



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 09:53 AM UTC

PDB ID : 8P5R / pdb_00008p5r
Title : Crystal structure of full-length, homohexameric 2-oxoglutarate dehydrogenase KGD from Mycobacterium smegmatis in complex with GarA
Authors : Wagner, T.; Mechaly, A.M.; Alzari, P.M.; Bellinzoni, M.
Deposited on : 2023-05-24
Resolution : 4.56 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 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

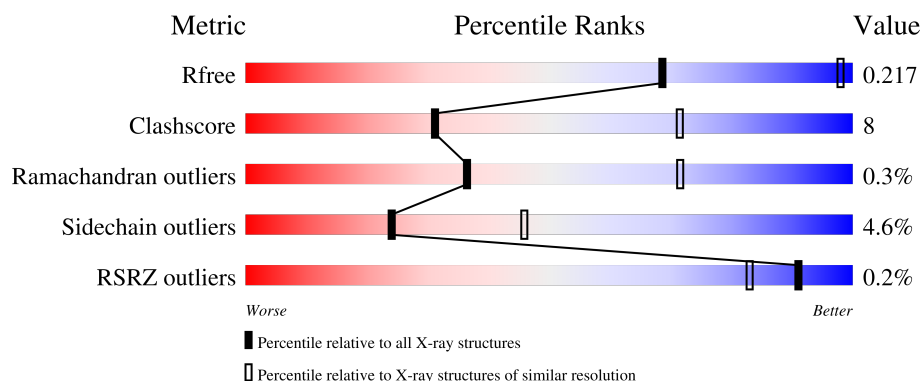
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.56 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.



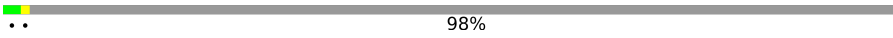
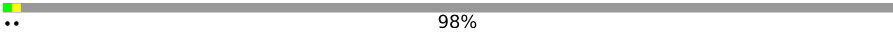
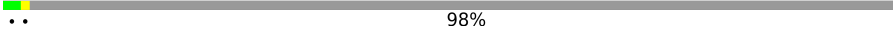
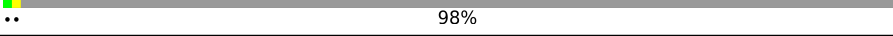
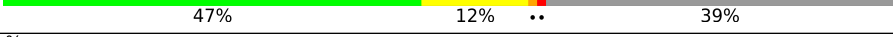
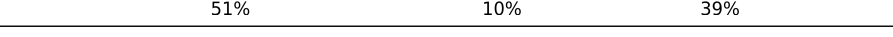
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1000 (5.20-3.92)
Clashscore	190562	1009 (5.14-3.94)
Ramachandran outliers	187476	1067 (5.22-3.90)
Sidechain outliers	187428	1049 (5.22-3.90)
RSRZ outliers	180081	1136 (5.22-3.90)

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	1250	
1	B	1250	
1	C	1250	
1	D	1250	
1	E	1250	

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Mol	Chain	Length	Quality of chain
1	F	1250	 72%15%12%
1	N	1250	 98%
1	O	1250	 98%
1	P	1250	 98%
1	Q	1250	 98%
2	G	158	 49%13%38%
2	H	158	 47%12%39%
2	I	158	 47%14%39%
2	J	158	 49%11%39%
2	K	158	 52%9%39%
2	L	158	 51%10%39%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 57005 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 Multifunctional 2-oxoglutarate metabolism enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1106	Total	C	N	O	S	0	0	0
			8579	5394	1535	1619	31			
1	B	1108	Total	C	N	O	S	0	0	0
			8591	5404	1534	1622	31			
1	C	1109	Total	C	N	O	S	0	0	0
			8593	5407	1531	1624	31			
1	D	1107	Total	C	N	O	S	0	0	0
			8544	5379	1519	1615	31			
1	E	1109	Total	C	N	O	S	0	0	0
			8537	5373	1516	1617	31			
1	F	1105	Total	C	N	O	S	0	0	0
			8513	5357	1517	1608	31			
1	N	30	Total	C	N	O	S	0	0	0
			266	172	41	52	1			
1	O	30	Total	C	N	O	S	0	0	0
			266	172	41	52	1			
1	P	30	Total	C	N	O	S	0	0	0
			266	172	41	52	1			
1	Q	30	Total	C	N	O	S	0	0	0
			266	172	41	52	1			

There are 240 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	MET	-	initiating methionine	UNP A0R2B1
A	-21	GLY	-	expression tag	UNP A0R2B1
A	-20	SER	-	expression tag	UNP A0R2B1
A	-19	SER	-	expression tag	UNP A0R2B1
A	-18	HIS	-	expression tag	UNP A0R2B1
A	-17	HIS	-	expression tag	UNP A0R2B1
A	-16	HIS	-	expression tag	UNP A0R2B1
A	-15	HIS	-	expression tag	UNP A0R2B1
A	-14	HIS	-	expression tag	UNP A0R2B1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	HIS	-	expression tag	UNP A0R2B1
A	-12	SER	-	expression tag	UNP A0R2B1
A	-11	SER	-	expression tag	UNP A0R2B1
A	-10	GLY	-	expression tag	UNP A0R2B1
A	-9	LEU	-	expression tag	UNP A0R2B1
A	-8	VAL	-	expression tag	UNP A0R2B1
A	-7	PRO	-	expression tag	UNP A0R2B1
A	-6	ARG	-	expression tag	UNP A0R2B1
A	-5	GLY	-	expression tag	UNP A0R2B1
A	-4	SER	-	expression tag	UNP A0R2B1
A	-3	HIS	-	expression tag	UNP A0R2B1
A	-2	MET	-	expression tag	UNP A0R2B1
A	-1	ALA	-	expression tag	UNP A0R2B1
A	0	SER	-	expression tag	UNP A0R2B1
A	1	VAL	-	expression tag	UNP A0R2B1
B	-22	MET	-	initiating methionine	UNP A0R2B1
B	-21	GLY	-	expression tag	UNP A0R2B1
B	-20	SER	-	expression tag	UNP A0R2B1
B	-19	SER	-	expression tag	UNP A0R2B1
B	-18	HIS	-	expression tag	UNP A0R2B1
B	-17	HIS	-	expression tag	UNP A0R2B1
B	-16	HIS	-	expression tag	UNP A0R2B1
B	-15	HIS	-	expression tag	UNP A0R2B1
B	-14	HIS	-	expression tag	UNP A0R2B1
B	-13	HIS	-	expression tag	UNP A0R2B1
B	-12	SER	-	expression tag	UNP A0R2B1
B	-11	SER	-	expression tag	UNP A0R2B1
B	-10	GLY	-	expression tag	UNP A0R2B1
B	-9	LEU	-	expression tag	UNP A0R2B1
B	-8	VAL	-	expression tag	UNP A0R2B1
B	-7	PRO	-	expression tag	UNP A0R2B1
B	-6	ARG	-	expression tag	UNP A0R2B1
B	-5	GLY	-	expression tag	UNP A0R2B1
B	-4	SER	-	expression tag	UNP A0R2B1
B	-3	HIS	-	expression tag	UNP A0R2B1
B	-2	MET	-	expression tag	UNP A0R2B1
B	-1	ALA	-	expression tag	UNP A0R2B1
B	0	SER	-	expression tag	UNP A0R2B1
B	1	VAL	-	expression tag	UNP A0R2B1
C	-22	MET	-	initiating methionine	UNP A0R2B1
C	-21	GLY	-	expression tag	UNP A0R2B1
C	-20	SER	-	expression tag	UNP A0R2B1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-19	SER	-	expression tag	UNP A0R2B1
C	-18	HIS	-	expression tag	UNP A0R2B1
C	-17	HIS	-	expression tag	UNP A0R2B1
C	-16	HIS	-	expression tag	UNP A0R2B1
C	-15	HIS	-	expression tag	UNP A0R2B1
C	-14	HIS	-	expression tag	UNP A0R2B1
C	-13	HIS	-	expression tag	UNP A0R2B1
C	-12	SER	-	expression tag	UNP A0R2B1
C	-11	SER	-	expression tag	UNP A0R2B1
C	-10	GLY	-	expression tag	UNP A0R2B1
C	-9	LEU	-	expression tag	UNP A0R2B1
C	-8	VAL	-	expression tag	UNP A0R2B1
C	-7	PRO	-	expression tag	UNP A0R2B1
C	-6	ARG	-	expression tag	UNP A0R2B1
C	-5	GLY	-	expression tag	UNP A0R2B1
C	-4	SER	-	expression tag	UNP A0R2B1
C	-3	HIS	-	expression tag	UNP A0R2B1
C	-2	MET	-	expression tag	UNP A0R2B1
C	-1	ALA	-	expression tag	UNP A0R2B1
C	0	SER	-	expression tag	UNP A0R2B1
C	1	VAL	-	expression tag	UNP A0R2B1
D	-22	MET	-	initiating methionine	UNP A0R2B1
D	-21	GLY	-	expression tag	UNP A0R2B1
D	-20	SER	-	expression tag	UNP A0R2B1
D	-19	SER	-	expression tag	UNP A0R2B1
D	-18	HIS	-	expression tag	UNP A0R2B1
D	-17	HIS	-	expression tag	UNP A0R2B1
D	-16	HIS	-	expression tag	UNP A0R2B1
D	-15	HIS	-	expression tag	UNP A0R2B1
D	-14	HIS	-	expression tag	UNP A0R2B1
D	-13	HIS	-	expression tag	UNP A0R2B1
D	-12	SER	-	expression tag	UNP A0R2B1
D	-11	SER	-	expression tag	UNP A0R2B1
D	-10	GLY	-	expression tag	UNP A0R2B1
D	-9	LEU	-	expression tag	UNP A0R2B1
D	-8	VAL	-	expression tag	UNP A0R2B1
D	-7	PRO	-	expression tag	UNP A0R2B1
D	-6	ARG	-	expression tag	UNP A0R2B1
D	-5	GLY	-	expression tag	UNP A0R2B1
D	-4	SER	-	expression tag	UNP A0R2B1
D	-3	HIS	-	expression tag	UNP A0R2B1
D	-2	MET	-	expression tag	UNP A0R2B1

