



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 18, 2026 – 03:40 AM UTC

PDB ID : 5Z2P / pdb_00005z2p
Title : ThDP-Mn²⁺ complex of R413K variant of EcMenD soaked with 2-ketoglutarate for 5 min
Authors : Qin, M.M.; Guo, Z.H.
Deposited on : 2018-01-03
Resolution : 2.30 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

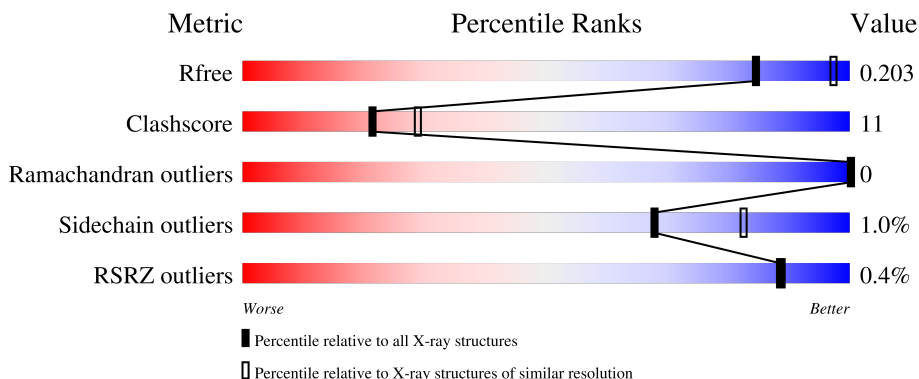
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	556	 87% 11% .
1	B	556	 83% 16% .
1	C	556	 81% 18% .
1	D	556	 83% 17% .
1	E	556	 81% 18% .

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Mol	Chain	Length	Quality of chain
1	F	556	 81% 18% .
1	G	556	 82% 17% .
1	H	556	 % 81% 19%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	TD6	A	601	-	-	X	-
4	FMT	A	604	-	-	X	-
4	FMT	A	605	-	-	X	-
4	FMT	A	607	-	-	X	-
4	FMT	A	608	-	-	X	-
4	FMT	B	605	-	-	X	-
4	FMT	C	603	-	-	X	-
4	FMT	D	603	-	-	X	-
4	FMT	F	604	-	-	X	-
4	FMT	F	606	-	-	X	-
4	FMT	F	608	-	-	X	-
5	GOL	D	604	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 36992 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.

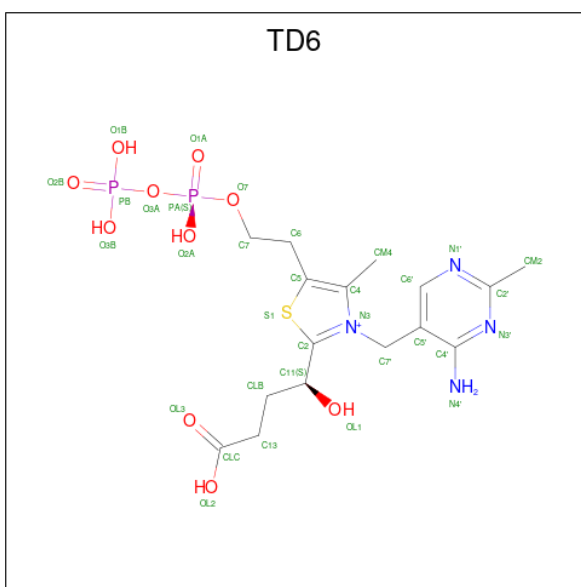
- Molecule 1 is a protein called 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	556	Total	C	N	O	S	0	0	0
			4266	2716	766	770	14			
1	B	556	Total	C	N	O	S	0	0	0
			4276	2717	767	777	15			
1	C	556	Total	C	N	O	S	0	0	0
			4271	2715	767	775	14			
1	D	556	Total	C	N	O	S	0	0	0
			4273	2717	765	777	14			
1	E	556	Total	C	N	O	S	0	0	0
			4267	2715	765	773	14			
1	F	556	Total	C	N	O	S	0	0	0
			4284	2724	768	778	14			
1	G	556	Total	C	N	O	S	0	0	0
			4240	2700	761	765	14			
1	H	556	Total	C	N	O	S	0	0	0
			4246	2701	764	767	14			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	413	LYS	ARG	engineered mutation	UNP P17109
B	413	LYS	ARG	engineered mutation	UNP P17109
C	413	LYS	ARG	engineered mutation	UNP P17109
D	413	LYS	ARG	engineered mutation	UNP P17109
E	413	LYS	ARG	engineered mutation	UNP P17109
F	413	LYS	ARG	engineered mutation	UNP P17109
G	413	LYS	ARG	engineered mutation	UNP P17109
H	413	LYS	ARG	engineered mutation	UNP P17109

- Molecule 2 is (4S)-4-{3-[(4-amino-2-methylpyrimidin-5-yl)methyl]-5-(2-{[(S)-hydroxy(phosphonooxy)phosphoryl]oxy}ethyl)-4-methyl-1,3lambda 5 -thiazol-2-yl}-4-hydroxybutanoic acid (CCD ID: TD6) (formula: C₁₆H₂₅N₄O₁₀P₂S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 33	C 16	N 4	O 10	P 2	S 1	0	0
2	B	1	Total 33	C 16	N 4	O 10	P 2	S 1	0	0
2	C	1	Total 33	C 16	N 4	O 10	P 2	S 1	0	0
2	D	1	Total 33	C 16	N 4	O 10	P 2	S 1	1	0
2	E	1	Total 33	C 16	N 4	O 10	P 2	S 1	0	0
2	F	1	Total 33	C 16	N 4	O 10	P 2	S 1	0	0
2	G	1	Total 33	C 16	N 4	O 10	P 2	S 1	0	0
2	H	1	Total 33	C 16	N 4	O 10	P 2	S 1	0	0

- Molecule 3 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

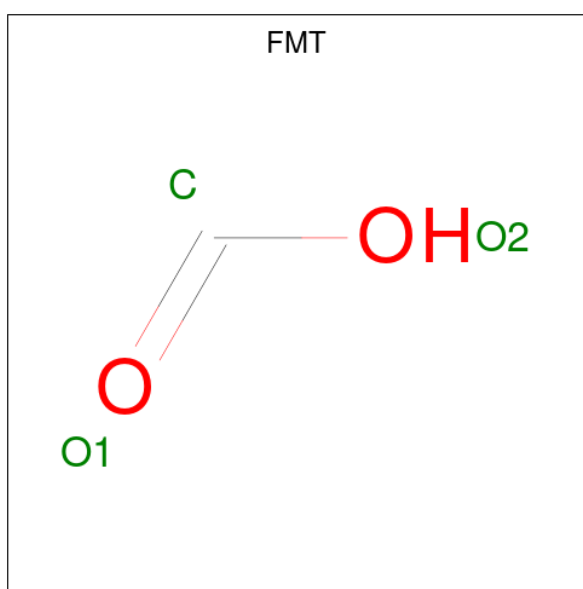
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mn 1 1	0	0
3	B	1	Total Mn 1 1	0	0
3	C	1	Total Mn 1 1	0	0
3	D	1	Total Mn 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	1	Total 1	Mn 1	0	0
3	F	1	Total 1	Mn 1	0	0
3	G	1	Total 1	Mn 1	0	0
3	H	1	Total 1	Mn 1	0	0

- Molecule 4 is FORMIC ACID (CCD ID: FMT) (formula: CH_2O_2).



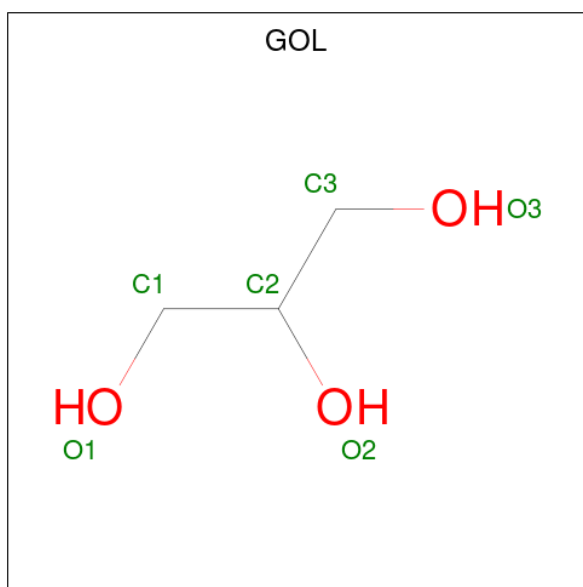
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 3	C 1	O 2	0	0
4	A	1	Total 3	C 1	O 2	0	0
4	A	1	Total 3	C 1	O 2	0	0
4	A	1	Total 3	C 1	O 2	0	0
4	A	1	Total 3	C 1	O 2	0	0
4	A	1	Total 3	C 1	O 2	0	0
4	B	1	Total 3	C 1	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			3	1	2		
4	B	1	Total	C	O	0	0
			3	1	2		
4	C	1	Total	C	O	0	0
			3	1	2		
4	D	1	Total	C	O	0	0
			3	1	2		
4	E	1	Total	C	O	0	0
			3	1	2		
4	E	1	Total	C	O	0	0
			3	1	2		
4	E	1	Total	C	O	0	0
			3	1	2		
4	F	1	Total	C	O	0	0
			3	1	2		
4	F	1	Total	C	O	0	0
			3	1	2		
4	F	1	Total	C	O	0	0
			3	1	2		
4	F	1	Total	C	O	0	0
			3	1	2		
4	F	1	Total	C	O	0	0
			3	1	2		
4	F	1	Total	C	O	0	0
			3	1	2		
4	G	1	Total	C	O	0	0
			3	1	2		
4	G	1	Total	C	O	0	0
			3	1	2		
4	H	1	Total	C	O	0	0
			3	1	2		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	C	O	0	0
			6	3	3		
5	G	1	Total	C	O	0	0
			6	3	3		

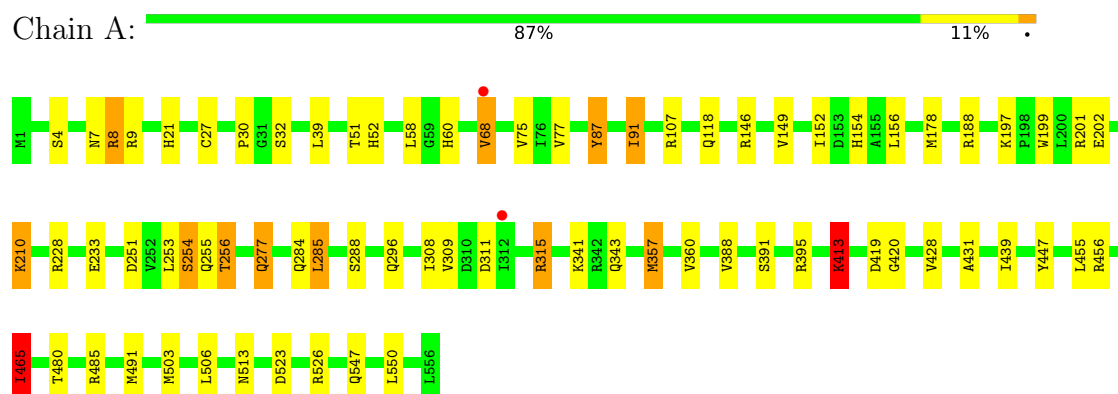
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	329	Total	O	0	0
			329	329		
6	B	351	Total	O	0	0
			351	351		
6	C	346	Total	O	0	0
			346	346		
6	D	317	Total	O	0	0
			317	317		
6	E	333	Total	O	0	0
			333	333		
6	F	320	Total	O	0	0
			320	320		
6	G	261	Total	O	0	0
			261	261		
6	H	259	Total	O	0	0
			259	259		

