



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 10, 2021 – 09:22 PM EDT

PDB ID : 3EXH
Title : Crystal structure of the pyruvate dehydrogenase (E1p) component of human pyruvate dehydrogenase complex
Authors : Kato, M.; Wynn, R.M.; Chuang, J.L.; Tso, S.-C.; Machius, M.; Li, J.; Chuang, D.T.
Deposited on : 2008-10-16
Resolution : 2.44 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 2.23.2
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) : 2.23.2

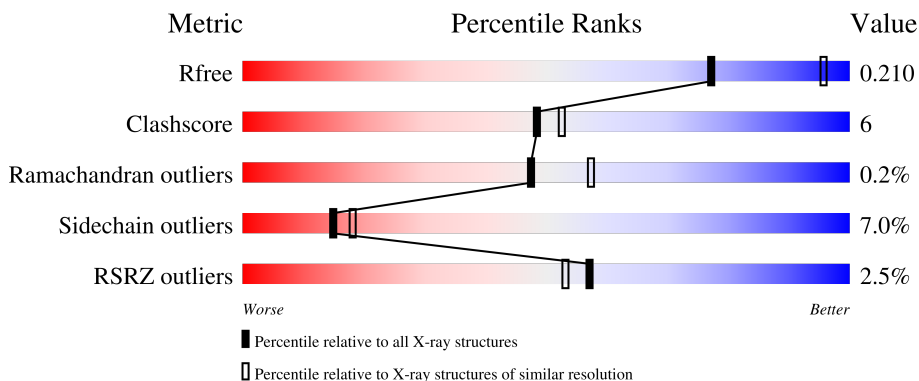
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.44 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.



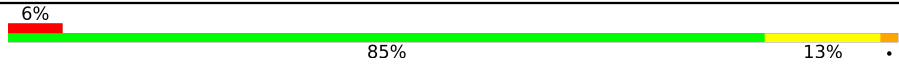

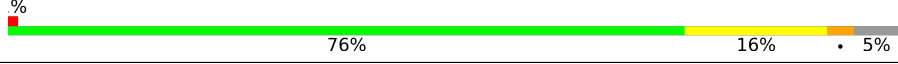
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1564 (2.46-2.42)
Clashscore	141614	1631 (2.46-2.42)
Ramachandran outliers	138981	1617 (2.46-2.42)
Sidechain outliers	138945	1617 (2.46-2.42)
RSRZ outliers	127900	1547 (2.46-2.42)

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	382	 76% 16% • 6%
1	E	382	 69% 15% • 13%
2	B	329	 85% 13% •
2	D	329	 87% 12% •
2	F	329	 88% 11% •

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Mol	Chain	Length	Quality of chain
2	H	329	 <p>6% 85% 13% • 5%</p>
3	C	382	 <p>% 77% 15% • 5%</p>
3	G	382	 <p>% 76% 16% • 5%</p>

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 22035 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 Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	359	2802	1760	493	525	24	0	0	0
1	E	331	2573	1621	448	482	22	0	0	0

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	expression tag	UNP P08559
A	-19	GLY	-	expression tag	UNP P08559
A	-18	SER	-	expression tag	UNP P08559
A	-17	SER	-	expression tag	UNP P08559
A	-16	HIS	-	expression tag	UNP P08559
A	-15	HIS	-	expression tag	UNP P08559
A	-14	HIS	-	expression tag	UNP P08559
A	-13	HIS	-	expression tag	UNP P08559
A	-12	HIS	-	expression tag	UNP P08559
A	-11	HIS	-	expression tag	UNP P08559
A	-10	SER	-	expression tag	UNP P08559
A	-9	SER	-	expression tag	UNP P08559
A	-8	GLY	-	expression tag	UNP P08559
A	-7	LEU	-	expression tag	UNP P08559
A	-6	VAL	-	expression tag	UNP P08559
A	-5	PRO	-	expression tag	UNP P08559
A	-4	ARG	-	expression tag	UNP P08559
A	-3	GLY	-	expression tag	UNP P08559
A	-2	SER	-	expression tag	UNP P08559
A	-1	HIS	-	expression tag	UNP P08559
A	0	MET	-	expression tag	UNP P08559
A	203	ALA	SER	engineered mutation	UNP P08559
A	271	ALA	SER	engineered mutation	UNP P08559
E	-20	MET	-	expression tag	UNP P08559

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-19	GLY	-	expression tag	UNP P08559
E	-18	SER	-	expression tag	UNP P08559
E	-17	SER	-	expression tag	UNP P08559
E	-16	HIS	-	expression tag	UNP P08559
E	-15	HIS	-	expression tag	UNP P08559
E	-14	HIS	-	expression tag	UNP P08559
E	-13	HIS	-	expression tag	UNP P08559
E	-12	HIS	-	expression tag	UNP P08559
E	-11	HIS	-	expression tag	UNP P08559
E	-10	SER	-	expression tag	UNP P08559
E	-9	SER	-	expression tag	UNP P08559
E	-8	GLY	-	expression tag	UNP P08559
E	-7	LEU	-	expression tag	UNP P08559
E	-6	VAL	-	expression tag	UNP P08559
E	-5	PRO	-	expression tag	UNP P08559
E	-4	ARG	-	expression tag	UNP P08559
E	-3	GLY	-	expression tag	UNP P08559
E	-2	SER	-	expression tag	UNP P08559
E	-1	HIS	-	expression tag	UNP P08559
E	0	MET	-	expression tag	UNP P08559
E	203	ALA	SER	engineered mutation	UNP P08559
E	271	ALA	SER	engineered mutation	UNP P08559

- Molecule 2 is a protein called Pyruvate dehydrogenase E1 component subunit beta, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	329	Total	C	N	O	S	0	0	0
			2519	1604	427	469	19			
2	D	329	Total	C	N	O	S	0	0	0
			2519	1604	427	469	19			
2	F	329	Total	C	N	O	S	0	0	0
			2519	1604	427	469	19			
2	H	329	Total	C	N	O	S	0	0	0
			2519	1604	427	469	19			

- Molecule 3 is a protein called Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
3	C	362	Total	C	N	O	P	S	0	0	0
			2825	1772	496	532	1	24			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	P				S
3	G	362	2825	1772	496	532	1	24	0	0	0