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-1	ALA	-	expression tag	UNP A0R2B1
D	0	SER	-	expression tag	UNP A0R2B1
D	1	VAL	-	expression tag	UNP A0R2B1
E	-22	MET	-	initiating methionine	UNP A0R2B1
E	-21	GLY	-	expression tag	UNP A0R2B1
E	-20	SER	-	expression tag	UNP A0R2B1
E	-19	SER	-	expression tag	UNP A0R2B1
E	-18	HIS	-	expression tag	UNP A0R2B1
E	-17	HIS	-	expression tag	UNP A0R2B1
E	-16	HIS	-	expression tag	UNP A0R2B1
E	-15	HIS	-	expression tag	UNP A0R2B1
E	-14	HIS	-	expression tag	UNP A0R2B1
E	-13	HIS	-	expression tag	UNP A0R2B1
E	-12	SER	-	expression tag	UNP A0R2B1
E	-11	SER	-	expression tag	UNP A0R2B1
E	-10	GLY	-	expression tag	UNP A0R2B1
E	-9	LEU	-	expression tag	UNP A0R2B1
E	-8	VAL	-	expression tag	UNP A0R2B1
E	-7	PRO	-	expression tag	UNP A0R2B1
E	-6	ARG	-	expression tag	UNP A0R2B1
E	-5	GLY	-	expression tag	UNP A0R2B1
E	-4	SER	-	expression tag	UNP A0R2B1
E	-3	HIS	-	expression tag	UNP A0R2B1
E	-2	MET	-	expression tag	UNP A0R2B1
E	-1	ALA	-	expression tag	UNP A0R2B1
E	0	SER	-	expression tag	UNP A0R2B1
E	1	VAL	-	expression tag	UNP A0R2B1
F	-22	MET	-	initiating methionine	UNP A0R2B1
F	-21	GLY	-	expression tag	UNP A0R2B1
F	-20	SER	-	expression tag	UNP A0R2B1
F	-19	SER	-	expression tag	UNP A0R2B1
F	-18	HIS	-	expression tag	UNP A0R2B1
F	-17	HIS	-	expression tag	UNP A0R2B1
F	-16	HIS	-	expression tag	UNP A0R2B1
F	-15	HIS	-	expression tag	UNP A0R2B1
F	-14	HIS	-	expression tag	UNP A0R2B1
F	-13	HIS	-	expression tag	UNP A0R2B1
F	-12	SER	-	expression tag	UNP A0R2B1
F	-11	SER	-	expression tag	UNP A0R2B1
F	-10	GLY	-	expression tag	UNP A0R2B1
F	-9	LEU	-	expression tag	UNP A0R2B1
F	-8	VAL	-	expression tag	UNP A0R2B1

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-7	PRO	-	expression tag	UNP A0R2B1
F	-6	ARG	-	expression tag	UNP A0R2B1
F	-5	GLY	-	expression tag	UNP A0R2B1
F	-4	SER	-	expression tag	UNP A0R2B1
F	-3	HIS	-	expression tag	UNP A0R2B1
F	-2	MET	-	expression tag	UNP A0R2B1
F	-1	ALA	-	expression tag	UNP A0R2B1
F	0	SER	-	expression tag	UNP A0R2B1
F	1	VAL	-	expression tag	UNP A0R2B1
N	-22	MET	-	initiating methionine	UNP A0R2B1
N	-21	GLY	-	expression tag	UNP A0R2B1
N	-20	SER	-	expression tag	UNP A0R2B1
N	-19	SER	-	expression tag	UNP A0R2B1
N	-18	HIS	-	expression tag	UNP A0R2B1
N	-17	HIS	-	expression tag	UNP A0R2B1
N	-16	HIS	-	expression tag	UNP A0R2B1
N	-15	HIS	-	expression tag	UNP A0R2B1
N	-14	HIS	-	expression tag	UNP A0R2B1
N	-13	HIS	-	expression tag	UNP A0R2B1
N	-12	SER	-	expression tag	UNP A0R2B1
N	-11	SER	-	expression tag	UNP A0R2B1
N	-10	GLY	-	expression tag	UNP A0R2B1
N	-9	LEU	-	expression tag	UNP A0R2B1
N	-8	VAL	-	expression tag	UNP A0R2B1
N	-7	PRO	-	expression tag	UNP A0R2B1
N	-6	ARG	-	expression tag	UNP A0R2B1
N	-5	GLY	-	expression tag	UNP A0R2B1
N	-4	SER	-	expression tag	UNP A0R2B1
N	-3	HIS	-	expression tag	UNP A0R2B1
N	-2	MET	-	expression tag	UNP A0R2B1
N	-1	ALA	-	expression tag	UNP A0R2B1
N	0	SER	-	expression tag	UNP A0R2B1
N	1	VAL	-	expression tag	UNP A0R2B1
O	-22	MET	-	initiating methionine	UNP A0R2B1
O	-21	GLY	-	expression tag	UNP A0R2B1
O	-20	SER	-	expression tag	UNP A0R2B1
O	-19	SER	-	expression tag	UNP A0R2B1
O	-18	HIS	-	expression tag	UNP A0R2B1
O	-17	HIS	-	expression tag	UNP A0R2B1
O	-16	HIS	-	expression tag	UNP A0R2B1
O	-15	HIS	-	expression tag	UNP A0R2B1
O	-14	HIS	-	expression tag	UNP A0R2B1

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Chain	Residue	Modelled	Actual	Comment	Reference
O	-13	HIS	-	expression tag	UNP A0R2B1
O	-12	SER	-	expression tag	UNP A0R2B1
O	-11	SER	-	expression tag	UNP A0R2B1
O	-10	GLY	-	expression tag	UNP A0R2B1
O	-9	LEU	-	expression tag	UNP A0R2B1
O	-8	VAL	-	expression tag	UNP A0R2B1
O	-7	PRO	-	expression tag	UNP A0R2B1
O	-6	ARG	-	expression tag	UNP A0R2B1
O	-5	GLY	-	expression tag	UNP A0R2B1
O	-4	SER	-	expression tag	UNP A0R2B1
O	-3	HIS	-	expression tag	UNP A0R2B1
O	-2	MET	-	expression tag	UNP A0R2B1
O	-1	ALA	-	expression tag	UNP A0R2B1
O	0	SER	-	expression tag	UNP A0R2B1
O	1	VAL	-	expression tag	UNP A0R2B1
P	-22	MET	-	initiating methionine	UNP A0R2B1
P	-21	GLY	-	expression tag	UNP A0R2B1
P	-20	SER	-	expression tag	UNP A0R2B1
P	-19	SER	-	expression tag	UNP A0R2B1
P	-18	HIS	-	expression tag	UNP A0R2B1
P	-17	HIS	-	expression tag	UNP A0R2B1
P	-16	HIS	-	expression tag	UNP A0R2B1
P	-15	HIS	-	expression tag	UNP A0R2B1
P	-14	HIS	-	expression tag	UNP A0R2B1
P	-13	HIS	-	expression tag	UNP A0R2B1
P	-12	SER	-	expression tag	UNP A0R2B1
P	-11	SER	-	expression tag	UNP A0R2B1
P	-10	GLY	-	expression tag	UNP A0R2B1
P	-9	LEU	-	expression tag	UNP A0R2B1
P	-8	VAL	-	expression tag	UNP A0R2B1
P	-7	PRO	-	expression tag	UNP A0R2B1
P	-6	ARG	-	expression tag	UNP A0R2B1
P	-5	GLY	-	expression tag	UNP A0R2B1
P	-4	SER	-	expression tag	UNP A0R2B1
P	-3	HIS	-	expression tag	UNP A0R2B1
P	-2	MET	-	expression tag	UNP A0R2B1
P	-1	ALA	-	expression tag	UNP A0R2B1
P	0	SER	-	expression tag	UNP A0R2B1
P	1	VAL	-	expression tag	UNP A0R2B1
Q	-22	MET	-	initiating methionine	UNP A0R2B1
Q	-21	GLY	-	expression tag	UNP A0R2B1
Q	-20	SER	-	expression tag	UNP A0R2B1

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	-19	SER	-	expression tag	UNP A0R2B1
Q	-18	HIS	-	expression tag	UNP A0R2B1
Q	-17	HIS	-	expression tag	UNP A0R2B1
Q	-16	HIS	-	expression tag	UNP A0R2B1
Q	-15	HIS	-	expression tag	UNP A0R2B1
Q	-14	HIS	-	expression tag	UNP A0R2B1
Q	-13	HIS	-	expression tag	UNP A0R2B1
Q	-12	SER	-	expression tag	UNP A0R2B1
Q	-11	SER	-	expression tag	UNP A0R2B1
Q	-10	GLY	-	expression tag	UNP A0R2B1
Q	-9	LEU	-	expression tag	UNP A0R2B1
Q	-8	VAL	-	expression tag	UNP A0R2B1
Q	-7	PRO	-	expression tag	UNP A0R2B1
Q	-6	ARG	-	expression tag	UNP A0R2B1
Q	-5	GLY	-	expression tag	UNP A0R2B1
Q	-4	SER	-	expression tag	UNP A0R2B1
Q	-3	HIS	-	expression tag	UNP A0R2B1
Q	-2	MET	-	expression tag	UNP A0R2B1
Q	-1	ALA	-	expression tag	UNP A0R2B1
Q	0	SER	-	expression tag	UNP A0R2B1
Q	1	VAL	-	expression tag	UNP A0R2B1

