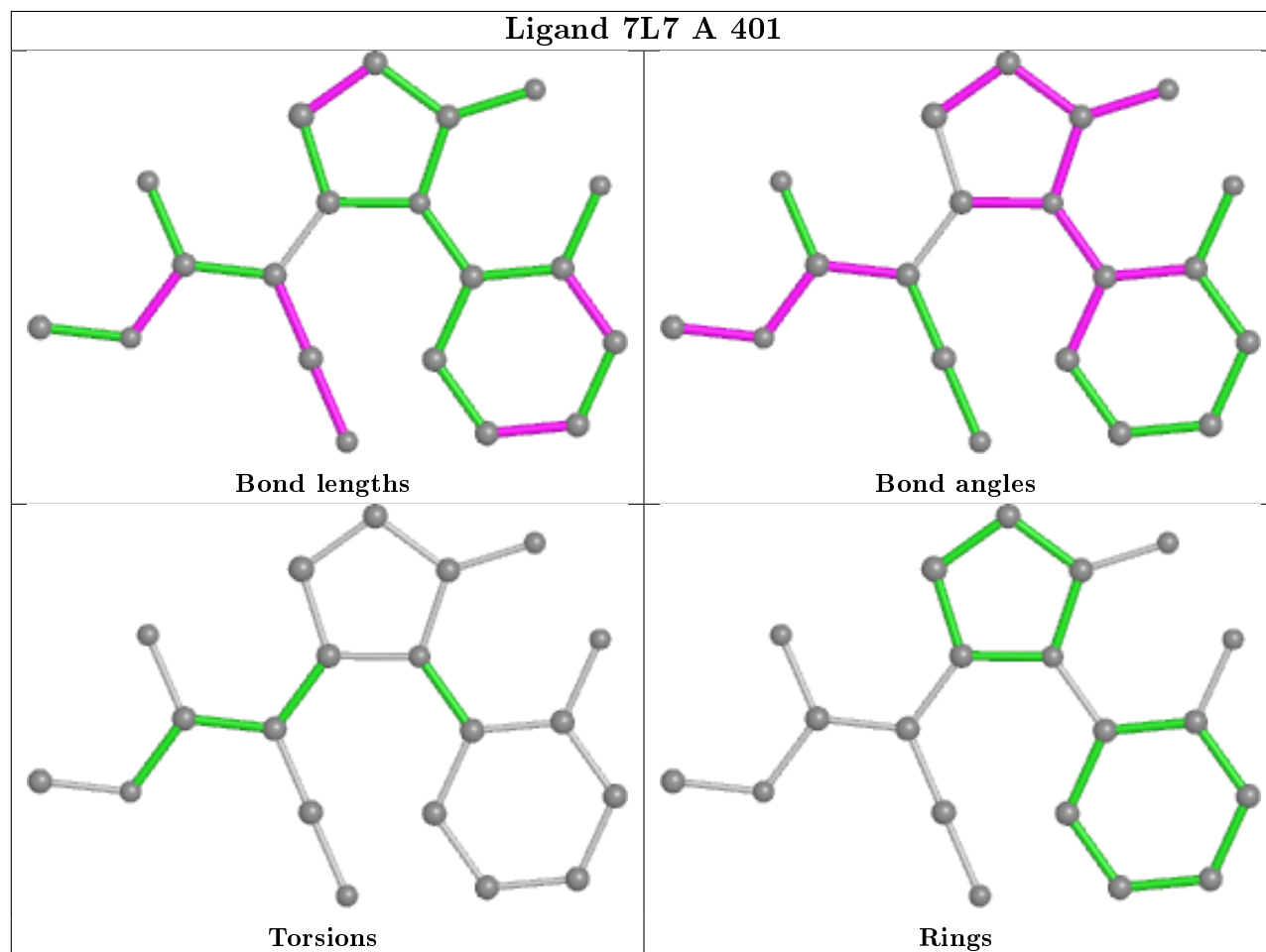
There are no ring outliers.