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-20	MET	-	expression tag	UNP P08559
C	-19	GLY	-	expression tag	UNP P08559
C	-18	SER	-	expression tag	UNP P08559
C	-17	SER	-	expression tag	UNP P08559
C	-16	HIS	-	expression tag	UNP P08559
C	-15	HIS	-	expression tag	UNP P08559
C	-14	HIS	-	expression tag	UNP P08559
C	-13	HIS	-	expression tag	UNP P08559
C	-12	HIS	-	expression tag	UNP P08559
C	-11	HIS	-	expression tag	UNP P08559
C	-10	SER	-	expression tag	UNP P08559
C	-9	SER	-	expression tag	UNP P08559
C	-8	GLY	-	expression tag	UNP P08559
C	-7	LEU	-	expression tag	UNP P08559
C	-6	VAL	-	expression tag	UNP P08559
C	-5	PRO	-	expression tag	UNP P08559
C	-4	ARG	-	expression tag	UNP P08559
C	-3	GLY	-	expression tag	UNP P08559
C	-2	SER	-	expression tag	UNP P08559
C	-1	HIS	-	expression tag	UNP P08559
C	0	MET	-	expression tag	UNP P08559
C	203	ALA	SER	engineered mutation	UNP P08559
C	271	ALA	SER	engineered mutation	UNP P08559
G	-20	MET	-	expression tag	UNP P08559
G	-19	GLY	-	expression tag	UNP P08559
G	-18	SER	-	expression tag	UNP P08559
G	-17	SER	-	expression tag	UNP P08559
G	-16	HIS	-	expression tag	UNP P08559
G	-15	HIS	-	expression tag	UNP P08559
G	-14	HIS	-	expression tag	UNP P08559
G	-13	HIS	-	expression tag	UNP P08559
G	-12	HIS	-	expression tag	UNP P08559
G	-11	HIS	-	expression tag	UNP P08559
G	-10	SER	-	expression tag	UNP P08559
G	-9	SER	-	expression tag	UNP P08559
G	-8	GLY	-	expression tag	UNP P08559

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-7	LEU	-	expression tag	UNP P08559
G	-6	VAL	-	expression tag	UNP P08559
G	-5	PRO	-	expression tag	UNP P08559
G	-4	ARG	-	expression tag	UNP P08559
G	-3	GLY	-	expression tag	UNP P08559
G	-2	SER	-	expression tag	UNP P08559
G	-1	HIS	-	expression tag	UNP P08559
G	0	MET	-	expression tag	UNP P08559
G	203	ALA	SER	engineered mutation	UNP P08559
G	271	ALA	SER	engineered mutation	UNP P08559

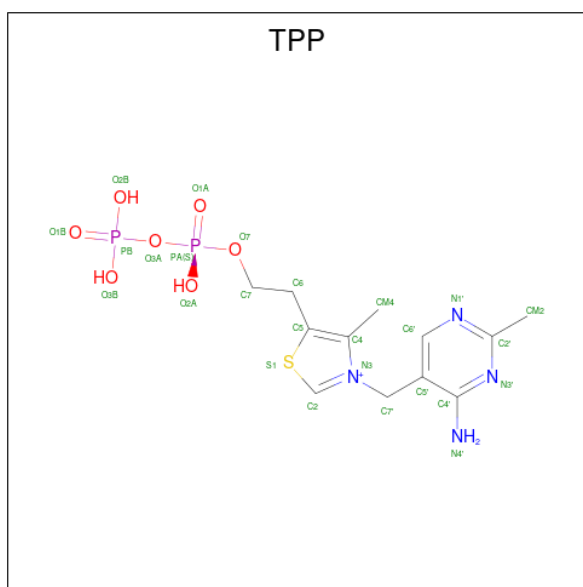
- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Mn 1 1	0	0
4	C	1	Total Mn 1 1	0	0
4	E	1	Total Mn 1 1	0	0
4	G	1	Total Mn 1 1	0	0

- Molecule 5 is POTASSIUM ION (three-letter code: K) (formula: K).

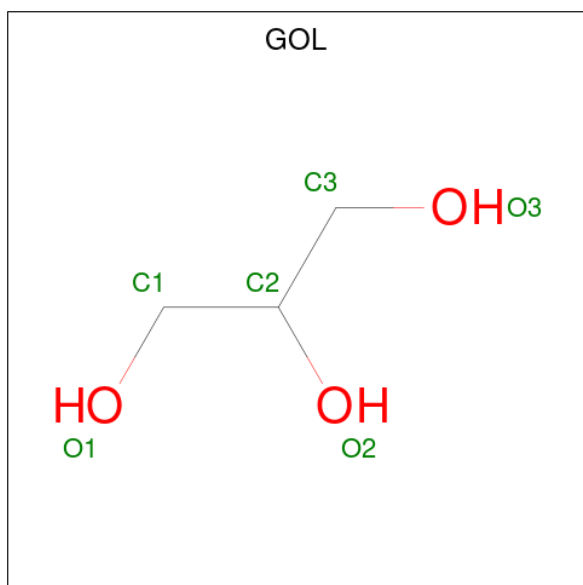
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total K 1 1	0	0
5	C	1	Total K 1 1	0	0
5	E	1	Total K 1 1	0	0
5	G	1	Total K 1 1	0	0

- Molecule 6 is THIAMINE DIPHOSPHATE (three-letter code: TPP) (formula: C₁₂H₁₉N₄O₇P₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			S
6	A	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
6	C	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
6	E	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
6	G	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	C	1	Total	C	O	0	0
			6	3	3		
7	E	1	Total	C	O	0	0
			6	3	3		
7	G	1	Total	C	O	0	0
			6	3	3		