- Molecule 2 is a protein called Glycogen accumulation regulator GarA.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	G	98	Total	C	N	O	0	0	0
			744	464	135	145			
2	H	96	Total	C	N	O	0	0	0
			710	438	131	141			
2	I	97	Total	C	N	O	0	0	0
			740	462	134	144			
2	J	97	Total	C	N	O	0	0	0
			740	462	134	144			
2	K	97	Total	C	N	O	0	0	0
			740	462	134	144			
2	L	97	Total	C	N	O	0	0	0
			740	462	134	144			

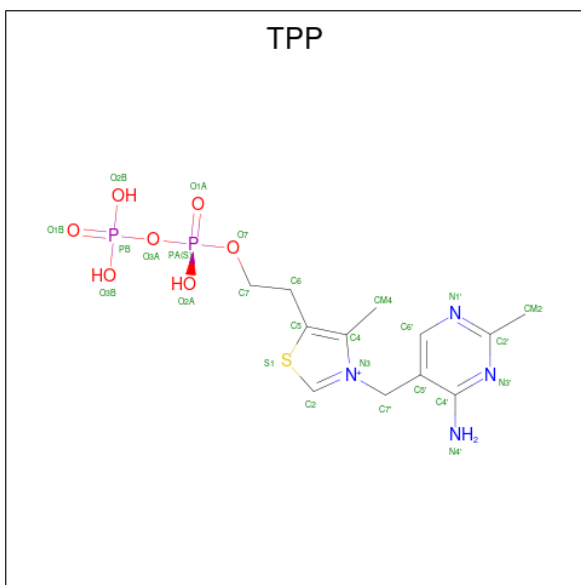
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Mg 1	0	0
3	B	1	Total 1	Mg 1	0	0
3	C	1	Total 1	Mg 1	0	0
3	D	1	Total 1	Mg 1	0	0
3	E	1	Total 1	Mg 1	0	0
3	F	1	Total 1	Mg 1	0	0

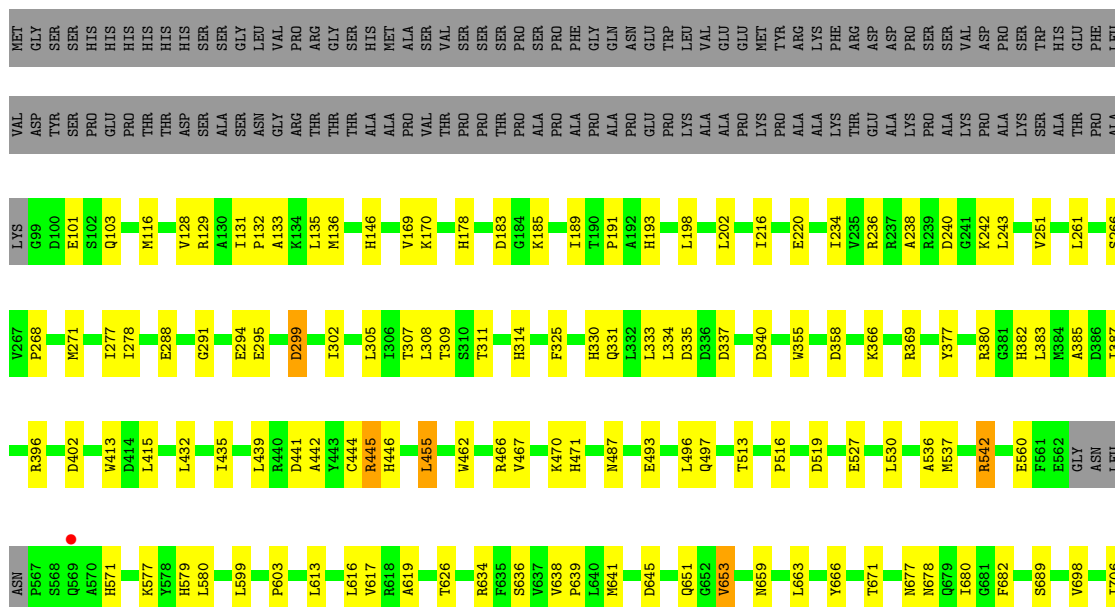
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

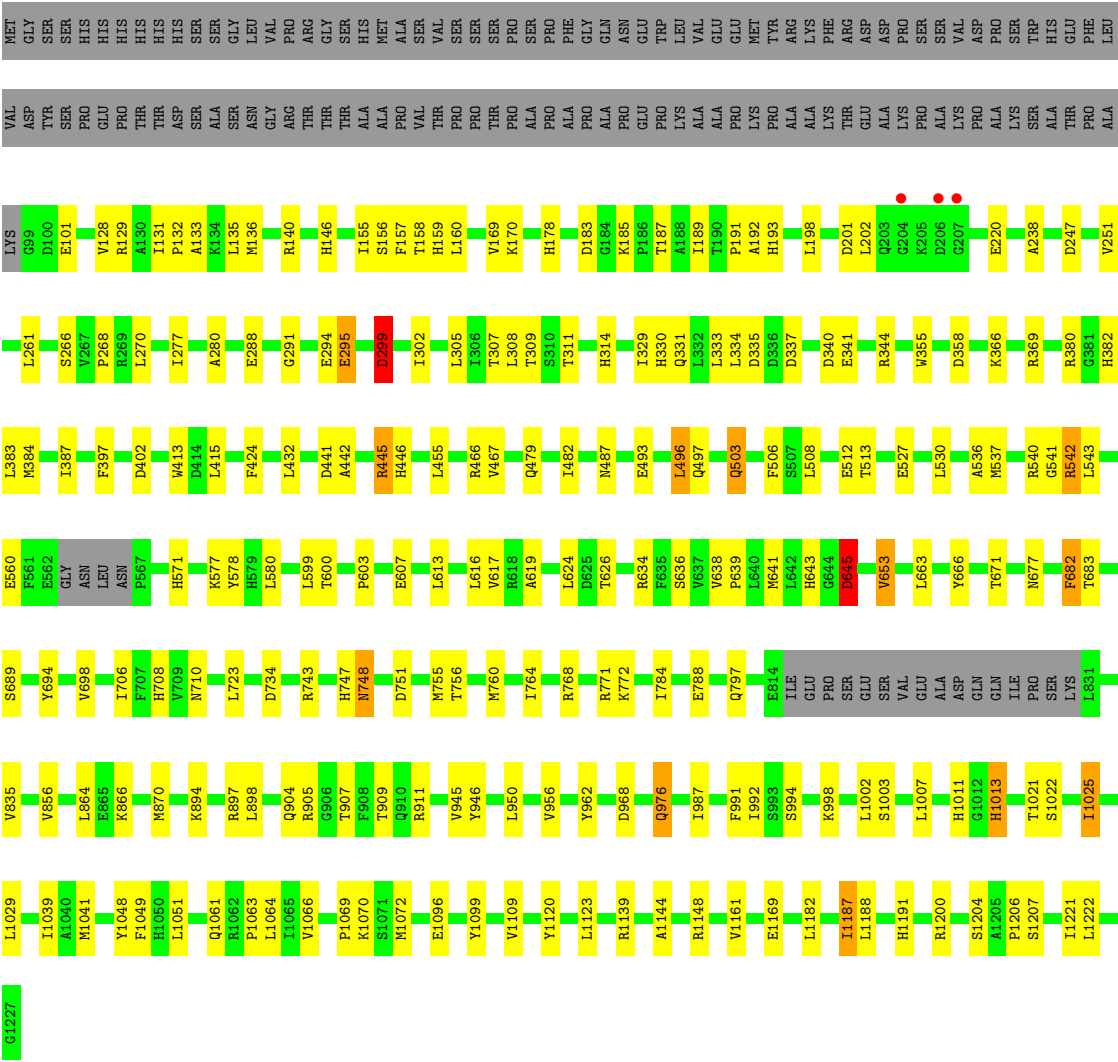
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total 2	Ca 2	0	0
4	B	2	Total 2	Ca 2	0	0
4	C	1	Total 1	Ca 1	0	0
4	D	1	Total 1	Ca 1	0	0
4	E	1	Total 1	Ca 1	0	0
4	F	1	Total 1	Ca 1	0	0

- Molecule 5 is THIAMINE DIPHOSPHATE (CCD ID: TPP) (formula: C₁₂H₁₉N₄O₇P₂S) (labeled as "Ligand of Interest" by depositor).