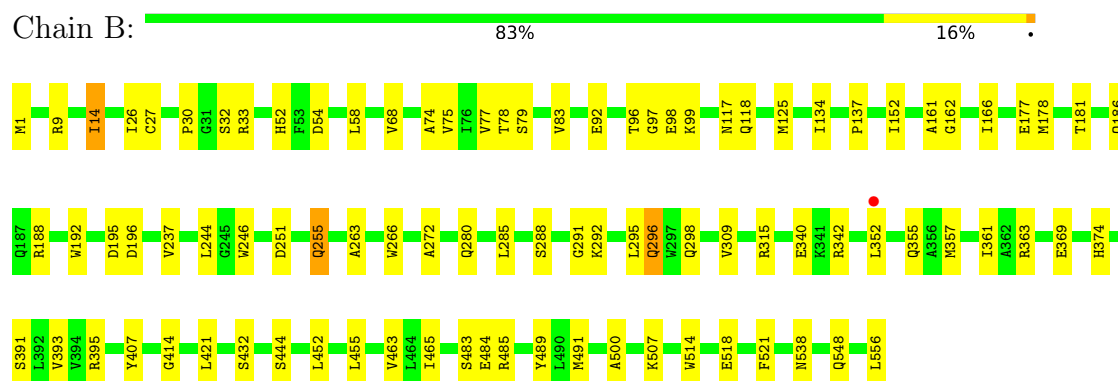
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

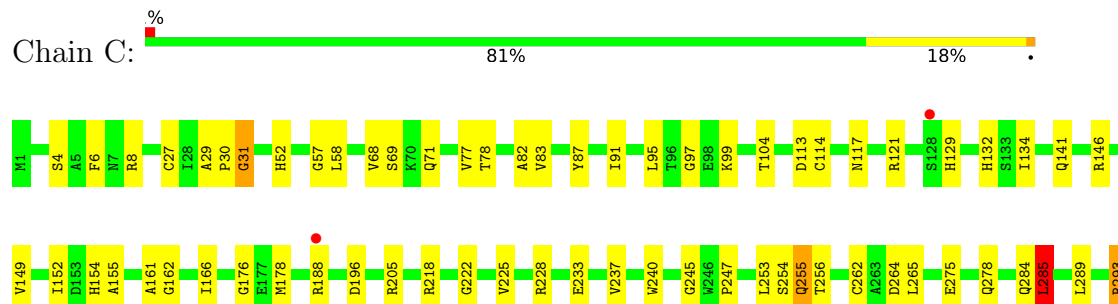
- Molecule 1: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase

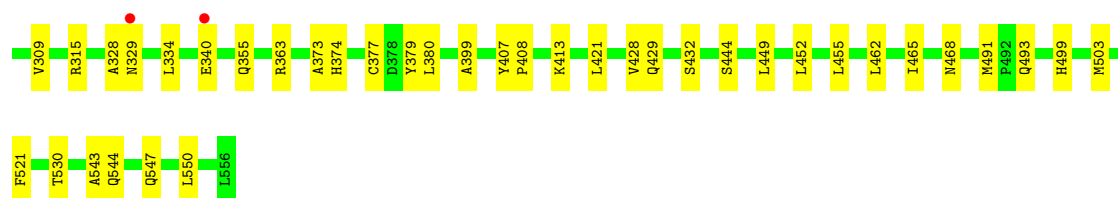


- Molecule 1: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase



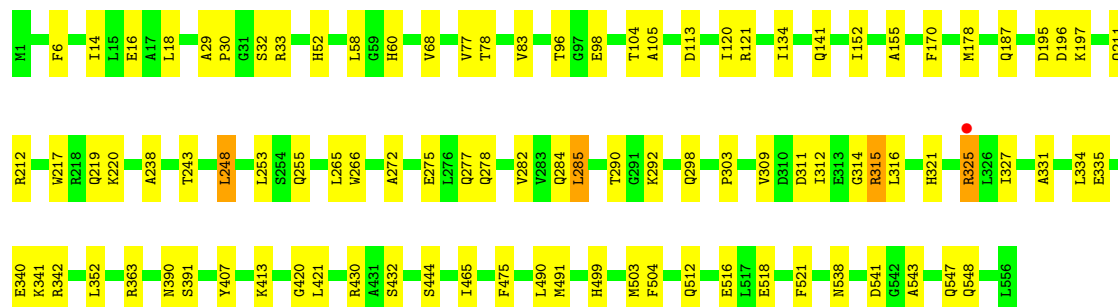
- Molecule 1: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase





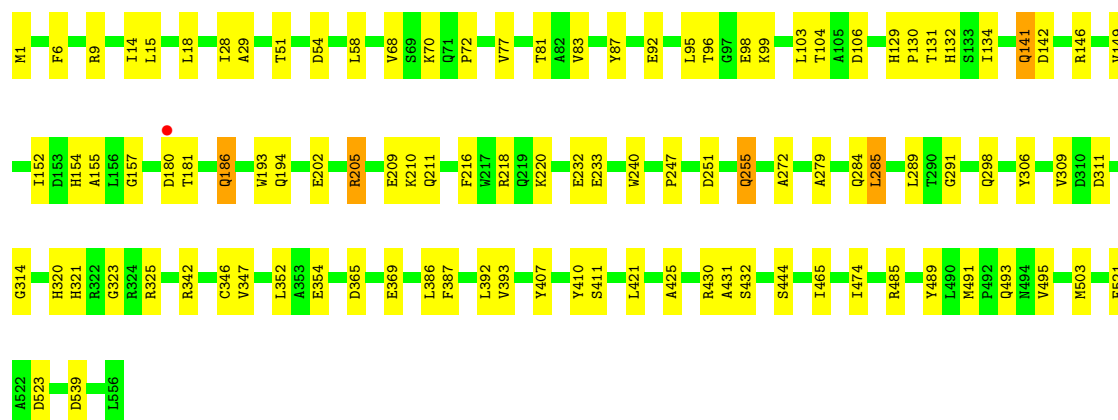
- Molecule 1: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase

Chain D: 83% 17%



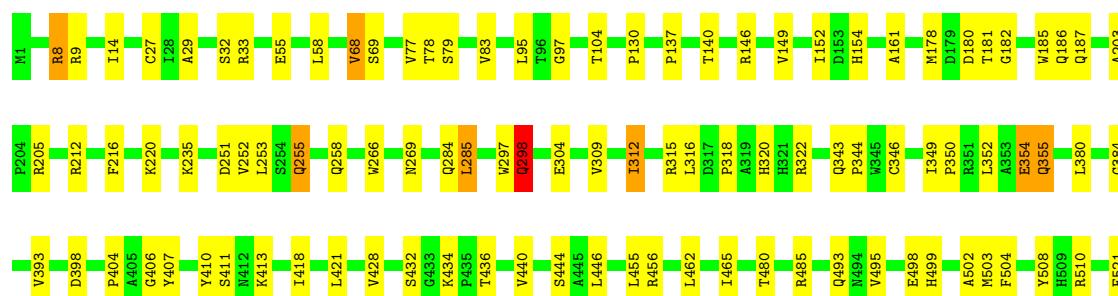
- Molecule 1: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase

Chain E: 81% 18%



- Molecule 1: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase

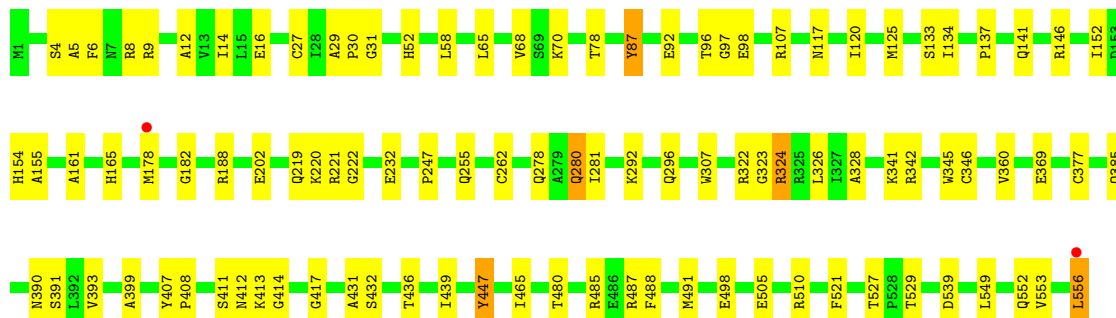
Chain F: 81% 18%





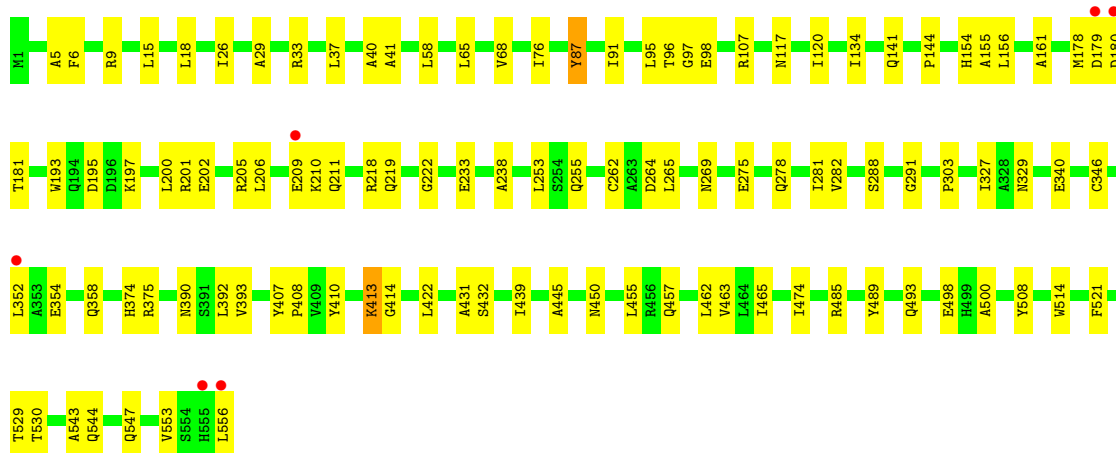
- Molecule 1: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase