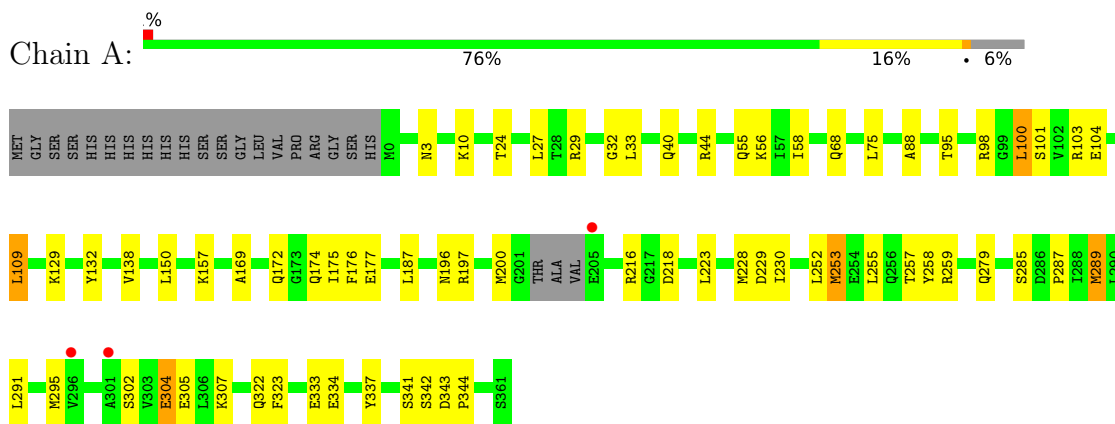
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	93	Total	O	0	0
			93	93		
8	B	114	Total	O	0	0
			114	114		
8	C	80	Total	O	0	0
			80	80		
8	D	97	Total	O	0	0
			97	97		
8	E	89	Total	O	0	0
			89	89		
8	F	121	Total	O	0	0
			121	121		
8	G	97	Total	O	0	0
			97	97		
8	H	101	Total	O	0	0
			101	101		

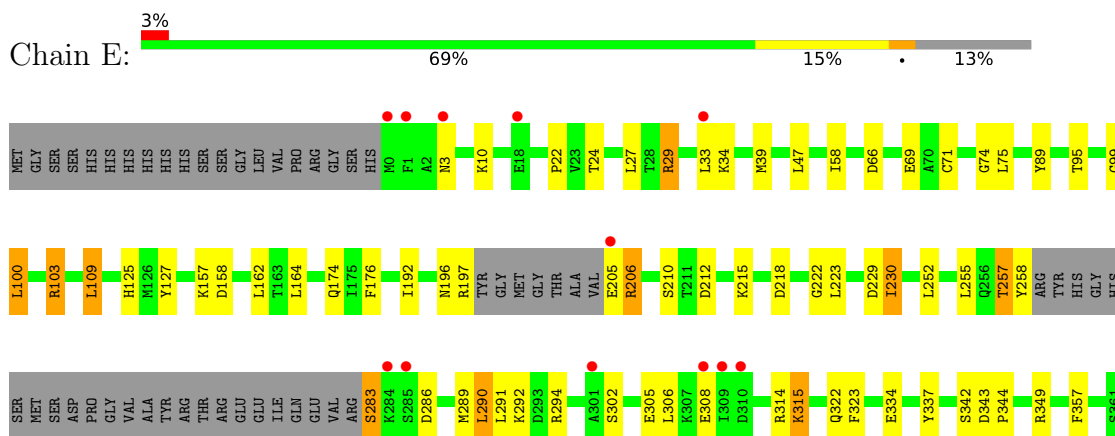
3 Residue-property plots [i](#)

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.

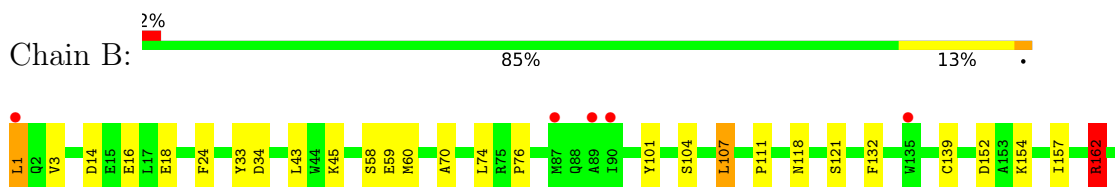
- Molecule 1: Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial



- Molecule 1: Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial

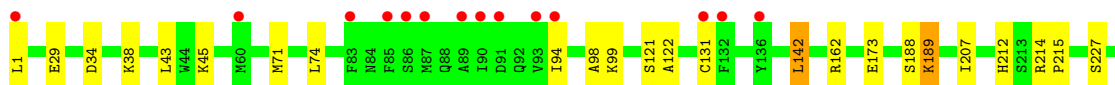
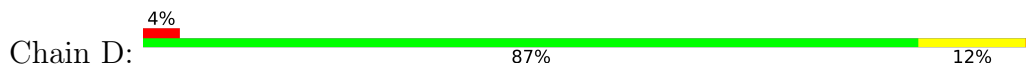


- Molecule 2: Pyruvate dehydrogenase E1 component subunit beta, mitochondrial

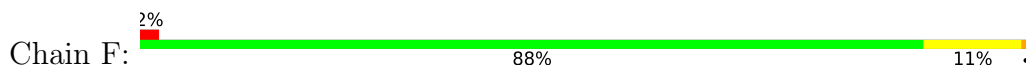




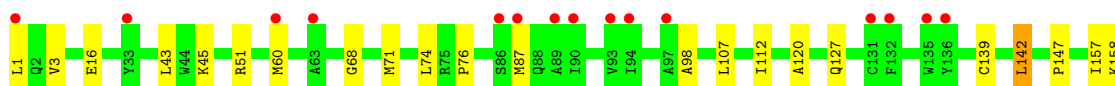
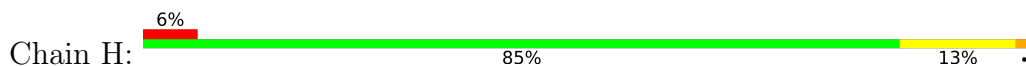
- Molecule 2: Pyruvate dehydrogenase E1 component subunit beta, mitochondrial



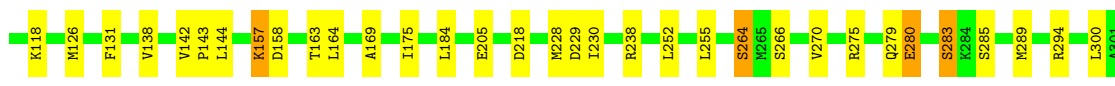
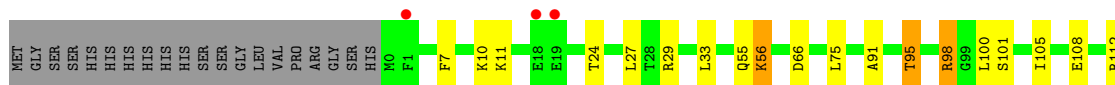
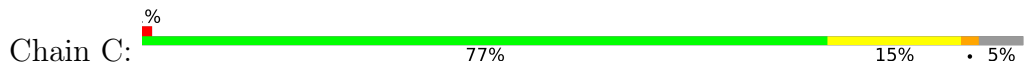
- Molecule 2: Pyruvate dehydrogenase E1 component subunit beta, mitochondrial