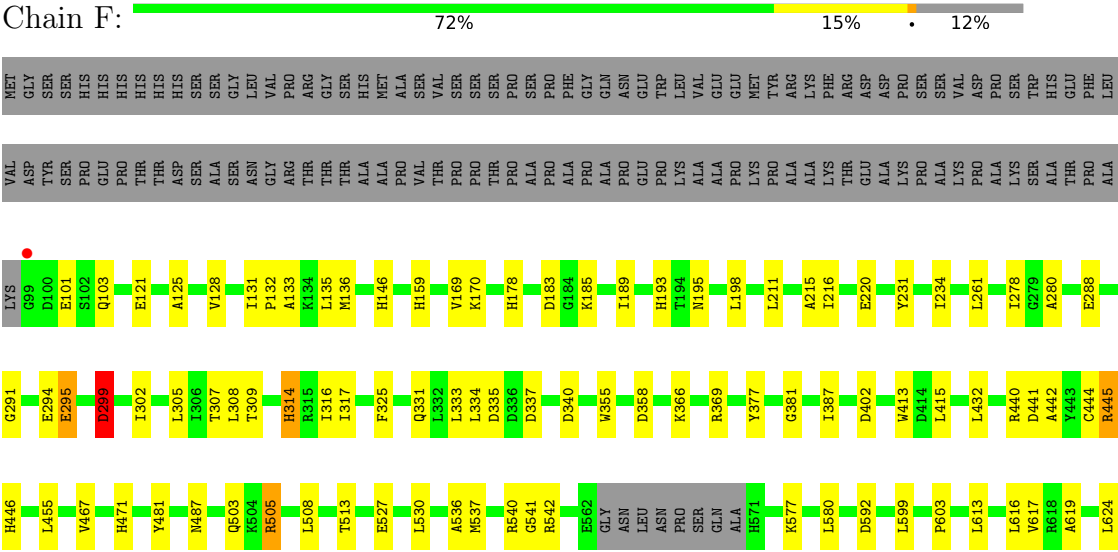


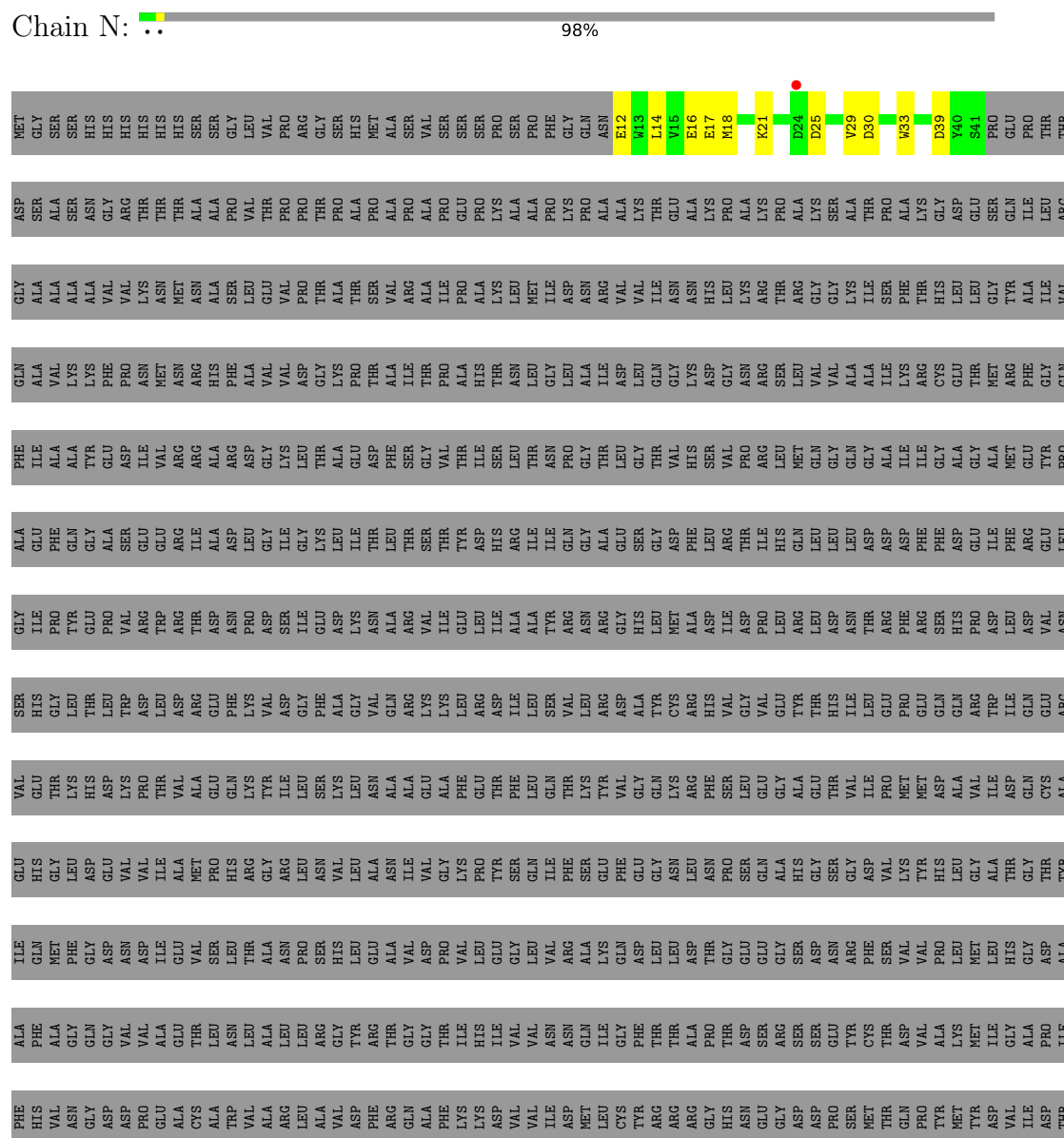
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total 26	C 12	N 4	O 7	P 2	S 1	0	0
5	B	1	Total 26	C 12	N 4	O 7	P 2	S 1	0	0
5	C	1	Total 26	C 12	N 4	O 7	P 2	S 1	0	0
5	D	1	Total 26	C 12	N 4	O 7	P 2	S 1	0	0
5	E	1	Total 26	C 12	N 4	O 7	P 2	S 1	0	0
5	F	1	Total 26	C 12	N 4	O 7	P 2	S 1	0	0





• Molecule 1: Multifunctional 2-oxoglutarate metabolism enzyme





[illegible]

- Molecule 1: Multifunctional 2-oxoglutarate metabolism enzyme

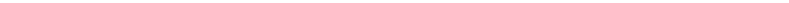
Chain 0:

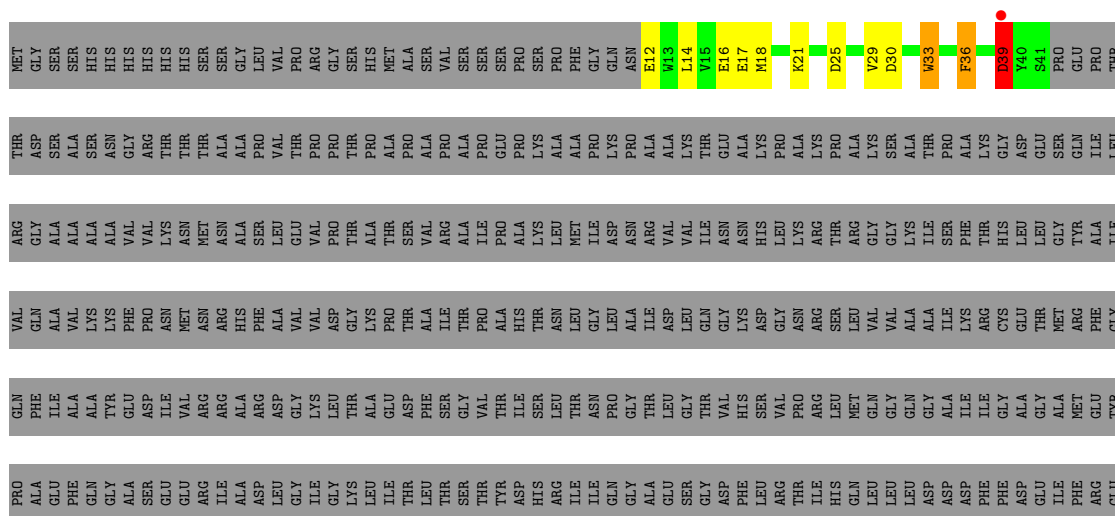
98%

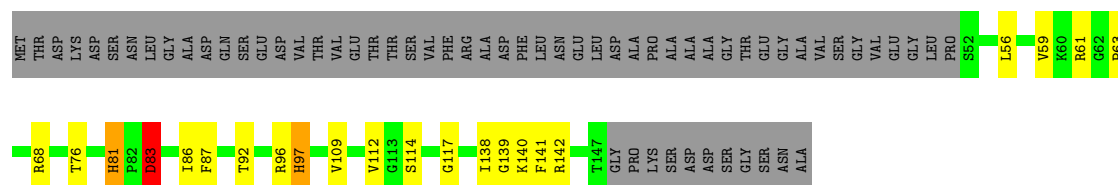
[illegible]

[illegible]

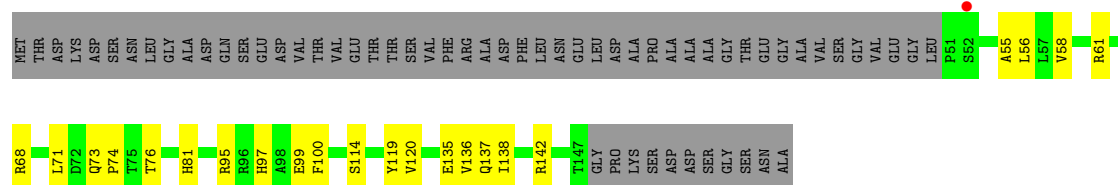
- Molecule 1: Multifunctional 2-oxoglutarate metabolism enzyme

Chain Q:  98%

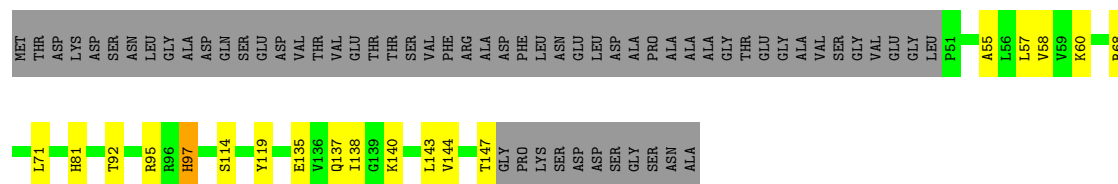




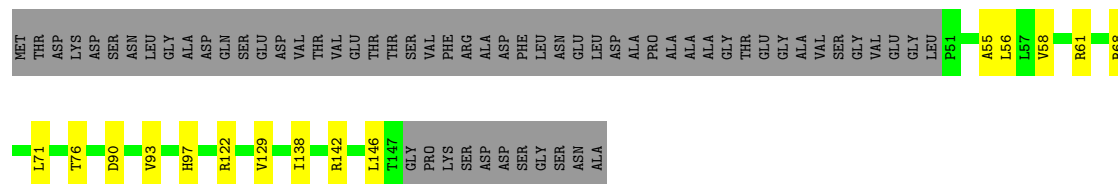
• Molecule 2: Glycogen accumulation regulator GarA