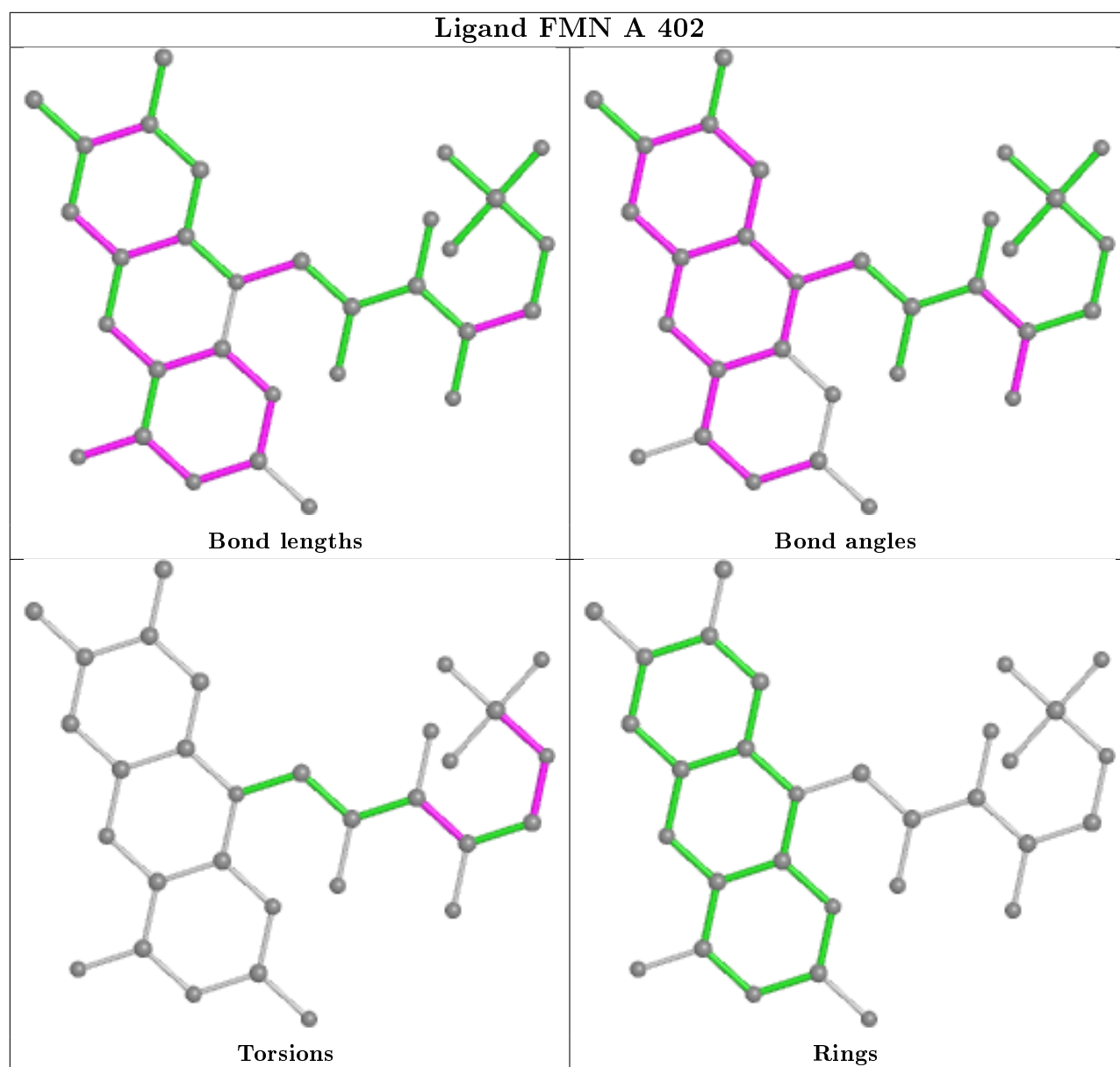
5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	407	ACT	1	0
6	A	408	ACT	1	0
6	A	406	ACT	1	0
2	A	401	7L7	4	0
6	A	409	ACT	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [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	363/390 (93%)	0.03	23 (6%)	20 20	11, 24, 47, 95	13 (3%)

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	72	ARG	7.6
1	A	211	VAL	7.4
1	A	213	VAL	7.1
1	A	73	PHE	6.7
1	A	362	TRP	6.6
1	A	189	VAL	6.3
1	A	33	GLY	5.8
1	A	37	PHE	5.4
1	A	70	ARG	4.6
1	A	212	ASN	4.5
1	A	74	GLN	4.2
1	A	41	HIS	4.2
1	A	36	ARG	4.0
1	A	40	GLU	3.6
1	A	313	SER	3.5
1	A	134	VAL	3.4
1	A	71	ALA	3.3
1	A	34	ASP	3.2
1	A	48	GLY	3.2
1	A	187	THR	2.4
1	A	190	ASP	2.4
1	A	46	LEU	2.2
1	A	224	LEU	2.2