- Molecule 2: Pyruvate dehydrogenase E1 component subunit beta, mitochondrial

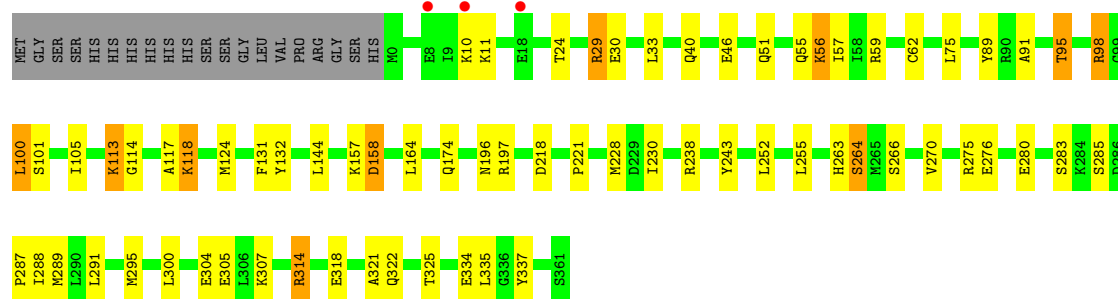


- Molecule 3: Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial



- Molecule 3: Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial

Chain G:  %



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	257.06Å 115.61Å 127.59Å 90.00° 113.64° 90.00°	Depositor
Resolution (Å)	50.00 – 2.44 47.46 – 2.44	Depositor EDS
% Data completeness (in resolution range)	97.8 (50.00-2.44) 97.8 (47.46-2.44)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.28 (at 2.45Å)	Xtrriage
Refinement program	REFMAC 5.4.0069	Depositor
R, R_{free}	0.165 , 0.211 0.166 , 0.210	Depositor DCC
R_{free} test set	6182 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	28.4	Xtrriage
Anisotropy	0.144	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 41.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	22035	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: TPP, MN, SEP, K, GOL

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	0.95	2/2857 (0.1%)	0.89	2/3845 (0.1%)
1	E	0.93	1/2621 (0.0%)	0.88	5/3527 (0.1%)
2	B	0.99	0/2574	0.95	7/3488 (0.2%)
2	D	0.96	3/2574 (0.1%)	0.91	2/3488 (0.1%)
2	F	0.99	2/2574 (0.1%)	0.92	2/3488 (0.1%)
2	H	0.98	1/2574 (0.0%)	0.90	3/3488 (0.1%)
3	C	0.94	2/2870 (0.1%)	0.87	1/3864 (0.0%)
3	G	0.93	1/2870 (0.0%)	0.86	1/3864 (0.0%)
All	All	0.96	12/21514 (0.1%)	0.90	23/29052 (0.1%)

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	29	GLU	CG-CD	6.55	1.61	1.51
3	G	62	CYS	CB-SG	-6.08	1.72	1.82
1	A	176	PHE	CE2-CZ	5.89	1.48	1.37
3	C	205	GLU	CG-CD	5.55	1.60	1.51
2	F	136	TYR	CD1-CE1	-5.49	1.31	1.39

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	162	ARG	NE-CZ-NH2	-9.03	115.78	120.30
2	B	14	ASP	CB-CG-OD1	8.83	126.25	118.30
2	B	162	ARG	NE-CZ-NH1	8.21	124.40	120.30
1	E	197	ARG	NE-CZ-NH1	8.13	124.37	120.30
2	F	162	ARG	NE-CZ-NH1	7.13	123.87	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	2802	0	2755	39	0
1	E	2573	0	2543	41	0
2	B	2519	0	2517	27	0
2	D	2519	0	2517	20	0
2	F	2519	0	2517	24	0
2	H	2519	0	2517	27	0
3	C	2825	0	2775	34	0
3	G	2825	0	2775	44	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
5	E	1	0	0	0	0
5	G	1	0	0	0	0
6	A	26	0	16	2	0
6	C	26	0	16	4	0
6	E	26	0	16	3	0
6	G	26	0	16	7	0
7	A	12	0	16	0	0
7	C	6	0	8	0	0
7	E	6	0	8	0	0
7	G	6	0	8	0	0
8	A	93	0	0	2	0
8	B	114	0	0	1	0
8	C	80	0	0	1	0
8	D	97	0	0	0	0
8	E	89	0	0	3	0
8	F	121	0	0	2	0
8	G	97	0	0	5	0
8	H	101	0	0	3	0
All	All	22035	0	21020	253	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 6.

The worst 5 of 253 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)
3:G:264:SEP:O3P	3:G:266:SER:HB2	1.34	1.26
3:C:270:VAL:HG21	3:C:275:ARG:NH1	1.62	1.14
3:C:264:SEP:O3P	3:C:266:SER:HB2	1.48	1.11
1:E:206:ARG:HG3	1:E:206:ARG:HH11	1.03	1.06
1:A:68:GLN:HE22	1:A:196:ASN:HD22	1.07	1.03

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	355/382 (93%)	343 (97%)	9 (2%)	3 (1%)	19	22
1	E	325/382 (85%)	317 (98%)	7 (2%)	1 (0%)	41	49
2	B	327/329 (99%)	315 (96%)	12 (4%)	0	100	100
2	D	327/329 (99%)	319 (98%)	8 (2%)	0	100	100
2	F	327/329 (99%)	314 (96%)	13 (4%)	0	100	100
2	H	327/329 (99%)	315 (96%)	12 (4%)	0	100	100
3	C	359/382 (94%)	348 (97%)	10 (3%)	1 (0%)	41	49
3	G	359/382 (94%)	346 (96%)	12 (3%)	1 (0%)	41	49
All	All	2706/2844 (95%)	2617 (97%)	83 (3%)	6 (0%)	47	57

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	200	MET
3	C	218	ASP
1	E	218	ASP
3	G	218	ASP

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Mol	Chain	Res	Type
1	A	88	ALA