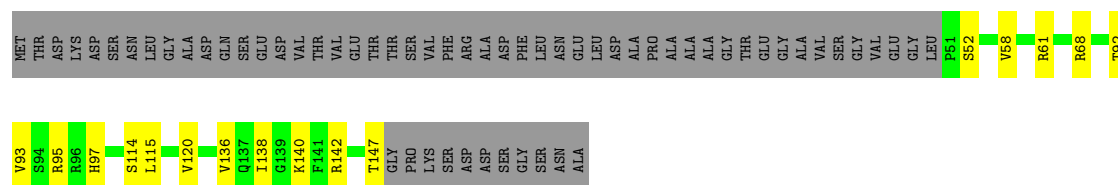
• Molecule 2: Glycogen accumulation regulator GarA



• Molecule 2: Glycogen accumulation regulator GarA



• Molecule 2: Glycogen accumulation regulator GarA



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	325.75Å 325.75Å 396.94Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.99 – 4.56 45.99 – 4.56	Depositor EDS
% Data completeness (in resolution range)	89.6 (45.99-4.56) 89.6 (45.99-4.56)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.92 (at 4.64Å)	Xtriage
Refinement program	BUSTER 2.10.4 (8-JUN-2022)	Depositor
R, R_{free}	0.198 , 0.229 0.190 , 0.217	Depositor DCC
R_{free} test set	6055 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	197.4	Xtriage
Anisotropy	0.084	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 791.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.390 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	57005	wwPDB-VP
Average B, all atoms (Å ²)	236.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.83% 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: MG, CA, TPP

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	0.59	0/8751	0.97	3/11855 (0.0%)
1	B	0.60	0/8764	0.97	6/11874 (0.1%)
1	C	0.59	0/8767	0.96	1/11877 (0.0%)
1	D	0.59	0/8717	0.96	1/11816 (0.0%)
1	E	0.60	0/8710	0.97	6/11812 (0.1%)
1	F	0.59	0/8685	0.97	1/11776 (0.0%)
1	N	0.72	0/276	0.92	0/375
1	O	0.72	0/276	0.92	0/375
1	P	0.72	0/276	0.91	0/375
1	Q	0.75	0/276	0.96	1/375 (0.3%)
2	G	0.57	0/757	0.87	0/1025
2	H	0.65	0/722	1.03	2/980 (0.2%)
2	I	0.53	0/753	0.82	0/1020
2	J	0.53	0/753	0.85	0/1020
2	K	0.60	0/753	0.87	0/1020
2	L	0.58	0/753	0.89	0/1020
All	All	0.60	0/57989	0.96	21/78595 (0.0%)

There are no bond length outliers.

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q	39	ASP	CA-CB-CG	7.43	120.03	112.60
1	E	645	ASP	CA-CB-CG	7.29	119.89	112.60
2	H	87	PHE	CA-CB-CG	6.86	120.66	113.80
1	B	645	ASP	CA-CB-CG	6.63	119.23	112.60
1	B	653	VAL	CA-C-N	5.68	128.54	120.53

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	8579	0	8402	144	0
1	B	8591	0	8414	143	0
1	C	8593	0	8408	141	0
1	D	8544	0	8341	137	0
1	E	8537	0	8299	140	0
1	F	8513	0	8287	136	0
1	N	266	0	233	15	0
1	O	266	0	233	17	0
1	P	266	0	233	13	0
1	Q	266	0	233	17	0
2	G	744	0	730	13	0
2	H	710	0	656	12	0
2	I	740	0	727	14	0
2	J	740	0	727	18	0
2	K	740	0	727	9	0
2	L	740	0	727	13	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
5	A	26	0	16	2	0
5	B	26	0	16	1	0
5	C	26	0	16	1	0
5	D	26	0	16	1	0
5	E	26	0	16	0	0
5	F	26	0	16	2	0
All	All	57005	0	55473	921	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 8.

The worst 5 of 921 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:634:ARG:HE	1:B:636:SER:HB3	1.05	1.08
1:E:542:ARG:HE	1:E:599:LEU:HD21	1.15	1.05
1:E:634:ARG:HE	1:E:636:SER:HB3	1.16	1.05
1:F:645:ASP:HB3	1:F:677:ASN:HA	1.41	1.01
1:F:634:ARG:HE	1:F:636:SER:HB3	1.26	1.01

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	1100/1250 (88%)	1029 (94%)	68 (6%)	3 (0%)	36	71
1	B	1102/1250 (88%)	1022 (93%)	76 (7%)	4 (0%)	30	67
1	C	1103/1250 (88%)	1028 (93%)	72 (6%)	3 (0%)	36	71
1	D	1101/1250 (88%)	1026 (93%)	71 (6%)	4 (0%)	30	67
1	E	1103/1250 (88%)	1022 (93%)	77 (7%)	4 (0%)	30	67
1	F	1099/1250 (88%)	1018 (93%)	77 (7%)	4 (0%)	30	67
1	N	28/1250 (2%)	24 (86%)	4 (14%)	0	100	100
1	O	28/1250 (2%)	24 (86%)	4 (14%)	0	100	100
1	P	28/1250 (2%)	24 (86%)	4 (14%)	0	100	100
1	Q	28/1250 (2%)	25 (89%)	2 (7%)	1 (4%)	2	20
2	G	96/158 (61%)	87 (91%)	8 (8%)	1 (1%)	12	47
2	H	94/158 (60%)	79 (84%)	14 (15%)	1 (1%)	11	45
2	I	95/158 (60%)	87 (92%)	8 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	J	95/158 (60%)	87 (92%)	8 (8%)	0	100	100
2	K	95/158 (60%)	87 (92%)	8 (8%)	0	100	100
2	L	95/158 (60%)	90 (95%)	5 (5%)	0	100	100
All	All	7290/13448 (54%)	6759 (93%)	506 (7%)	25 (0%)	36	71

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	358	ASP
1	B	358	ASP
1	C	358	ASP
1	C	445	ARG
1	D	358	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	892/1037 (86%)	850 (95%)	42 (5%)	23	45
1	B	894/1037 (86%)	853 (95%)	41 (5%)	24	46
1	C	893/1037 (86%)	855 (96%)	38 (4%)	26	48
1	D	885/1037 (85%)	846 (96%)	39 (4%)	25	47
1	E	880/1037 (85%)	840 (96%)	40 (4%)	24	46
1	F	878/1037 (85%)	845 (96%)	33 (4%)	29	51
1	N	30/1037 (3%)	26 (87%)	4 (13%)	4	16
1	O	30/1037 (3%)	25 (83%)	5 (17%)	2	11
1	P	30/1037 (3%)	26 (87%)	4 (13%)	4	16
1	Q	30/1037 (3%)	25 (83%)	5 (17%)	2	11
2	G	81/127 (64%)	79 (98%)	2 (2%)	42	62
2	H	72/127 (57%)	64 (89%)	8 (11%)	6	20
2	I	81/127 (64%)	79 (98%)	2 (2%)	42	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	J	81/127 (64%)	79 (98%)	2 (2%)	42	62
2	K	81/127 (64%)	78 (96%)	3 (4%)	30	51
2	L	81/127 (64%)	79 (98%)	2 (2%)	42	62
All	All	5919/11132 (53%)	5649 (95%)	270 (5%)	24	46

5 of 270 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	1204	SER
2	H	83	ASP
1	O	39	ASP
1	C	496	LEU
1	C	455	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	976	GLN
2	G	81	HIS
2	L	132	ASN
1	C	459	GLN
1	C	318	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 20 ligands modelled in this entry, 14 are monoatomic - leaving 6 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
5	TPP	A	1303	3	26,27,27	0.46	0	38,40,40	0.48	0
5	TPP	E	1303	3	26,27,27	0.49	0	38,40,40	0.41	0
5	TPP	C	1303	3	26,27,27	0.57	0	38,40,40	0.58	1 (2%)
5	TPP	F	1303	3	26,27,27	0.56	0	38,40,40	0.50	0
5	TPP	B	1303	3	26,27,27	0.52	0	38,40,40	0.54	0
5	TPP	D	1303	3	26,27,27	0.51	0	38,40,40	0.50	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	TPP	A	1303	3	-	7/17/17/17	0/2/2/2
5	TPP	E	1303	3	-	7/17/17/17	0/2/2/2
5	TPP	C	1303	3	-	3/17/17/17	0/2/2/2
5	TPP	F	1303	3	-	10/17/17/17	0/2/2/2
5	TPP	B	1303	3	-	7/17/17/17	0/2/2/2
5	TPP	D	1303	3	-	7/17/17/17	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	1303	TPP	O3B-PB-O3A	2.02	111.42	104.64