Chain G: 82% 17%



- Molecule 1: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase

Chain H: 81% 19%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	90.26Å 90.27Å 167.07Å 83.43° 76.14° 63.49°	Depositor
Resolution (Å)	20.64 – 2.30 20.64 – 2.30	Depositor EDS
% Data completeness (in resolution range)	78.2 (20.64-2.30) 78.1 (20.64-2.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.66 (at 2.30Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.165 , 0.207 0.167 , 0.203	Depositor DCC
R_{free} test set	2015 reflections (0.99%)	wwPDB-VP
Wilson B-factor (Å ²)	11.3	Xtriage
Anisotropy	0.357	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 50.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.029 for -h,-k,-h+l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	36992	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.99% 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: TD6, MN, FMT, 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	0.64	9/4374 (0.2%)	0.74	6/5974 (0.1%)
1	B	0.59	4/4384 (0.1%)	0.69	0/5988
1	C	0.66	11/4379 (0.3%)	0.73	3/5982 (0.1%)
1	D	0.55	4/4381 (0.1%)	0.70	1/5984 (0.0%)
1	E	0.63	7/4375 (0.2%)	0.69	1/5977 (0.0%)
1	F	0.60	7/4392 (0.2%)	0.70	2/5997 (0.0%)
1	G	0.57	5/4348 (0.1%)	0.68	1/5942 (0.0%)
1	H	0.63	4/4354 (0.1%)	0.73	2/5949 (0.0%)
All	All	0.61	51/34987 (0.1%)	0.71	16/47793 (0.0%)

The worst 5 of 51 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	87	TYR	C-O	-8.37	1.16	1.24
1	G	87	TYR	C-O	-8.08	1.16	1.24
1	G	326	LEU	C-O	-7.53	1.15	1.24
1	A	87	TYR	C-O	-7.53	1.17	1.24
1	E	365	ASP	C-O	-7.23	1.15	1.24

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	365	ASP	N-CA-C	8.53	120.58	111.28
1	A	68	VAL	N-CA-C	7.88	118.68	110.72
1	F	68	VAL	N-CA-C	6.97	117.09	110.53
1	A	91	ILE	CB-CA-C	-6.64	103.47	111.97
1	A	419	ASP	N-CA-C	6.01	120.62	113.28

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	4266	0	4205	86	0
1	B	4276	0	4203	86	0
1	C	4271	0	4193	88	0
1	D	4273	0	4200	89	0
1	E	4267	0	4199	81	1
1	F	4284	0	4225	113	0
1	G	4240	0	4155	100	0
1	H	4246	0	4163	96	0
2	A	33	0	20	9	0
2	B	33	0	20	6	0
2	C	33	0	21	5	0
2	D	33	0	21	7	0
2	E	33	0	20	3	0
2	F	33	0	20	5	0
2	G	33	0	21	8	0
2	H	33	0	20	2	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
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	A	18	0	6	16	0
4	B	9	0	3	5	0
4	C	3	0	1	2	0
4	D	3	0	1	3	0
4	E	9	0	3	1	0
4	F	18	0	6	12	0
4	G	6	0	2	0	0
4	H	3	0	1	0	0
5	D	6	0	8	3	1
5	G	6	0	8	3	0
6	A	329	0	0	17	0
6	B	351	0	0	14	0
6	C	346	0	0	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	D	317	0	0	21	0
6	E	333	0	0	23	0
6	F	320	0	0	15	0
6	G	261	0	0	22	0
6	H	259	0	0	20	0
All	All	36992	0	33745	745	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 745 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:G:552:GLN:O	1:G:556:LEU:CD1	1.77	1.31
1:F:411:SER:N	4:F:606:FMT:H	1.46	1.28
1:D:16:GLU:OE1	5:D:604:GOL:H2	1.04	1.20
1:D:315:ARG:NH2	6:D:701:HOH:O	1.74	1.16
1:D:16:GLU:OE1	5:D:604:GOL:C2	1.93	1.15

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:354:GLU:OE2	5:D:604:GOL:C1[1_465]	1.96	0.24

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	554/556 (100%)	540 (98%)	14 (2%)	0	100	100
1	B	554/556 (100%)	543 (98%)	11 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	554/556 (100%)	543 (98%)	11 (2%)	0	100	100
1	D	554/556 (100%)	540 (98%)	14 (2%)	0	100	100
1	E	554/556 (100%)	541 (98%)	13 (2%)	0	100	100
1	F	554/556 (100%)	543 (98%)	11 (2%)	0	100	100
1	G	554/556 (100%)	543 (98%)	11 (2%)	0	100	100
1	H	554/556 (100%)	543 (98%)	11 (2%)	0	100	100
All	All	4432/4448 (100%)	4336 (98%)	96 (2%)	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	435/452 (96%)	424 (98%)	11 (2%)	42	60
1	B	438/452 (97%)	436 (100%)	2 (0%)	81	90
1	C	436/452 (96%)	432 (99%)	4 (1%)	70	84
1	D	437/452 (97%)	433 (99%)	4 (1%)	70	84
1	E	436/452 (96%)	431 (99%)	5 (1%)	65	81
1	F	440/452 (97%)	435 (99%)	5 (1%)	65	81
1	G	428/452 (95%)	425 (99%)	3 (1%)	76	87
1	H	430/452 (95%)	429 (100%)	1 (0%)	87	94
All	All	3480/3616 (96%)	3445 (99%)	35 (1%)	68	82

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	255	GLN
1	F	285	LEU
1	G	324	ARG
1	B	255	GLN

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Mol	Chain	Res	Type
1	B	77	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	509	HIS
1	H	219	GLN
1	F	538	ASN
1	G	509	HIS
1	H	548	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](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 41 ligands modelled in this entry, 8 are monoatomic - leaving 33 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	$\# Z > 2$
4	FMT	H	603	-	2,2,2	0.66	0	1,1,1	0.61	0
2	TD6	D	601	3	31,34,34	3.89	13 (41%)	38,50,50	1.94	14 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	TD6	G	601	3	31,34,34	3.52	13 (41%)	38,50,50	2.36	14 (36%)
4	FMT	A	608	-	2,2,2	0.53	0	1,1,1	0.74	0
4	FMT	F	607	-	2,2,2	0.41	0	1,1,1	0.77	0
4	FMT	A	604	-	2,2,2	0.64	0	1,1,1	0.28	0
4	FMT	F	608	-	2,2,2	0.66	0	1,1,1	0.61	0
4	FMT	E	605	-	2,2,2	0.63	0	1,1,1	0.13	0
4	FMT	F	606	-	2,2,2	0.41	0	1,1,1	0.42	0
4	FMT	B	605	-	2,2,2	0.67	0	1,1,1	0.61	0
2	TD6	F	601	3	31,34,34	4.11	14 (45%)	38,50,50	2.12	19 (50%)
2	TD6	C	601	3	31,34,34	3.79	14 (45%)	38,50,50	1.99	12 (31%)
5	GOL	D	604	-	5,5,5	0.72	0	5,5,5	2.08	2 (40%)
2	TD6	B	601	3	31,34,34	3.97	15 (48%)	38,50,50	1.68	11 (28%)
4	FMT	A	605	-	2,2,2	0.50	0	1,1,1	0.37	0
4	FMT	C	603	-	2,2,2	0.67	0	1,1,1	0.61	0
4	FMT	F	603	-	2,2,2	0.67	0	1,1,1	0.23	0
4	FMT	B	604	-	2,2,2	0.38	0	1,1,1	0.44	0
4	FMT	G	603	-	2,2,2	0.64	0	1,1,1	0.17	0
4	FMT	A	603	-	2,2,2	0.57	0	1,1,1	0.01	0
4	FMT	F	605	-	2,2,2	0.45	0	1,1,1	0.51	0
4	FMT	B	603	-	2,2,2	0.60	0	1,1,1	0.37	0
4	FMT	D	603	-	2,2,2	0.67	0	1,1,1	0.61	0
5	GOL	G	605	-	5,5,5	0.36	0	5,5,5	0.86	0
4	FMT	A	607	-	2,2,2	0.67	0	1,1,1	0.62	0
2	TD6	A	601	3	31,34,34	3.85	13 (41%)	38,50,50	2.04	14 (36%)
4	FMT	G	604	-	2,2,2	0.24	0	1,1,1	0.10	0
2	TD6	E	601	3	31,34,34	3.84	13 (41%)	38,50,50	1.82	14 (36%)
4	FMT	A	606	-	2,2,2	0.97	0	1,1,1	0.04	0
4	FMT	F	604	-	2,2,2	0.64	0	1,1,1	0.11	0
4	FMT	E	603	-	2,2,2	0.45	0	1,1,1	0.00	0
2	TD6	H	601	3	31,34,34	3.88	14 (45%)	38,50,50	2.25	15 (39%)
4	FMT	E	604	-	2,2,2	0.68	0	1,1,1	0.04	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	GOL	G	605	-	-	0/4/4/4	-
2	TD6	A	601	3	-	9/25/26/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	TD6	D	601	3	-	9/25/26/26	0/2/2/2
2	TD6	G	601	3	-	6/25/26/26	0/2/2/2
2	TD6	F	601	3	-	7/25/26/26	0/2/2/2
2	TD6	C	601	3	-	6/25/26/26	0/2/2/2
2	TD6	E	601	3	-	5/25/26/26	0/2/2/2
5	GOL	D	604	-	-	2/4/4/4	-
2	TD6	B	601	3	-	7/25/26/26	0/2/2/2
2	TD6	H	601	3	-	7/25/26/26	0/2/2/2

The worst 5 of 109 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	TD6	C5-S1	-15.01	1.43	1.74
2	F	601	TD6	C5-S1	-14.47	1.44	1.74
2	D	601	TD6	C5-S1	-14.41	1.44	1.74
2	H	601	TD6	C5-S1	-14.04	1.45	1.74
2	A	601	TD6	C5-S1	-13.21	1.47	1.74

The worst 5 of 115 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	601	TD6	C13-CLB-C11	8.46	127.59	114.48
2	H	601	TD6	CM2-C2'-N1'	5.14	122.67	117.20
2	H	601	TD6	C4-C5-S1	-5.05	105.33	110.56
2	C	601	TD6	C13-CLB-C11	4.98	122.20	114.48
2	F	601	TD6	OL2-CLC-OL3	-4.88	110.78	123.33

There are no chirality outliers.