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	290/310 (94%)	269 (93%)	21 (7%)	14 17
1	E	267/310 (86%)	243 (91%)	24 (9%)	9 10
2	B	268/268 (100%)	253 (94%)	15 (6%)	21 27
2	D	268/268 (100%)	254 (95%)	14 (5%)	23 31
2	F	268/268 (100%)	255 (95%)	13 (5%)	25 33
2	H	268/268 (100%)	251 (94%)	17 (6%)	18 23
3	C	291/309 (94%)	266 (91%)	25 (9%)	10 11
3	G	291/309 (94%)	266 (91%)	25 (9%)	10 11
All	All	2211/2310 (96%)	2057 (93%)	154 (7%)	15 18

5 of 154 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	G	29	ARG
2	H	142	LEU
3	G	75	LEU
3	G	283	SER
2	H	279	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	257	ASN
3	G	263	HIS
2	F	328	ASN
3	G	51	GLN

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Mol	Chain	Res	Type
3	G	353	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SEP	G	264	3	8,9,10	1.51	1 (12%)	8,12,14	1.85	4 (50%)
3	SEP	C	264	3	8,9,10	1.73	2 (25%)	8,12,14	1.64	3 (37%)

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	SEP	G	264	3	-	2/5/8/10	-
3	SEP	C	264	3	-	2/5/8/10	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	264	SEP	P-O1P	3.60	1.62	1.50
3	G	264	SEP	P-O1P	2.99	1.60	1.50
3	C	264	SEP	P-O2P	2.42	1.64	1.54

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	264	SEP	O2P-P-OG	-2.43	100.27	106.73
3	C	264	SEP	OG-CB-CA	-2.33	105.88	108.14
3	G	264	SEP	O3P-P-O2P	2.32	116.52	107.64
3	G	264	SEP	O3P-P-OG	2.28	112.80	106.73
3	G	264	SEP	O3P-P-O1P	-2.12	102.37	110.68

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	264	SEP	CB-OG-P-O2P
3	C	264	SEP	CB-OG-P-O3P
3	G	264	SEP	CB-OG-P-O2P
3	G	264	SEP	CB-OG-P-O3P

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	264	SEP	2	0
3	C	264	SEP	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 8 are monoatomic - leaving 9 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	$\# Z > 2$
7	GOL	G	1905	-	5,5,5	0.57	0	5,5,5	0.79	0
6	TPP	E	1502	4	22,27,27	1.92	5 (22%)	29,40,40	3.10	14 (48%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	GOL	A	1901	-	5,5,5	0.20	0	5,5,5	1.30	1 (20%)
7	GOL	C	1903	-	5,5,5	0.42	0	5,5,5	0.77	0
6	TPP	G	1502	4	22,27,27	1.62	4 (18%)	29,40,40	2.41	12 (41%)
7	GOL	E	1904	-	5,5,5	0.33	0	5,5,5	0.53	0
6	TPP	A	1502	4	22,27,27	1.37	4 (18%)	29,40,40	2.33	12 (41%)
7	GOL	A	1902	-	5,5,5	0.34	0	5,5,5	0.55	0
6	TPP	C	1502	4	22,27,27	1.96	3 (13%)	29,40,40	2.43	16 (55%)

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
7	GOL	G	1905	-	-	4/4/4/4	-
6	TPP	E	1502	4	-	1/16/17/17	0/2/2/2
7	GOL	A	1901	-	-	4/4/4/4	-
7	GOL	C	1903	-	-	3/4/4/4	-
6	TPP	G	1502	4	-	2/16/17/17	0/2/2/2
7	GOL	E	1904	-	-	4/4/4/4	-
6	TPP	A	1502	4	-	4/16/17/17	0/2/2/2
7	GOL	A	1902	-	-	2/4/4/4	-
6	TPP	C	1502	4	-	0/16/17/17	0/2/2/2

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	1502	TPP	C6-C5	7.31	1.54	1.50
6	E	1502	TPP	C6-C5	6.47	1.53	1.50
6	G	1502	TPP	C7'-N3	-3.67	1.41	1.48
6	A	1502	TPP	C2'-N3'	3.54	1.40	1.34
6	G	1502	TPP	C6-C5	3.30	1.52	1.50

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	1502	TPP	C6-C5-C4	7.37	133.35	127.43
6	E	1502	TPP	C7'-N3-C2	-6.95	112.80	125.35
6	E	1502	TPP	CM4-C4-N3	6.00	130.18	122.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	G	1502	TPP	C7'-N3-C2	-5.03	116.27	125.35
6	A	1502	TPP	C6-C5-C4	4.78	131.27	127.43