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

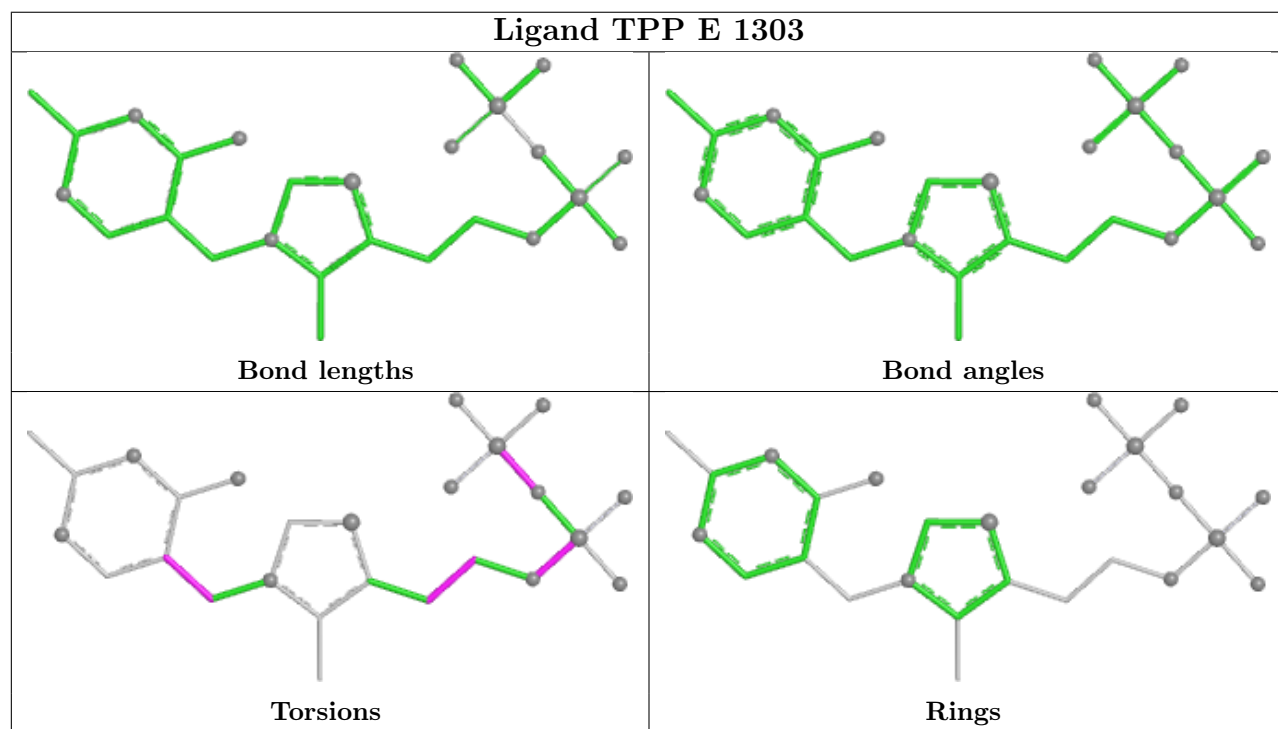
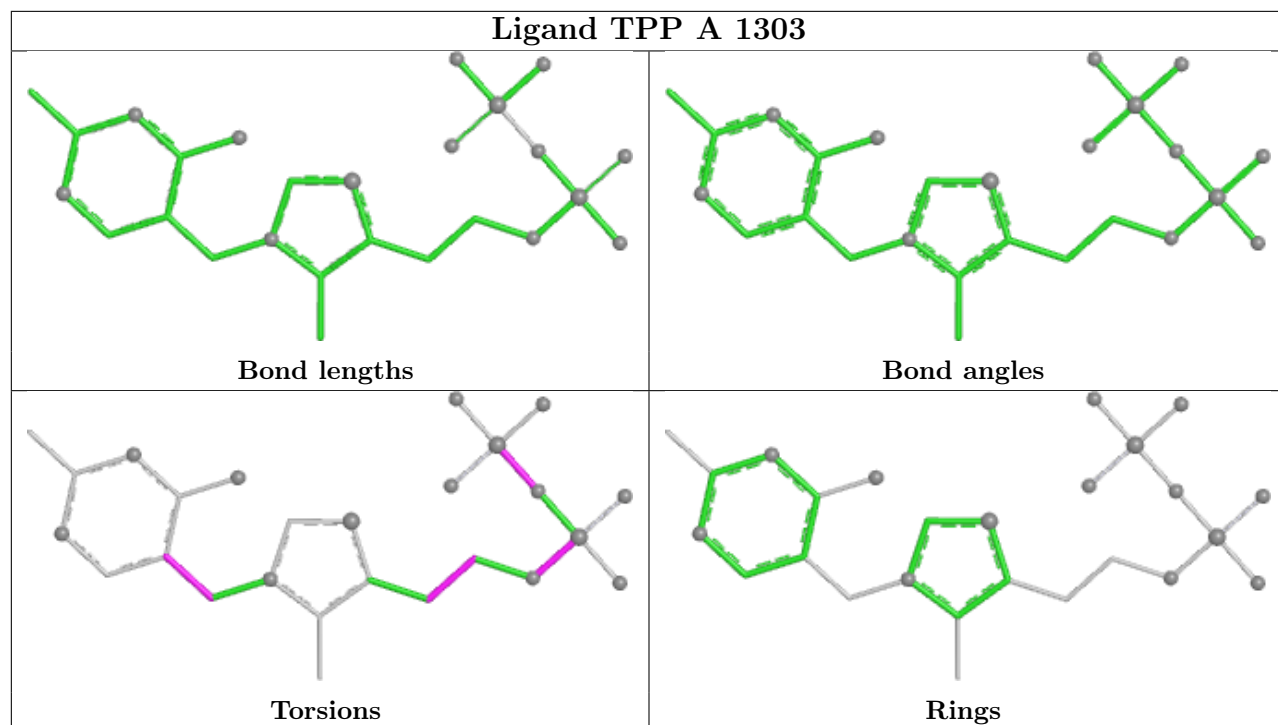
Mol	Chain	Res	Type	Atoms
5	A	1303	TPP	C5-C6-C7-O7
5	A	1303	TPP	C7-O7-PA-O1A
5	A	1303	TPP	C7-O7-PA-O2A
5	A	1303	TPP	PA-O3A-PB-O3B
5	B	1303	TPP	C5-C6-C7-O7

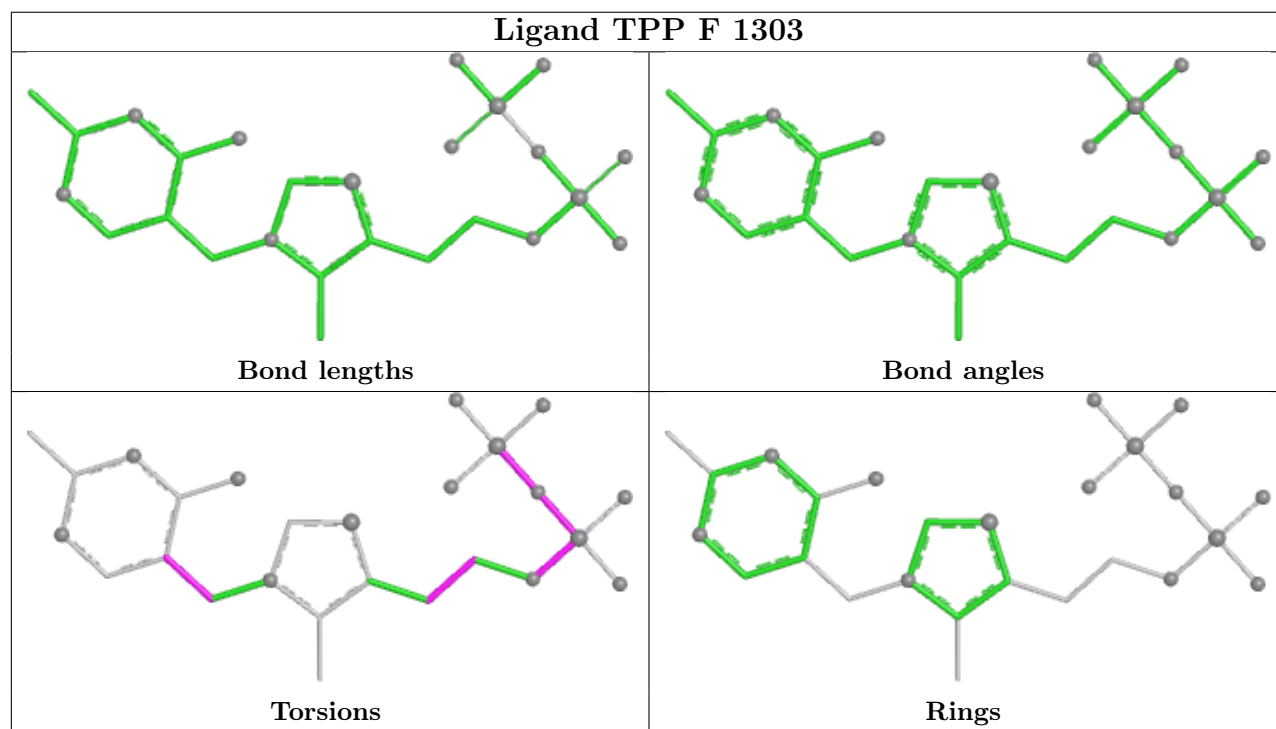
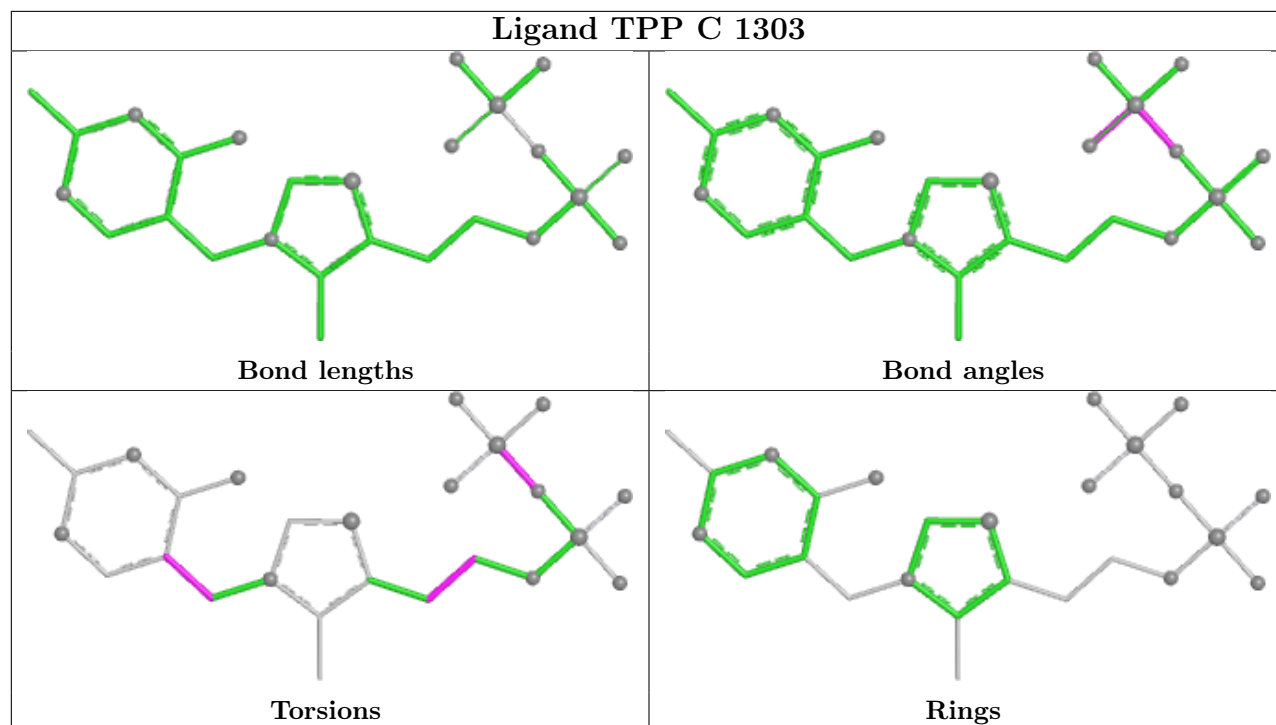
There are no ring outliers.