5 of 58 torsion outliers are listed below:

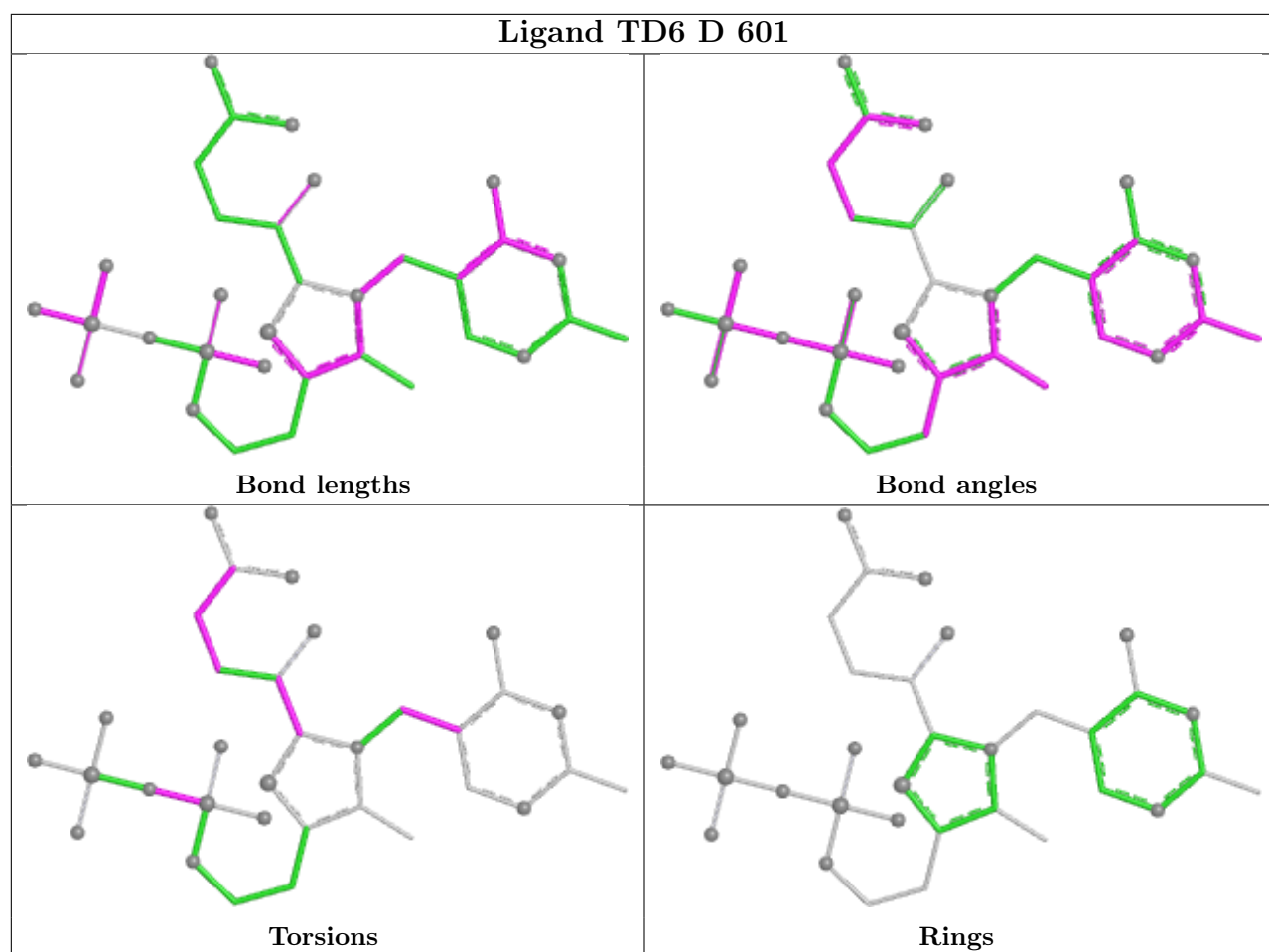
Mol	Chain	Res	Type	Atoms
2	A	601	TD6	CLB-C11-C2-S1
2	A	601	TD6	OL1-C11-C2-N3
2	A	601	TD6	PB-O3A-PA-O7
2	A	601	TD6	C2-C11-CLB-C13
2	A	601	TD6	CLC-C13-CLB-C11

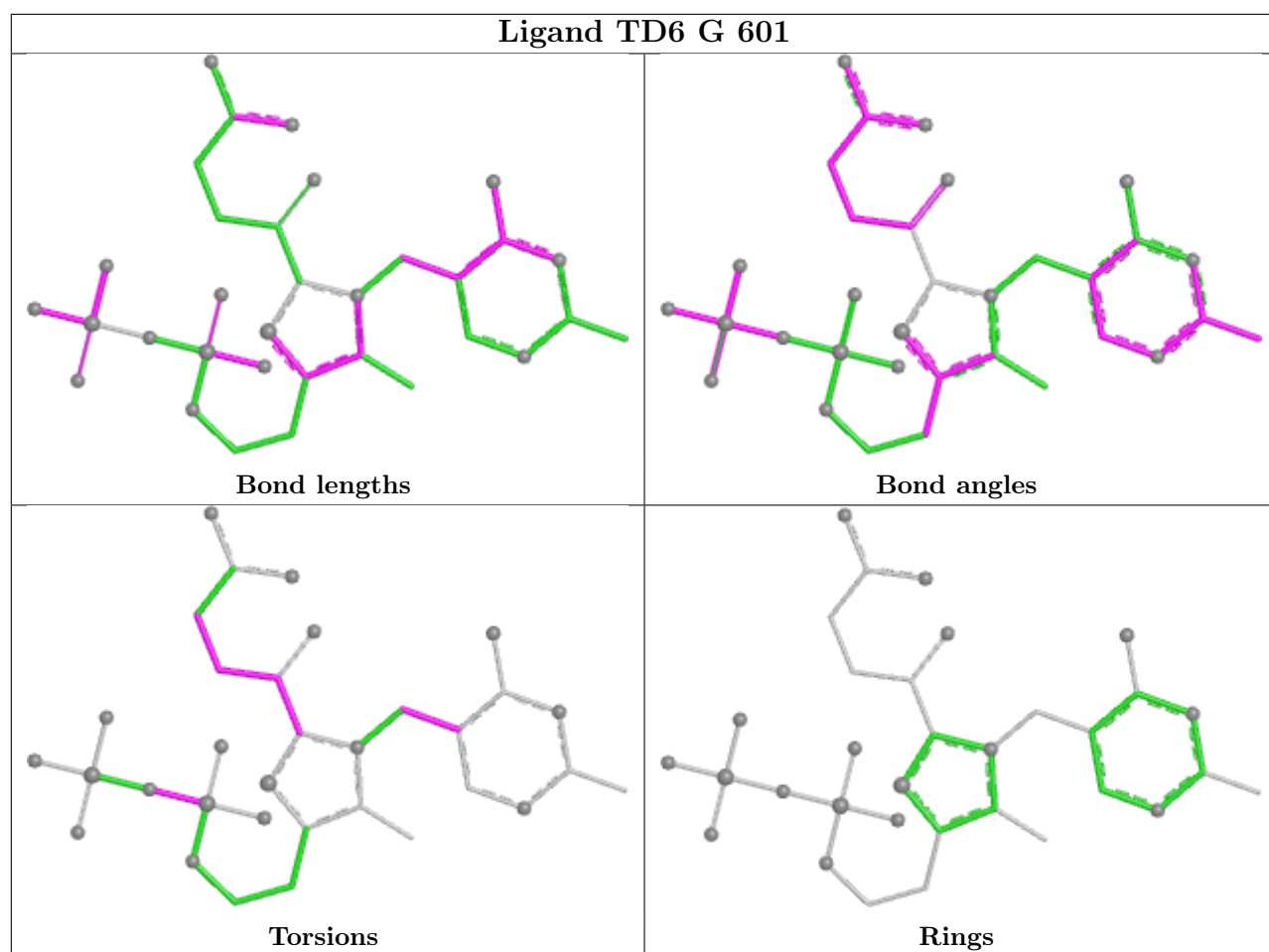
There are no ring outliers.

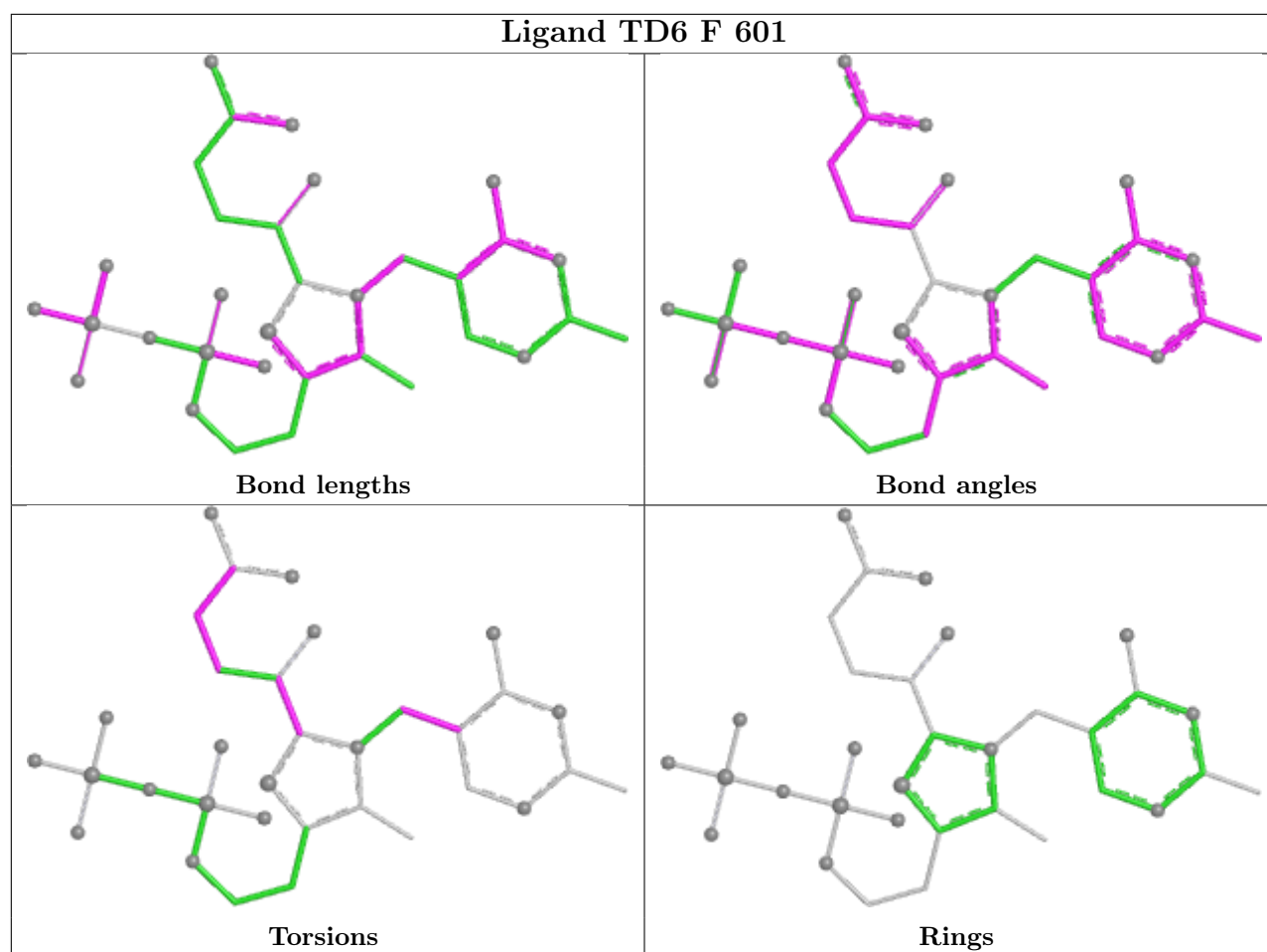
23 monomers are involved in 84 short contacts:

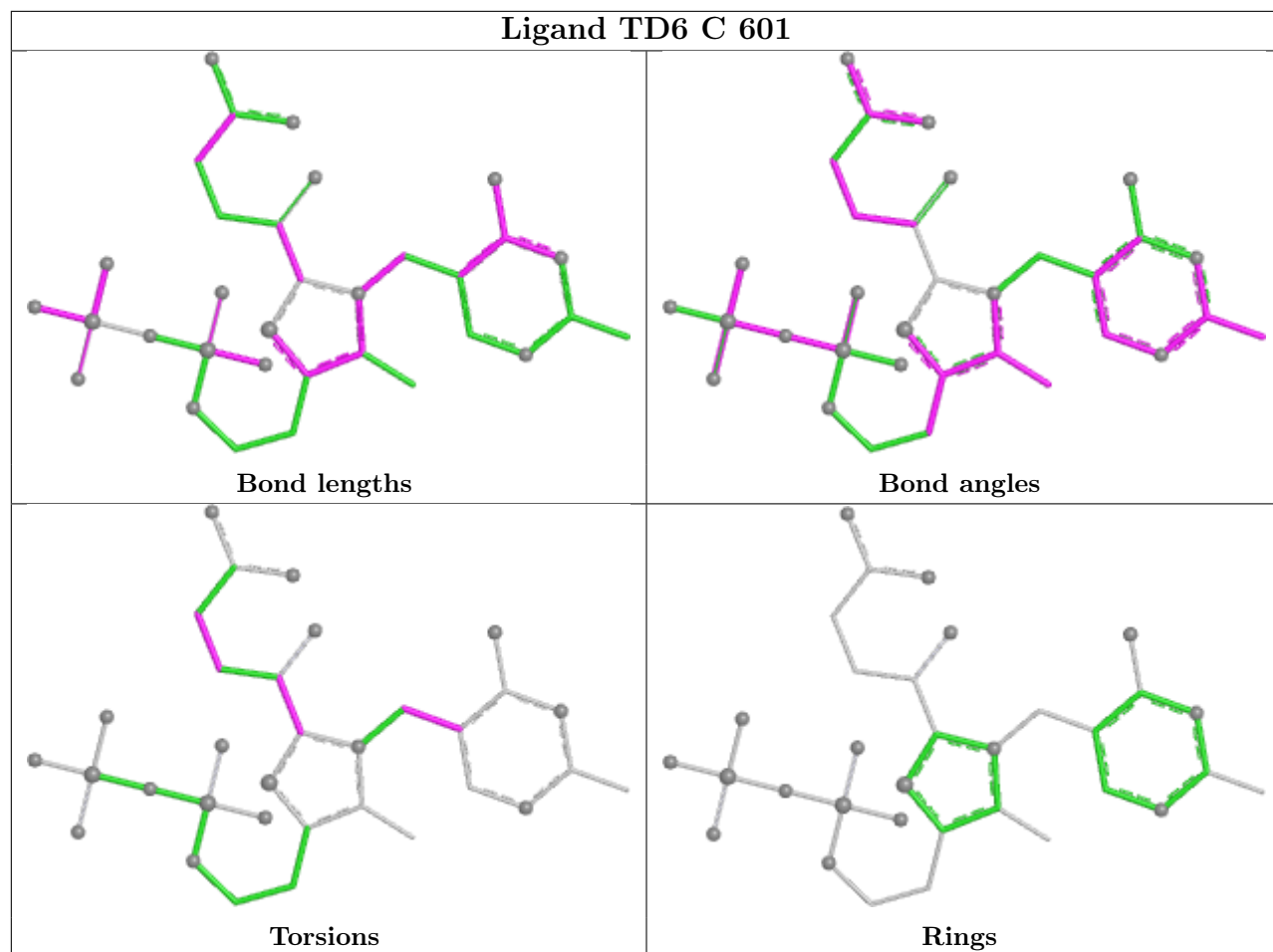
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	601	TD6	7	0
2	G	601	TD6	8	0
4	A	608	FMT	9	0
4	A	604	FMT	2	0
4	F	608	FMT	3	0
4	F	606	FMT	6	0
4	B	605	FMT	4	0
2	F	601	TD6	5	0
2	C	601	TD6	5	0
5	D	604	GOL	3	1
2	B	601	TD6	6	0
4	A	605	FMT	2	0
4	C	603	FMT	2	0
4	F	605	FMT	1	0
4	B	603	FMT	1	0
4	D	603	FMT	3	0
5	G	605	GOL	3	0
4	A	607	FMT	3	0
2	A	601	TD6	9	0
2	E	601	TD6	3	0
4	F	604	FMT	2	0
4	E	603	FMT	1	0
2	H	601	TD6	2	0

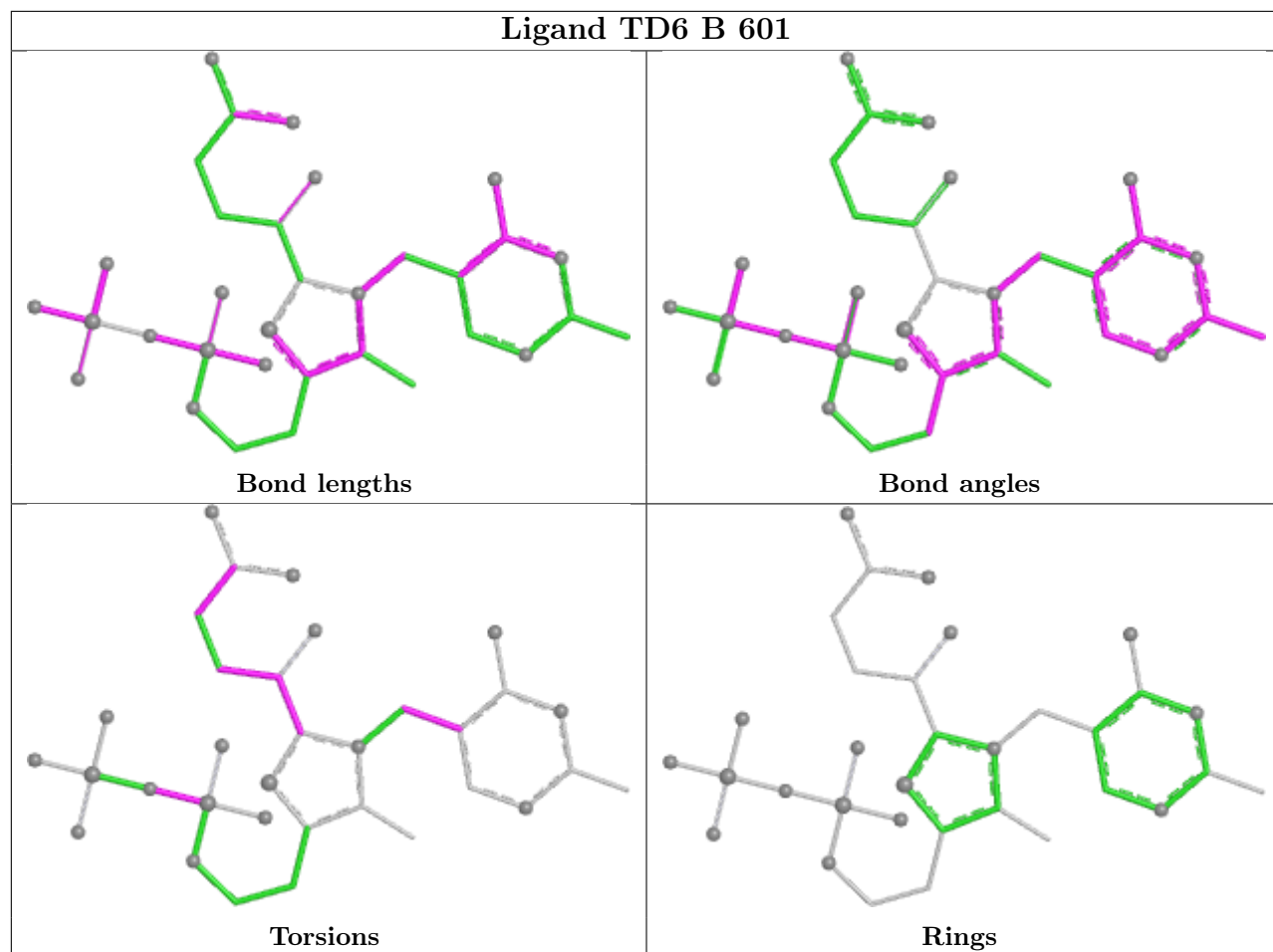
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