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

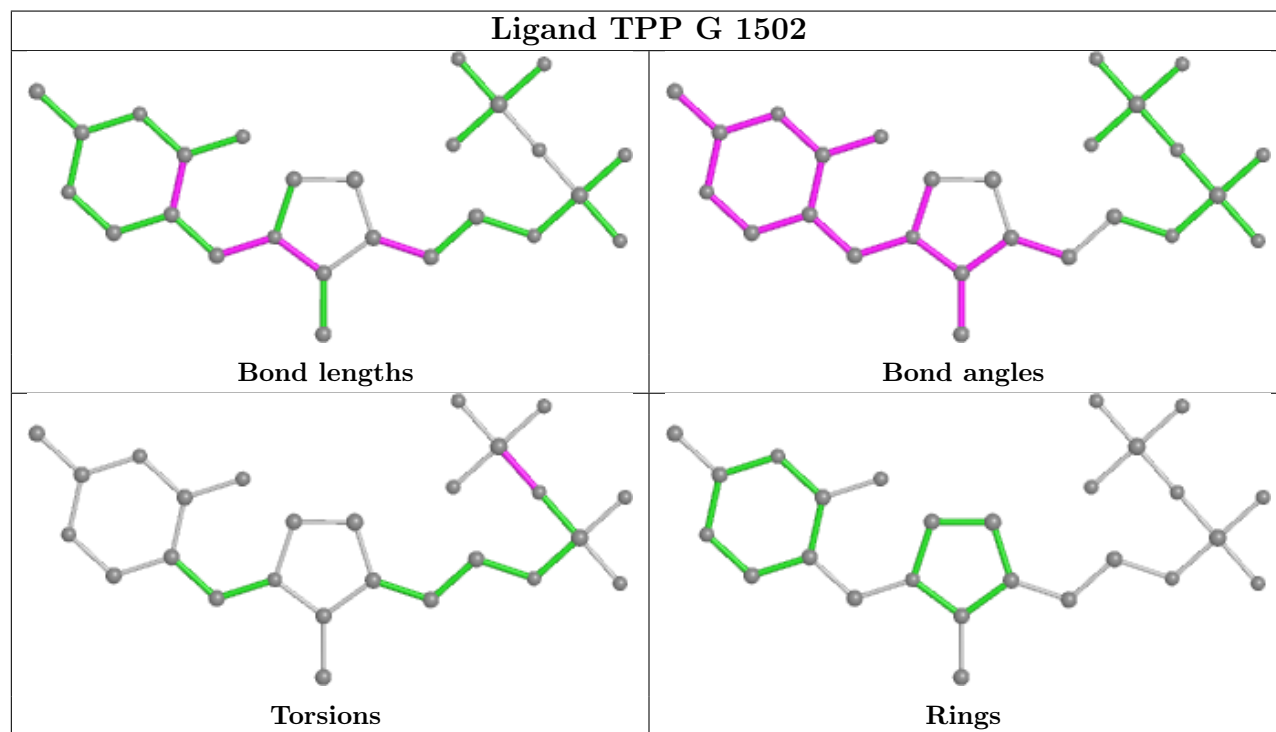
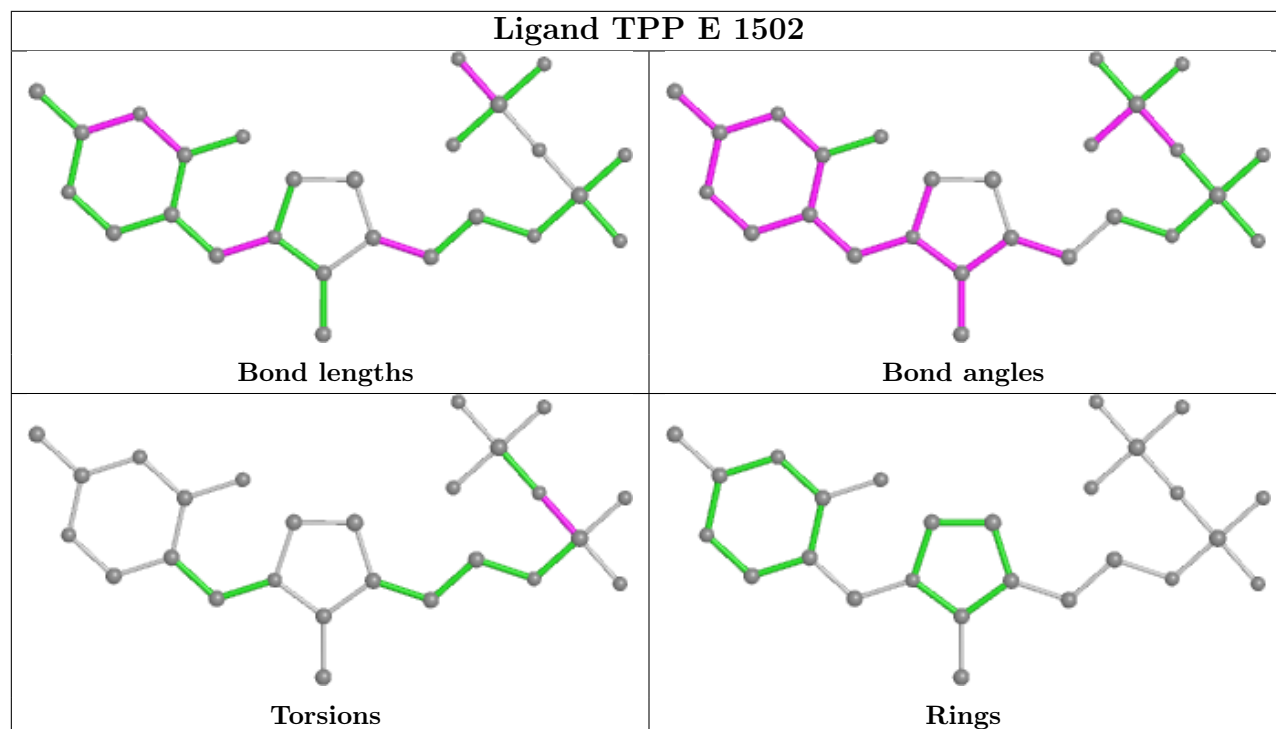
Mol	Chain	Res	Type	Atoms
6	A	1502	TPP	C5-C6-C7-O7
6	A	1502	TPP	C7-O7-PA-O1A
6	E	1502	TPP	PB-O3A-PA-O7
6	G	1502	TPP	PA-O3A-PB-O2B
7	A	1901	GOL	O1-C1-C2-O2