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

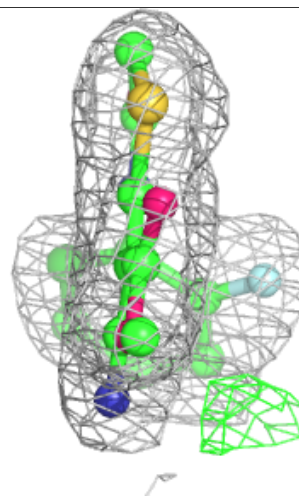
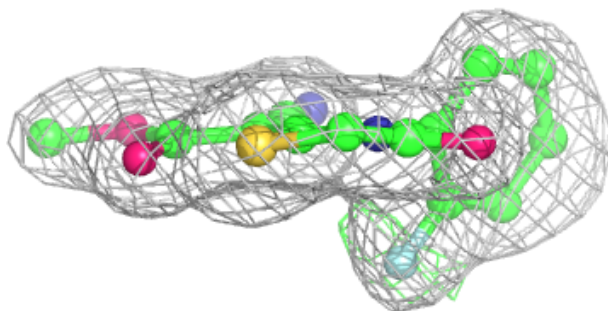
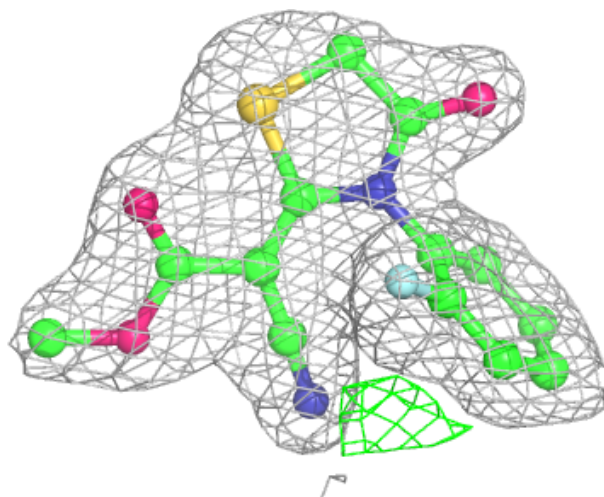
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	ACT	A	408	4/4	0.69	0.21	38,43,50,52	0
6	ACT	A	406	4/4	0.75	0.13	24,35,44,51	0
6	ACT	A	407	4/4	0.88	0.09	49,49,54,65	0
2	7L7	A	401	20/20	0.91	0.14	34,42,49,49	0
5	SO4	A	405	5/5	0.94	0.26	63,69,74,76	0
6	ACT	A	409	4/4	0.96	0.07	28,33,38,49	0
3	FMN	A	402	31/31	0.98	0.08	16,17,19,20	0
5	SO4	A	404	5/5	0.99	0.12	35,35,41,46	0
4	ORO	A	403	11/11	0.99	0.04	16,17,21,22	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.

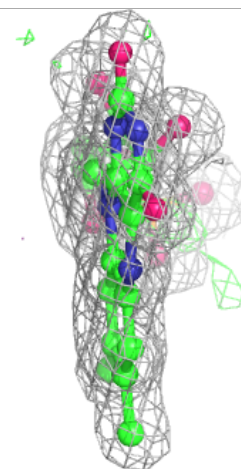
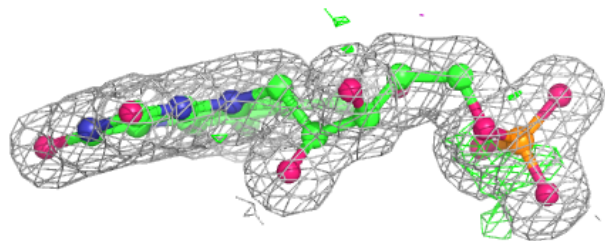
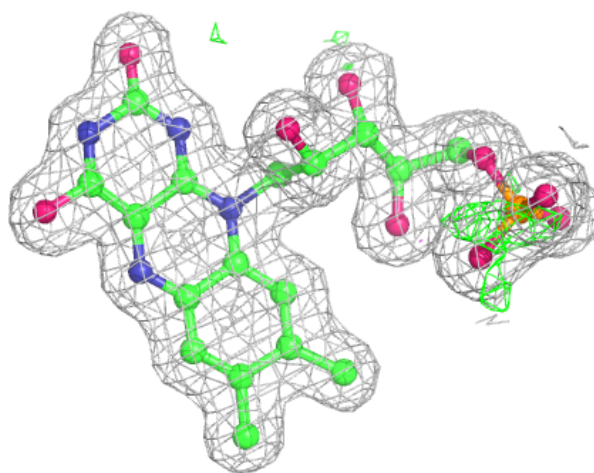
Electron density around 7L7 A 401:

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



Electron density around FMN A 402:

$2mF_o-DF_c$ (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.