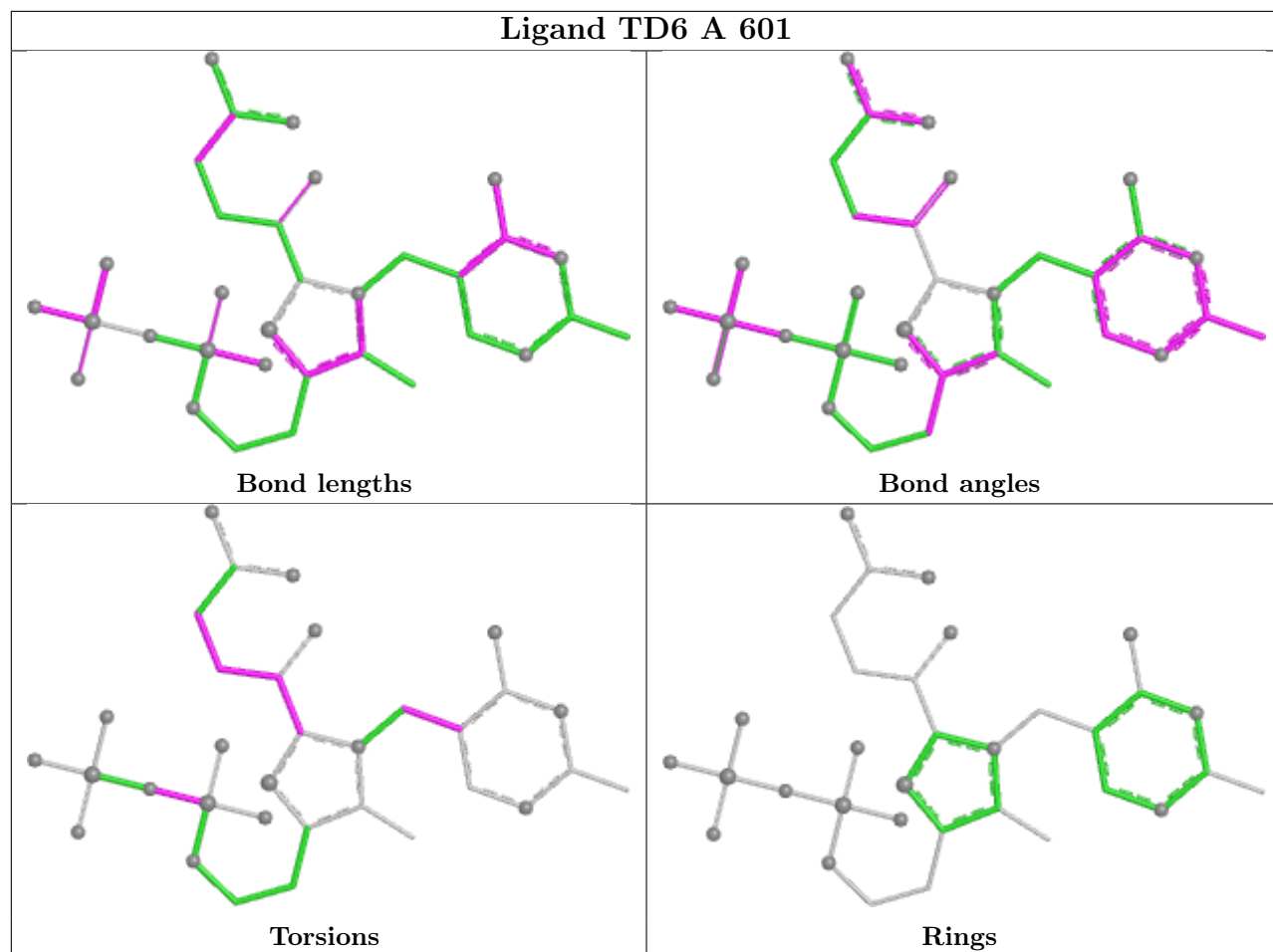


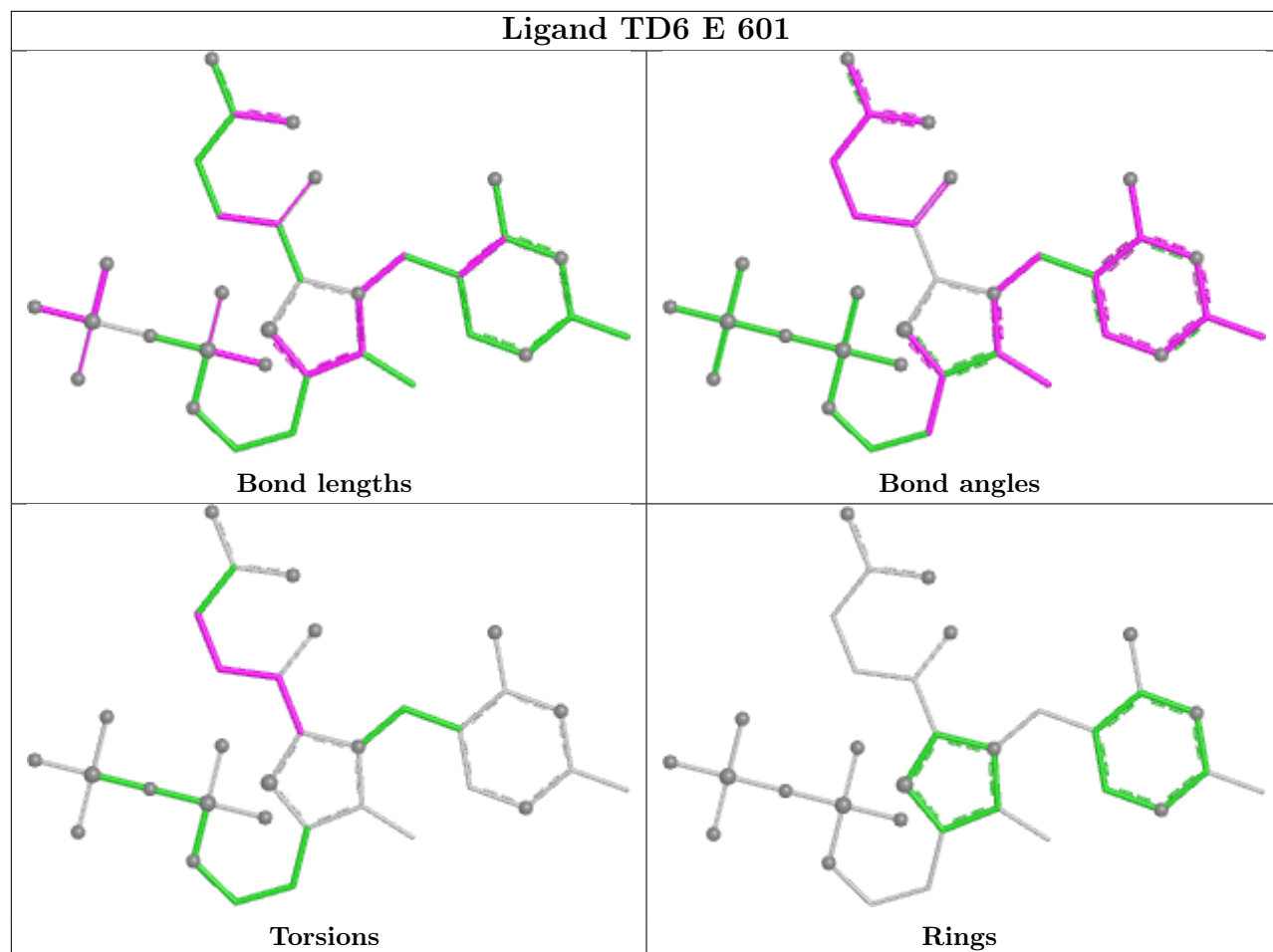


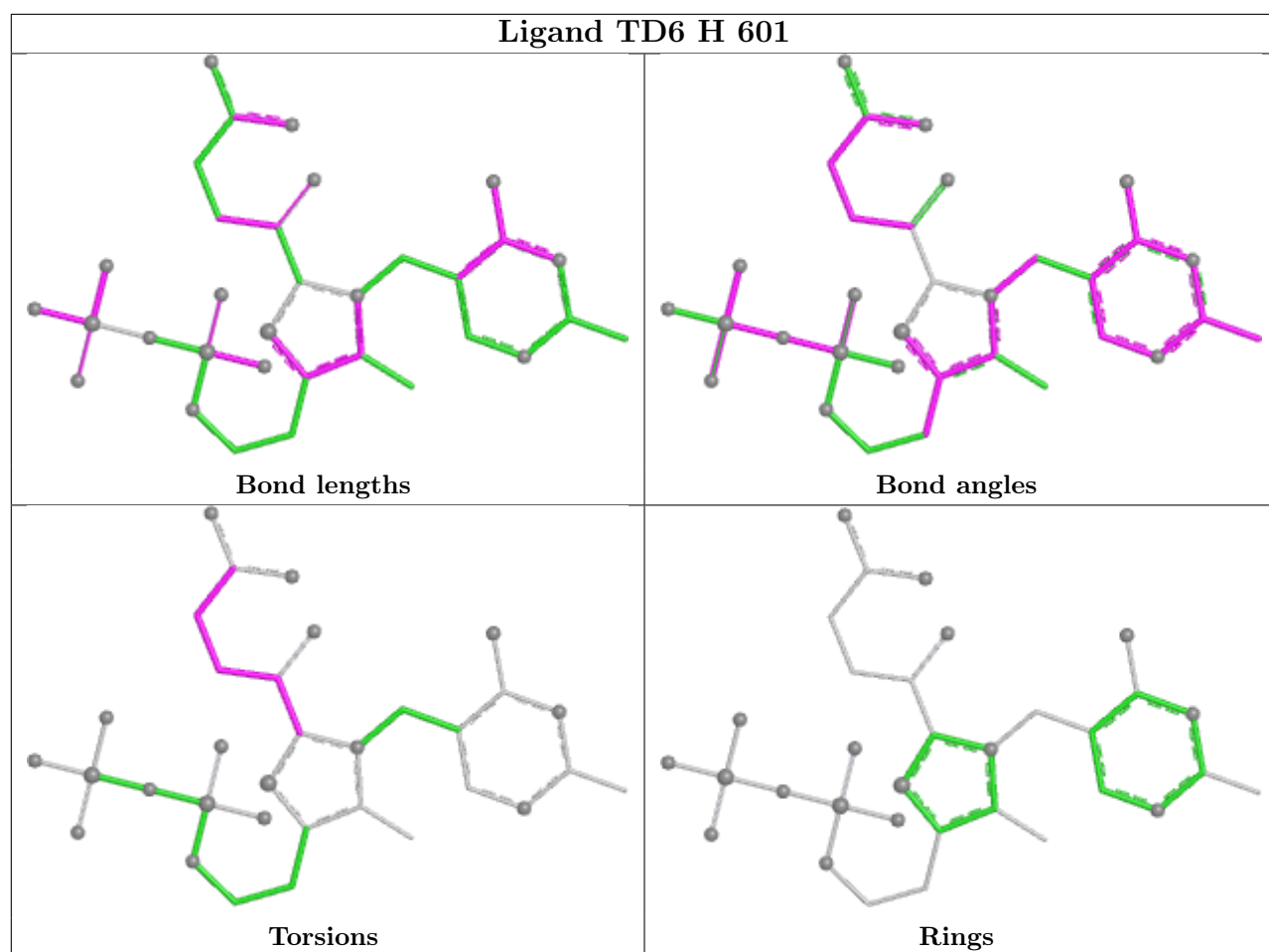












5.7 Other polymers [i](#)

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 [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	556/556 (100%)	-0.47	2 (0%) 88 89	6, 12, 24, 43	0
1	B	556/556 (100%)	-0.45	1 (0%) 91 91	6, 14, 24, 43	0
1	C	556/556 (100%)	-0.48	4 (0%) 84 85	7, 12, 23, 44	0
1	D	556/556 (100%)	-0.47	1 (0%) 91 91	6, 13, 24, 43	0
1	E	556/556 (100%)	-0.39	1 (0%) 91 91	8, 15, 26, 46	0
1	F	556/556 (100%)	-0.37	1 (0%) 91 91	9, 15, 27, 46	0
1	G	556/556 (100%)	-0.23	2 (0%) 88 89	10, 19, 32, 45	0
1	H	556/556 (100%)	-0.25	6 (1%) 78 79	8, 19, 33, 47	0
All	All	4448/4448 (100%)	-0.39	18 (0%) 88 89	6, 15, 29, 47	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	179	ASP	3.8
1	G	178	MET	3.7
1	G	556	LEU	3.5
1	C	188	ARG	2.8
1	A	68	VAL	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