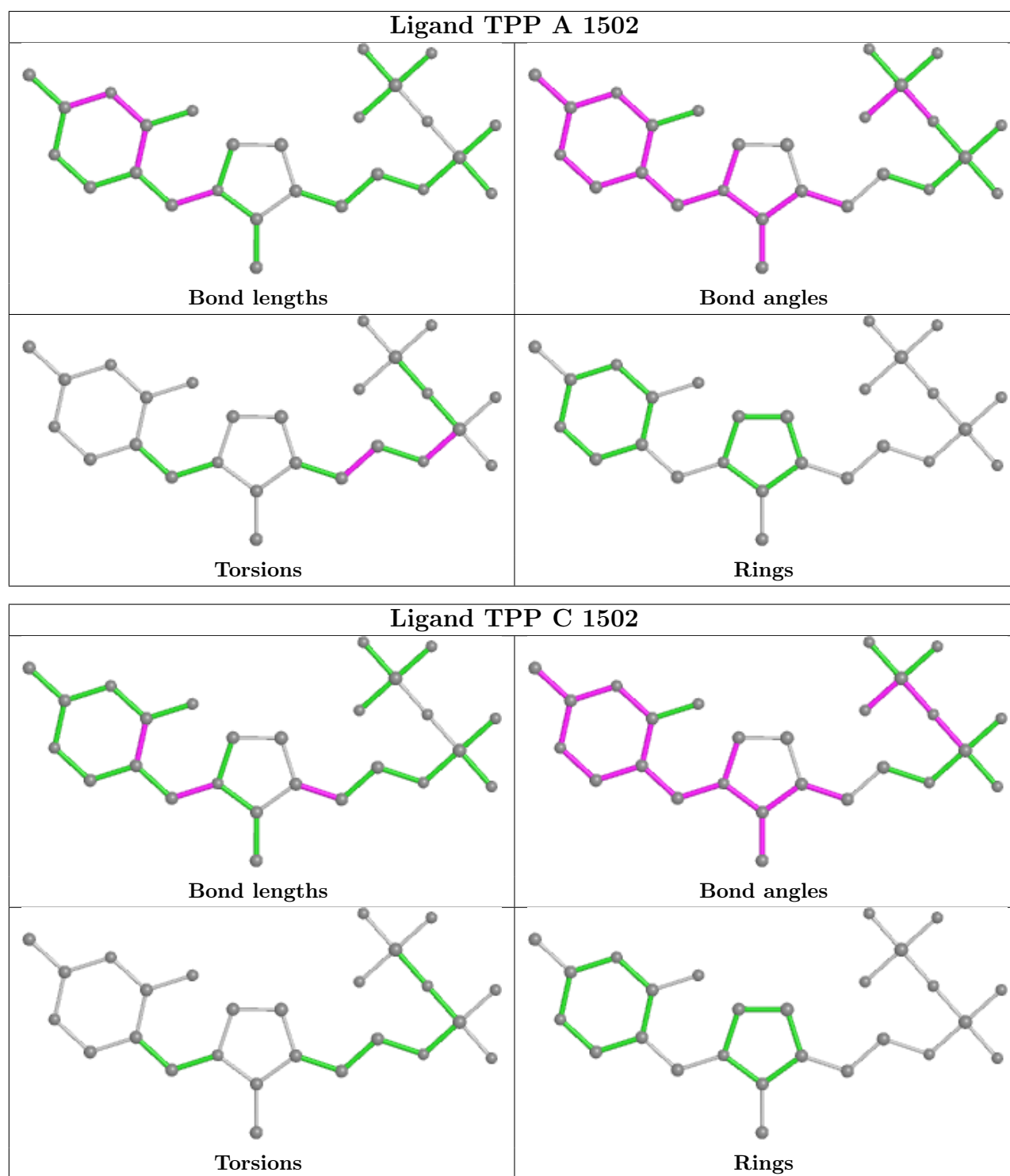
There are no ring outliers.

4 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	E	1502	TPP	3	0
6	G	1502	TPP	7	0
6	A	1502	TPP	2	0
6	C	1502	TPP	4	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

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	359/382 (93%)	-0.22	3 (0%) 86 85	10, 18, 32, 55	0
1	E	331/382 (86%)	-0.18	12 (3%) 42 39	10, 18, 29, 48	0
2	B	329/329 (100%)	-0.29	6 (1%) 68 64	10, 16, 27, 37	0
2	D	329/329 (100%)	-0.05	14 (4%) 35 32	10, 17, 28, 39	0
2	F	329/329 (100%)	-0.18	8 (2%) 59 54	11, 16, 27, 40	0
2	H	329/329 (100%)	0.03	20 (6%) 21 17	10, 17, 28, 41	0
3	C	361/382 (94%)	-0.28	3 (0%) 86 85	10, 18, 32, 44	0
3	G	361/382 (94%)	-0.24	3 (0%) 86 85	10, 18, 30, 42	0
All	All	2728/2844 (95%)	-0.18	69 (2%) 57 53	10, 17, 29, 55	0

The worst 5 of 69 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	90	ILE	4.7
2	D	90	ILE	4.1
2	D	1	LEU	3.6
3	C	18	GLU	3.4
2	F	1	LEU	3.4

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
3	SEP	G	264	10/11	0.94	0.15	27,31,37,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	SEP	C	264	10/11	0.96	0.15	30,35,44,45	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

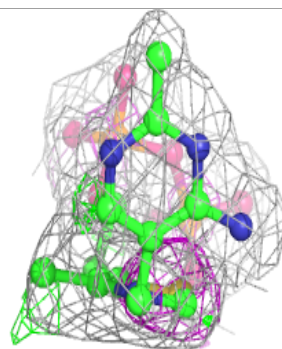
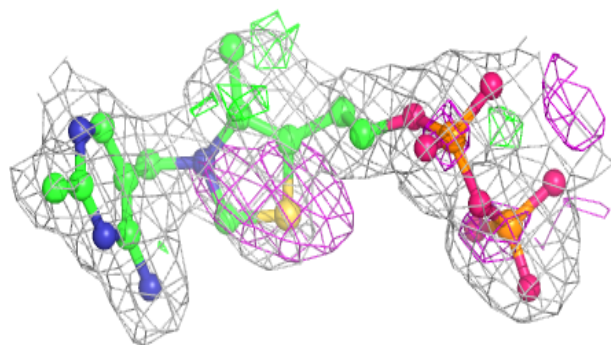
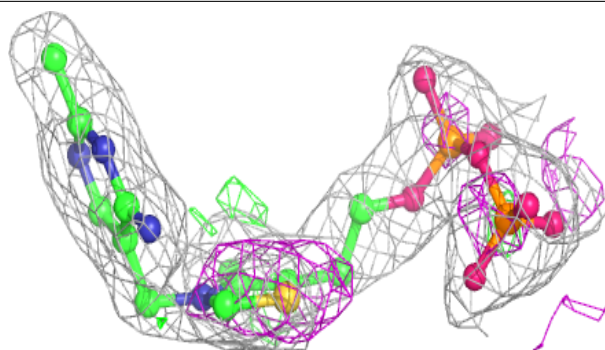
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	K	E	1501	1/1	0.79	0.10	48,48,48,48	0
7	GOL	C	1903	6/6	0.80	0.17	45,51,52,53	0
7	GOL	A	1902	6/6	0.88	0.15	46,51,52,52	0
7	GOL	A	1901	6/6	0.88	0.13	43,43,46,48	0
7	GOL	E	1904	6/6	0.88	0.15	45,48,50,52	0
7	GOL	G	1905	6/6	0.89	0.15	44,47,49,49	0
6	TPP	E	1502	26/26	0.96	0.12	7,16,31,40	0
6	TPP	G	1502	26/26	0.97	0.11	9,14,25,31	0
6	TPP	C	1502	26/26	0.97	0.11	10,14,26,34	0
6	TPP	A	1502	26/26	0.97	0.12	9,16,27,28	0
5	K	C	1501	1/1	0.98	0.13	32,32,32,32	0
5	K	A	1501	1/1	0.98	0.14	36,36,36,36	0
5	K	G	1501	1/1	0.98	0.14	41,41,41,41	0
4	MN	G	1500	1/1	0.99	0.02	13,13,13,13	0
4	MN	E	1500	1/1	1.00	0.01	14,14,14,14	0
4	MN	A	1500	1/1	1.00	0.02	14,14,14,14	0
4	MN	C	1500	1/1	1.00	0.01	12,12,12,12	0