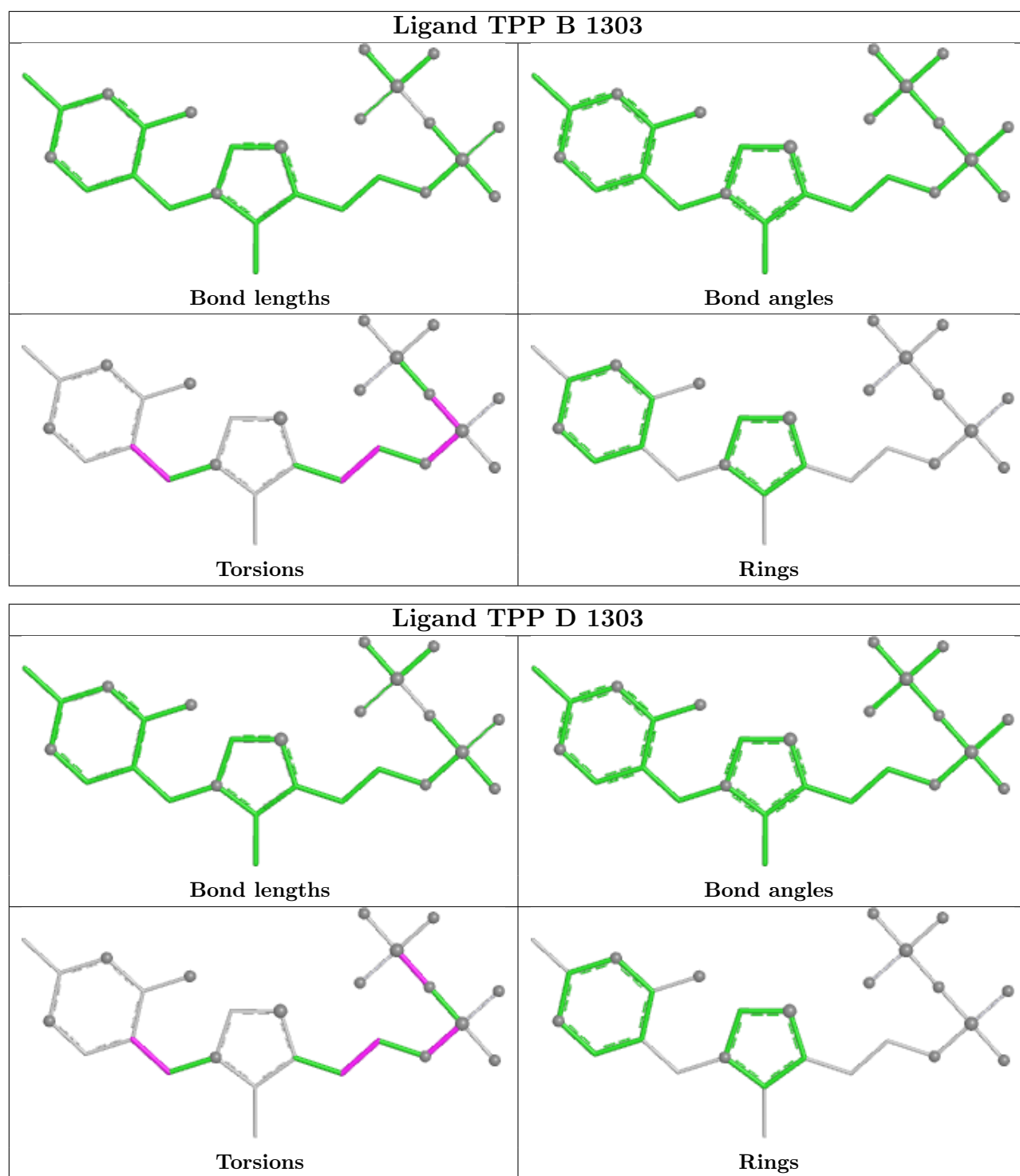
5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1303	TPP	2	0
5	C	1303	TPP	1	0
5	F	1303	TPP	2	0
5	B	1303	TPP	1	0
5	D	1303	TPP	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 ⓘ

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 ⓘ

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	1106/1250 (88%)	-0.69	0 100 100	155, 233, 300, 300	0
1	B	1108/1250 (88%)	-0.77	0 100 100	138, 225, 289, 300	0
1	C	1109/1250 (88%)	-0.64	1 (0%) 92 87	148, 231, 298, 300	0
1	D	1107/1250 (88%)	-0.64	7 (0%) 85 73	150, 232, 296, 300	0
1	E	1109/1250 (88%)	-0.78	3 (0%) 90 80	145, 225, 290, 300	0
1	F	1105/1250 (88%)	-0.67	2 (0%) 91 83	162, 233, 299, 300	0
1	N	30/1250 (2%)	0.18	1 (3%) 49 40	268, 300, 300, 300	0
1	O	30/1250 (2%)	0.05	0 100 100	280, 300, 300, 300	0
1	P	30/1250 (2%)	0.02	0 100 100	274, 300, 300, 300	0
1	Q	30/1250 (2%)	0.25	1 (3%) 49 40	259, 300, 300, 300	0
2	G	98/158 (62%)	-0.21	0 100 100	211, 283, 300, 300	0
2	H	96/158 (60%)	-0.61	0 100 100	179, 238, 300, 300	0
2	I	97/158 (61%)	-0.38	1 (1%) 79 64	207, 279, 300, 300	0
2	J	97/158 (61%)	-0.38	0 100 100	218, 281, 300, 300	0
2	K	97/158 (61%)	-0.63	0 100 100	183, 236, 295, 300	0
2	L	97/158 (61%)	-0.18	0 100 100	230, 284, 300, 300	0
All	All	7346/13448 (54%)	-0.66	16 (0%) 91 83	138, 233, 300, 300	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	746	GLY	3.5
1	Q	39	ASP	3.3
1	D	629	GLU	2.9
1	D	628	GLU	2.7
1	D	207	GLY	2.7

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](#)

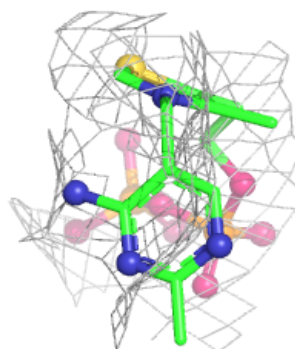
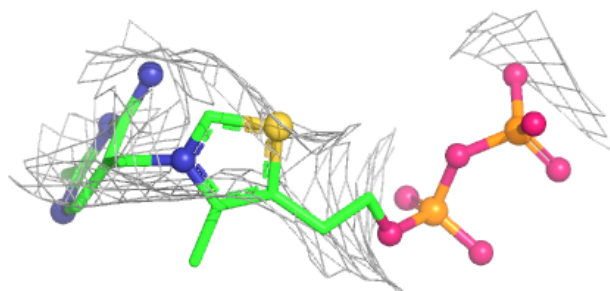
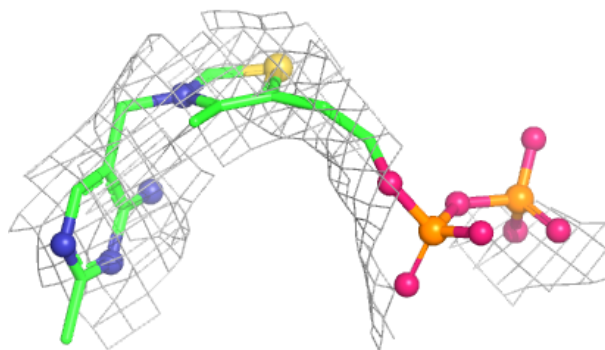
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
4	CA	A	1302	1/1	0.97	0.06	300,300,300,300	0
4	CA	B	1302	1/1	0.98	0.07	220,220,220,220	0
4	CA	C	1302	1/1	0.98	0.11	289,289,289,289	0
4	CA	D	1302	1/1	0.98	0.12	298,298,298,298	0
3	MG	D	1301	1/1	0.99	0.06	149,149,149,149	0
4	CA	B	1304	1/1	0.99	0.07	170,170,170,170	0
3	MG	C	1301	1/1	0.99	0.06	160,160,160,160	0
4	CA	A	1304	1/1	0.99	0.08	176,176,176,176	0
4	CA	F	1302	1/1	0.99	0.07	300,300,300,300	0
5	TPP	A	1303	26/26	0.99	0.06	226,226,226,226	0
5	TPP	C	1303	26/26	0.99	0.06	225,225,225,225	0
5	TPP	F	1303	26/26	0.99	0.07	230,230,230,230	0
4	CA	E	1302	1/1	1.00	0.04	239,239,239,239	0
3	MG	E	1301	1/1	1.00	0.03	190,190,190,190	0
3	MG	F	1301	1/1	1.00	0.05	119,119,119,119	0
5	TPP	B	1303	26/26	1.00	0.04	216,216,216,216	0
3	MG	A	1301	1/1	1.00	0.01	106,106,106,106	0
5	TPP	D	1303	26/26	1.00	0.04	223,223,223,223	0
5	TPP	E	1303	26/26	1.00	0.05	223,223,223,223	0
3	MG	B	1301	1/1	1.00	0.03	216,216,216,216	0