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
5	GOL	D	604	6/6	0.79	0.13	20,20,20,20	0
4	FMT	B	603	3/3	0.83	0.14	20,20,20,20	0
4	FMT	F	603	3/3	0.83	0.10	24,24,29,34	0
4	FMT	A	608	3/3	0.83	0.27	20,20,20,20	0
4	FMT	F	607	3/3	0.84	0.15	20,20,20,20	0
4	FMT	E	603	3/3	0.86	0.13	17,17,19,23	0
4	FMT	G	604	3/3	0.86	0.14	20,20,20,20	0
4	FMT	A	605	3/3	0.86	0.14	20,20,20,20	0
5	GOL	G	605	6/6	0.86	0.14	20,20,20,20	0
4	FMT	B	605	3/3	0.88	0.14	20,20,20,20	0
4	FMT	H	603	3/3	0.88	0.15	20,20,20,20	0
4	FMT	F	605	3/3	0.89	0.15	20,20,20,20	0
4	FMT	E	604	3/3	0.91	0.14	22,22,26,28	0
4	FMT	A	606	3/3	0.91	0.11	20,20,20,20	0
4	FMT	E	605	3/3	0.92	0.13	25,25,32,35	0
4	FMT	D	603	3/3	0.92	0.14	20,20,20,20	0
4	FMT	B	604	3/3	0.93	0.16	20,20,20,20	0
4	FMT	G	603	3/3	0.93	0.09	32,32,35,35	0
4	FMT	C	603	3/3	0.93	0.13	20,20,20,20	0
4	FMT	A	607	3/3	0.94	0.16	20,20,20,20	0
4	FMT	F	604	3/3	0.94	0.09	18,18,21,21	0
4	FMT	A	603	3/3	0.94	0.09	19,19,23,25	0
2	TD6	H	601	33/33	0.96	0.07	13,19,27,33	4
2	TD6	C	601	33/33	0.96	0.08	8,11,17,45	5
4	FMT	F	606	3/3	0.96	0.12	20,20,20,20	0
2	TD6	G	601	33/33	0.96	0.09	15,23,38,43	4
4	FMT	F	608	3/3	0.96	0.16	20,20,20,20	0
4	FMT	A	604	3/3	0.97	0.05	22,22,23,24	0
2	TD6	E	601	33/33	0.97	0.08	8,15,32,39	0
2	TD6	F	601	33/33	0.97	0.07	8,14,22,27	3
2	TD6	B	601	33/33	0.97	0.08	5,12,33,43	3
2	TD6	A	601	33/33	0.97	0.07	8,11,25,42	5
2	TD6	D	601	33/33	0.97	0.07	8,12,22,28	2
3	MN	H	602	1/1	0.98	0.05	21,21,21,21	0
3	MN	B	602	1/1	0.99	0.04	24,24,24,24	0
3	MN	D	602	1/1	0.99	0.04	12,12,12,12	0
3	MN	E	602	1/1	0.99	0.04	16,16,16,16	0

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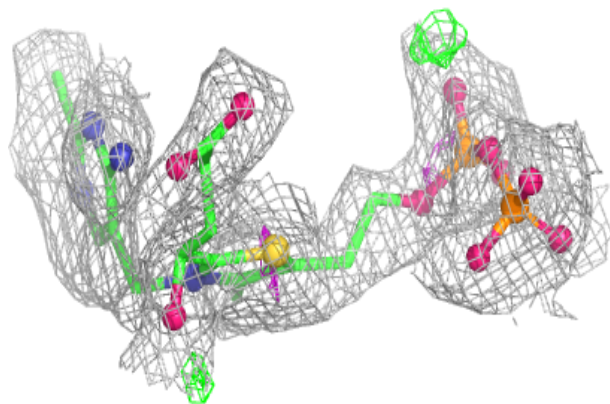
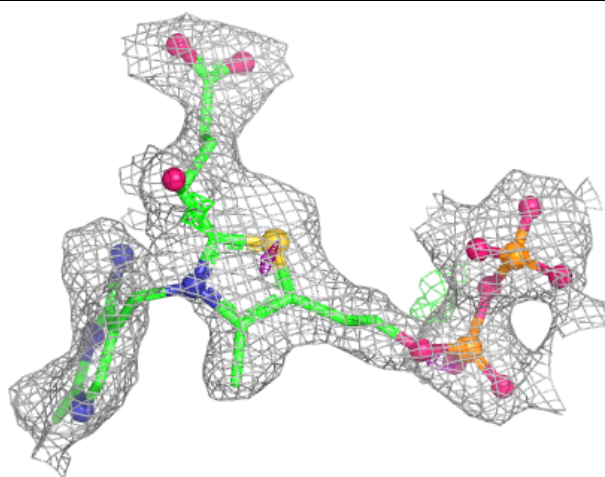
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MN	G	602	1/1	0.99	0.06	24,24,24,24	0
3	MN	A	602	1/1	0.99	0.03	12,12,12,12	0
3	MN	F	602	1/1	1.00	0.01	23,23,23,23	0
3	MN	C	602	1/1	1.00	0.03	11,11,11,11	0

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.

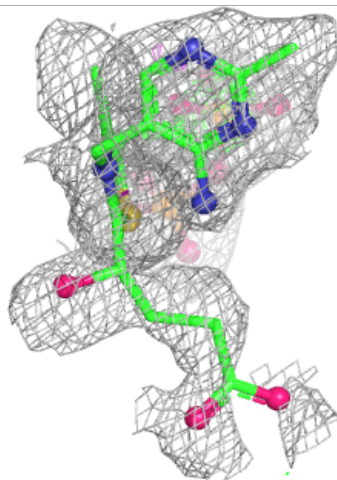
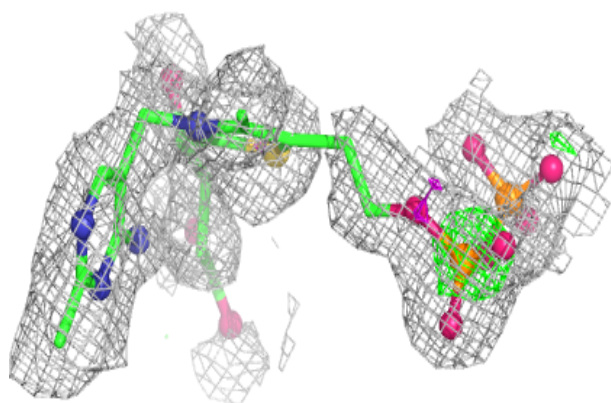
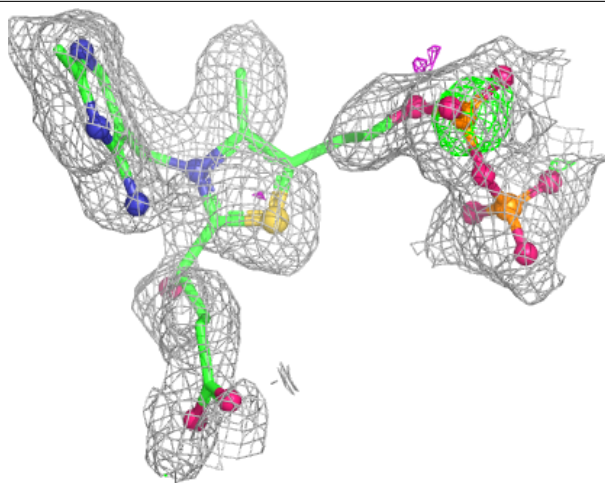
Electron density around TD6 H 601:

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



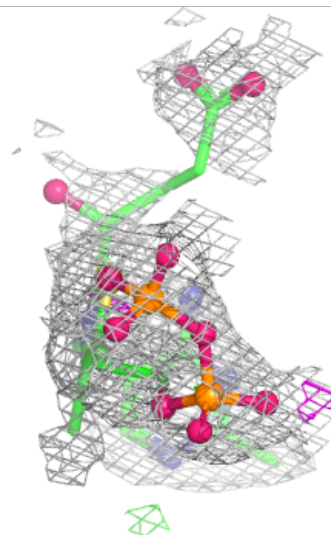
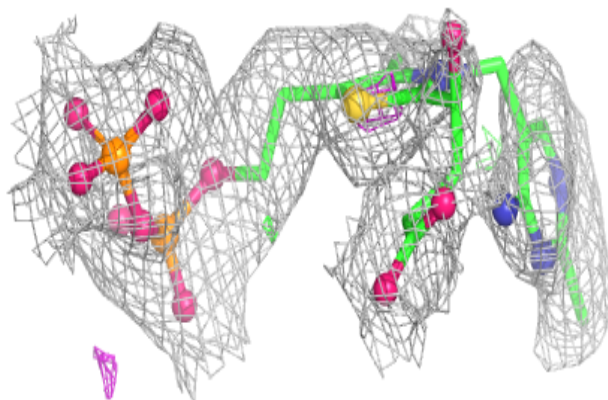
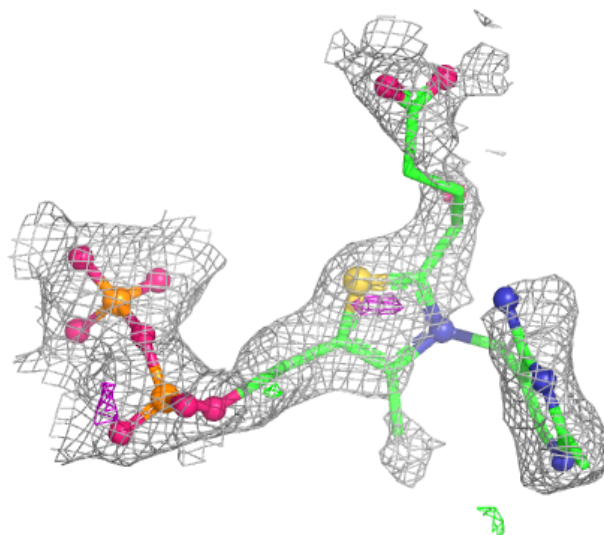
Electron density around TD6 C 601:

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



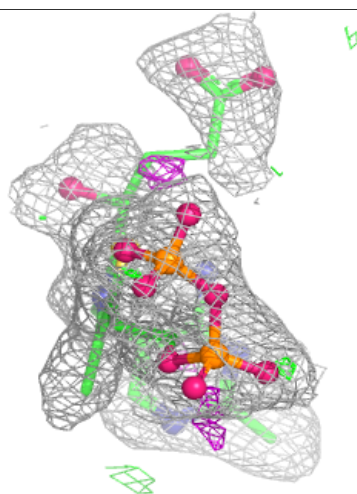
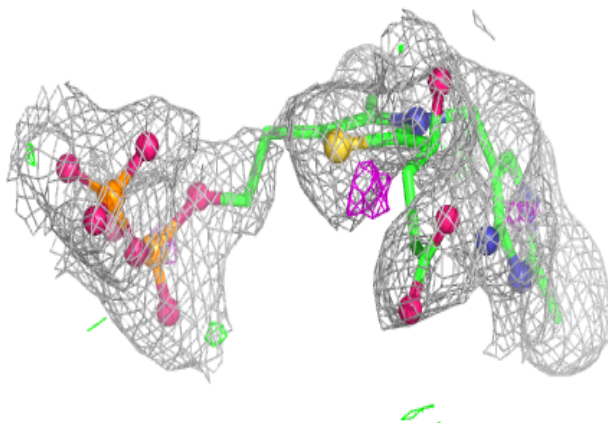
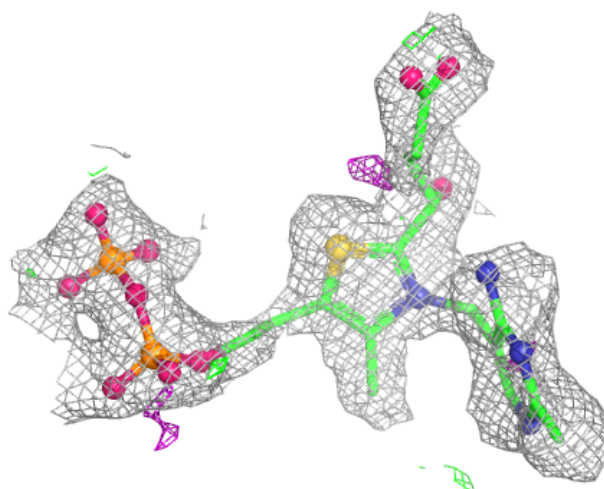
Electron density around TD6 G 601:

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



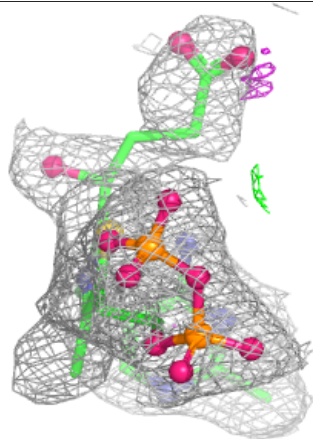
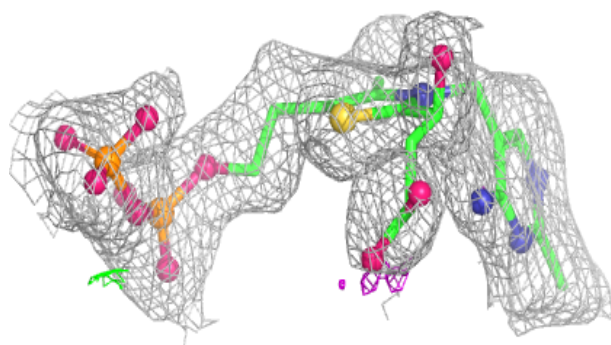
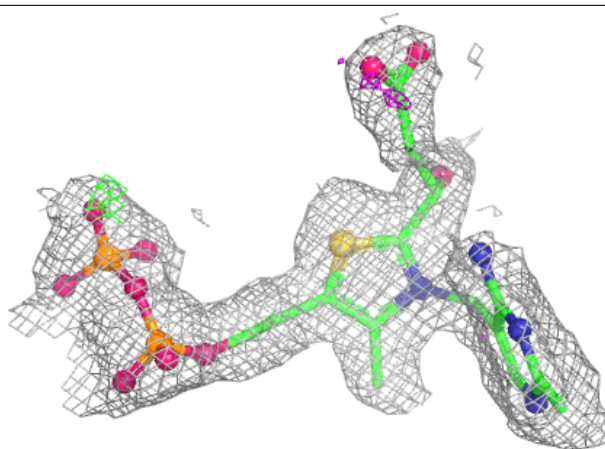
Electron density around TD6 E 601:

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



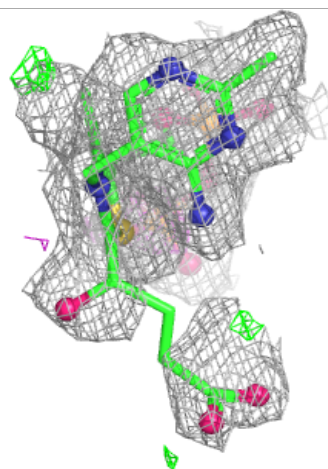
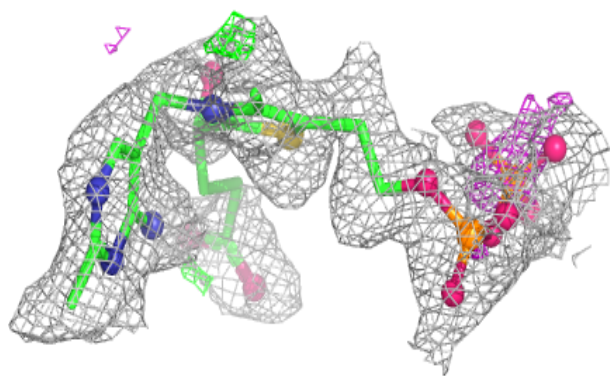
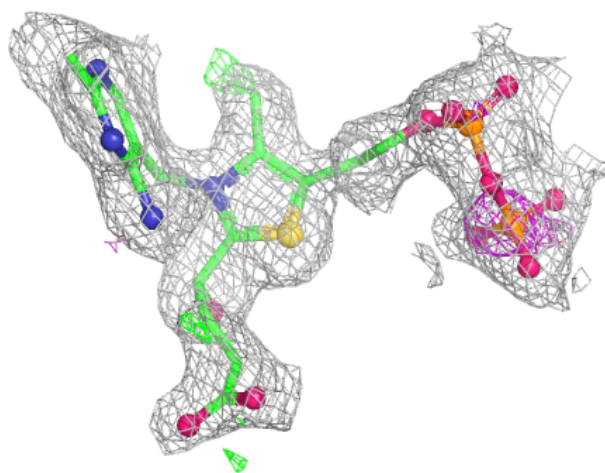
Electron density around TD6 F 601:

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



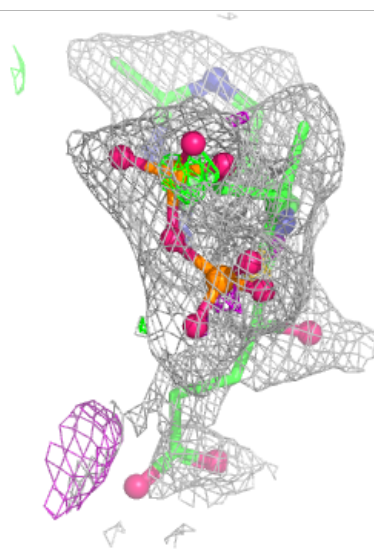
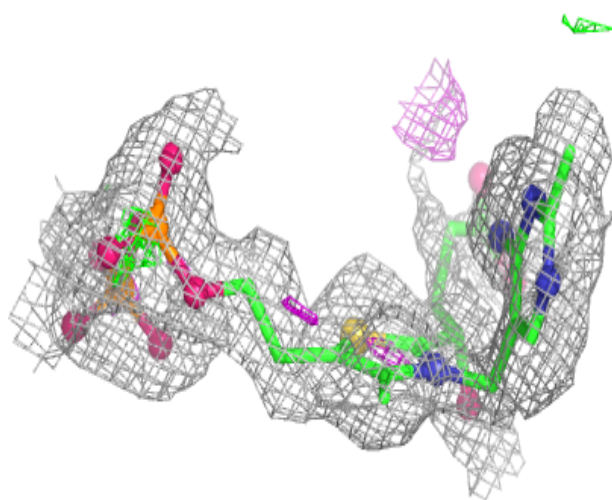
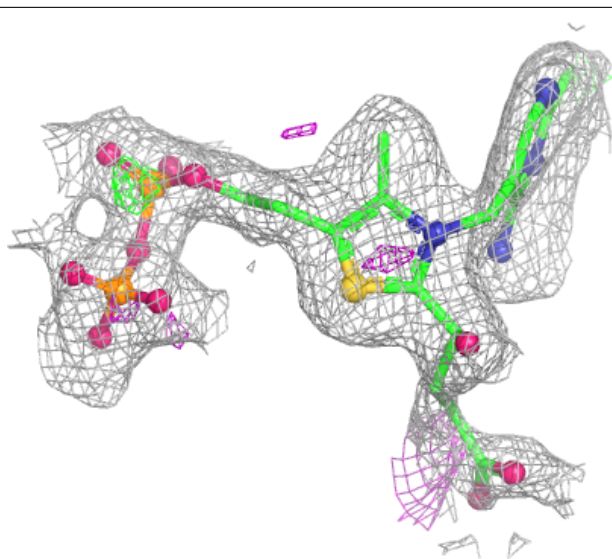
Electron density around TD6 B 601:

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



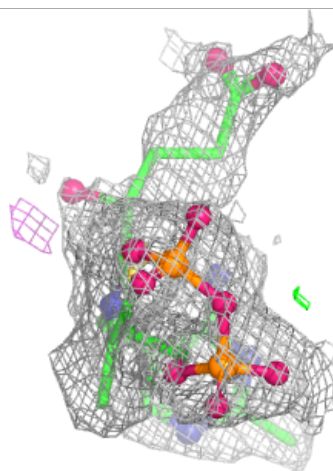
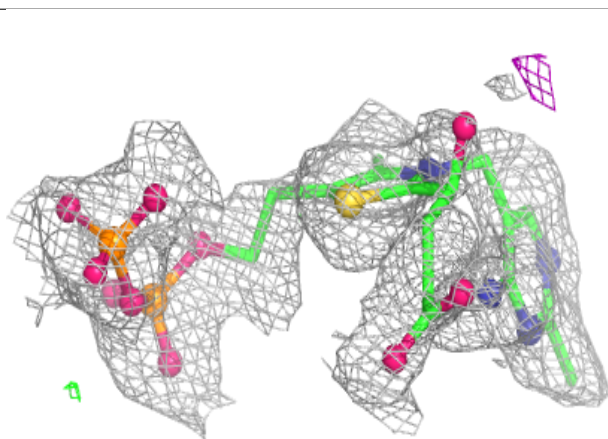
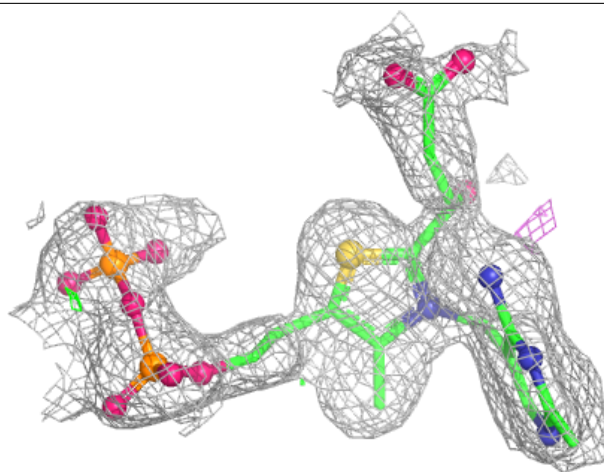
Electron density around TD6 A 601:

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



Electron density around TD6 D 601:

$2mF_o-DF_c$ (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.