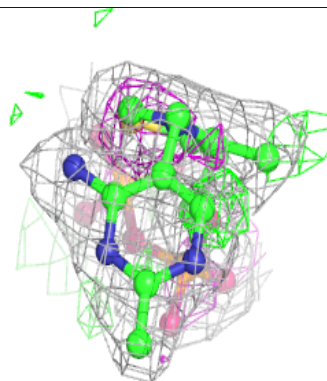
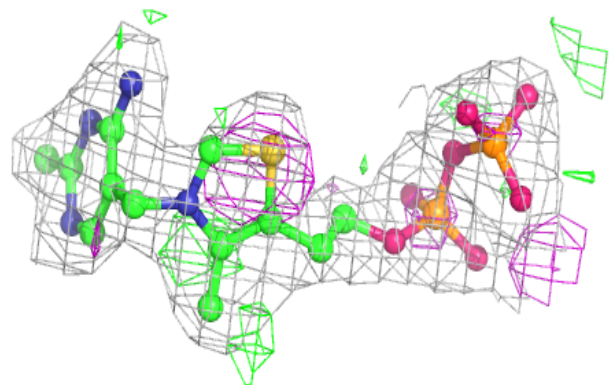
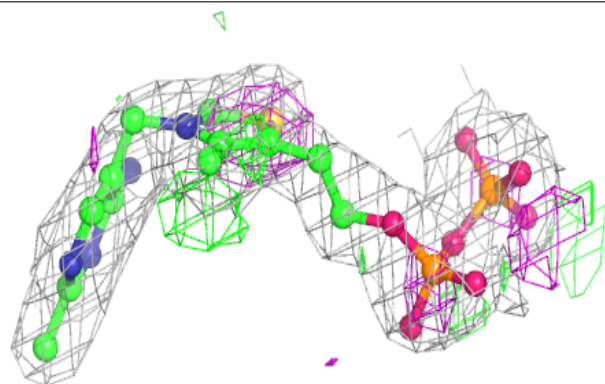
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around TPP E 1502:

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

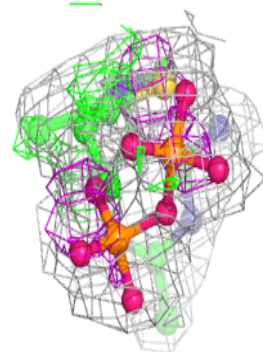
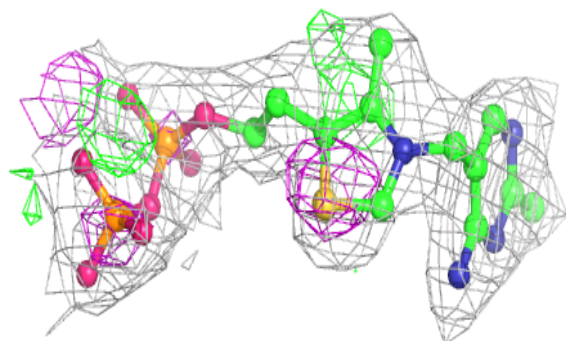
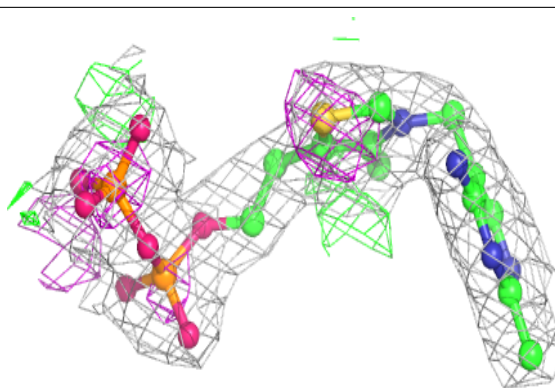
**Electron density around TPP G 1502:**

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

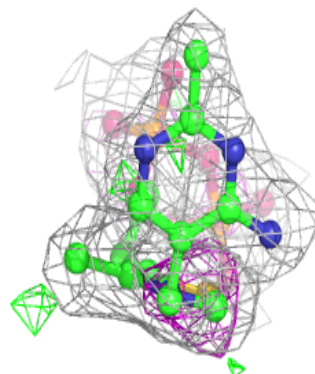
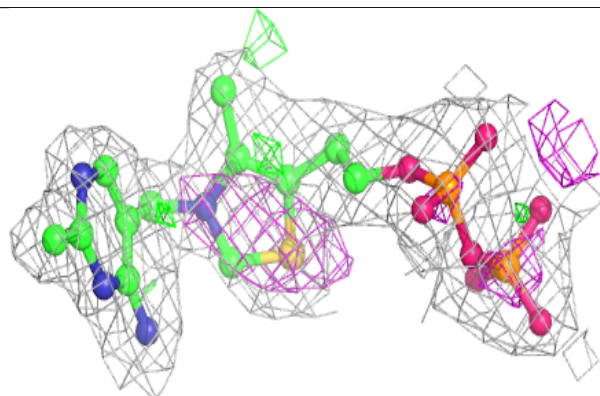
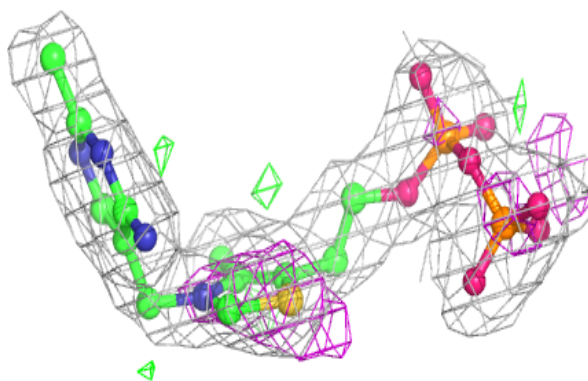


Electron density around TPP C 1502:

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

**Electron density around TPP A 1502:**

$2mF_o-DF_c$ (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.