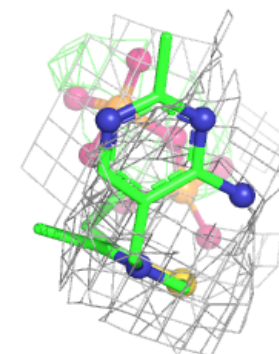
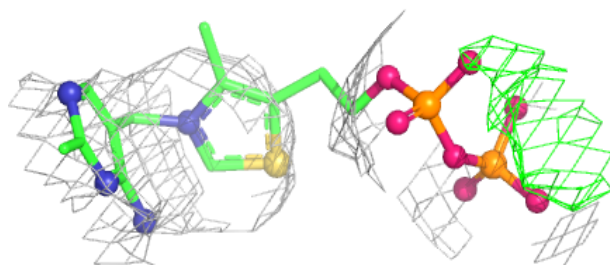
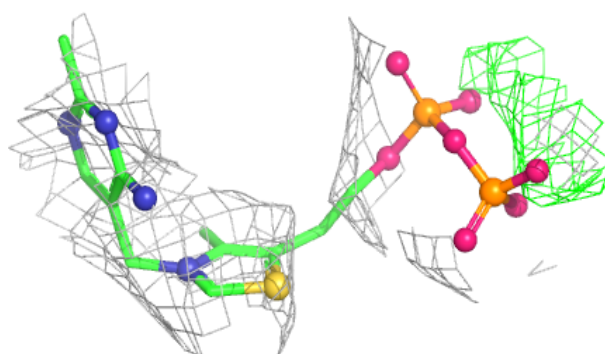
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around TPP A 1303:

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

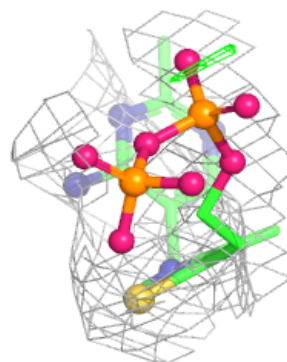
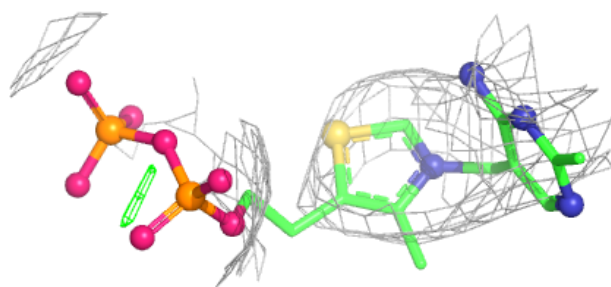
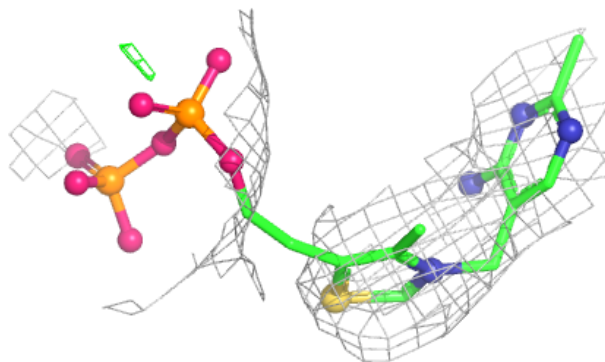
**Electron density around TPP C 1303:**

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

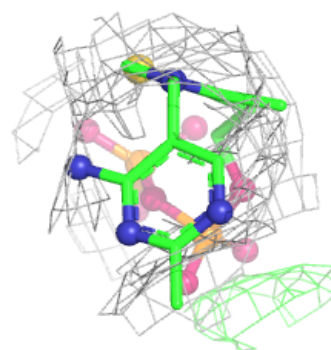
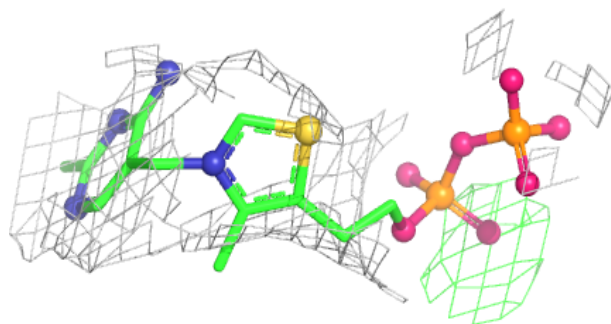
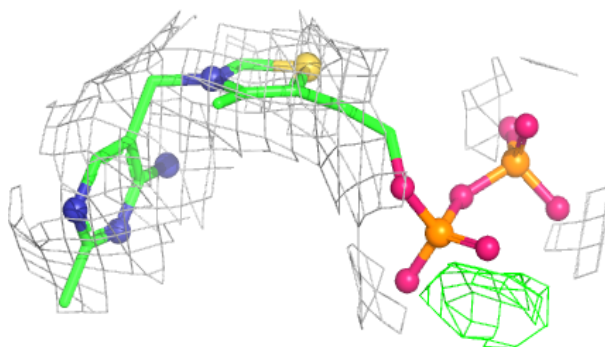


Electron density around TPP F 1303:

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

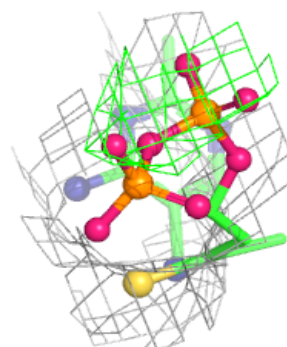
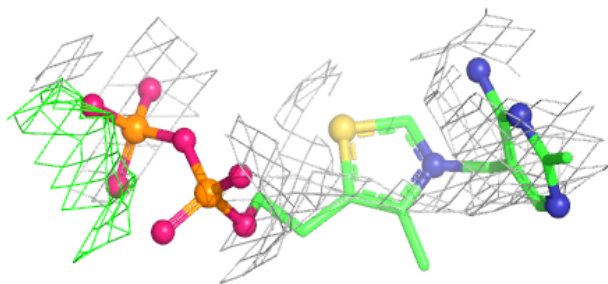
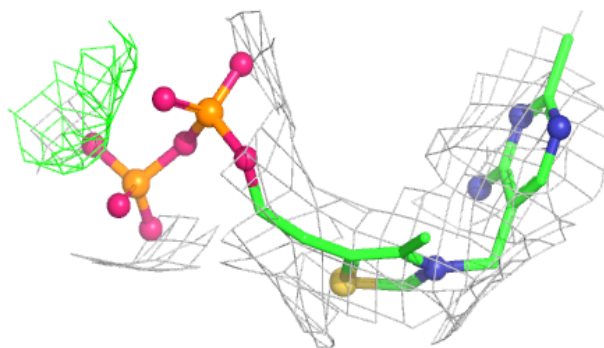
**Electron density around TPP B 1303:**

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

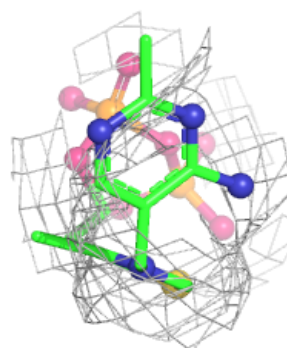
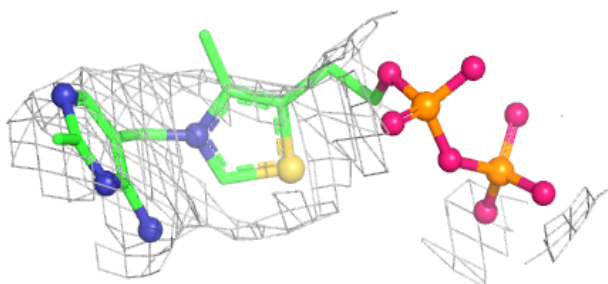
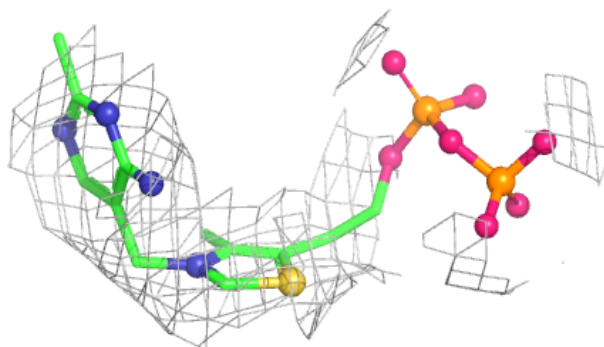


Electron density around TPP D 1303:

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

**Electron density around TPP E 1303:**

$2mF_o-DF_c$ (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.