



Full wwPDB X-ray Structure Validation Report

Jun 17, 2024 – 07:04 PM EDT

PDB ID : 5RW0
Title : PanDDA analysis group deposition – Crystal Structure of DHTKD1 in complex with Z2444997446
Authors : Bezerra, G.A.; Foster, W.R.; Bailey, H.J.; Shrestha, L.; Krojer, T.; Brandao-Neto, J.; Douangamath, A.; Burgess-Brown, N.; von Delft, F.; Arrowsmith, C.H.; Edwards, A.; Bountra, C.; Yue, W.W.
Deposited on : 2020-10-27
Resolution : 1.67 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the  symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references](#) ①) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.37.1
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) : 2.37.1

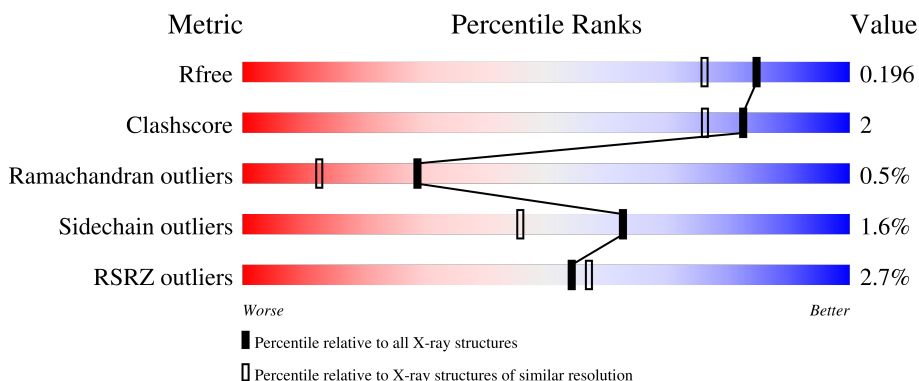
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.67 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	6780 (1.70-1.66)
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

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	898	 2% 90% 6% •
1	B	898	 3% 89% 7% •

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	WGD	A	1002	X	-	-	-
2	WGD	A	1003	X	-	-	-
2	WGD	B	1002	X	-	-	-

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 15420 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 Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	867	6775	4317	1169	1249	40	0	5	0
1	B	867	6740	4296	1163	1243	38	0	2	0

There are 46 discrepancies between the modelled and reference sequences:

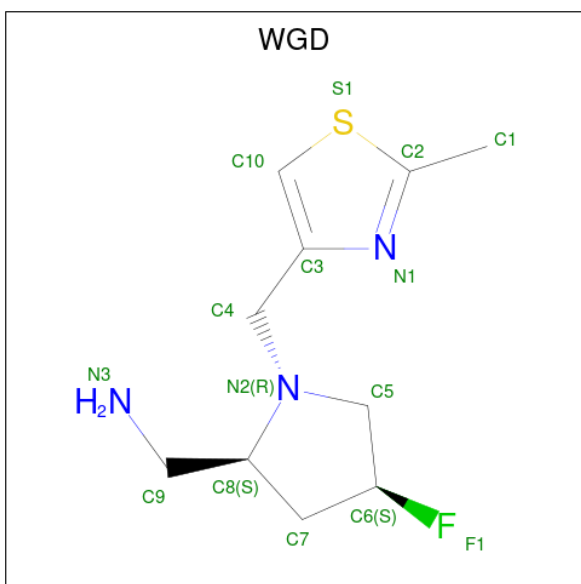
Chain	Residue	Modelled	Actual	Comment	Reference
A	22	MET	-	initiating methionine	UNP Q96HY7
A	23	HIS	-	expression tag	UNP Q96HY7
A	24	HIS	-	expression tag	UNP Q96HY7
A	25	HIS	-	expression tag	UNP Q96HY7
A	26	HIS	-	expression tag	UNP Q96HY7
A	27	HIS	-	expression tag	UNP Q96HY7
A	28	HIS	-	expression tag	UNP Q96HY7
A	29	SER	-	expression tag	UNP Q96HY7
A	30	SER	-	expression tag	UNP Q96HY7
A	31	GLY	-	expression tag	UNP Q96HY7
A	32	VAL	-	expression tag	UNP Q96HY7
A	33	ASP	-	expression tag	UNP Q96HY7
A	34	LEU	-	expression tag	UNP Q96HY7
A	35	GLY	-	expression tag	UNP Q96HY7
A	36	THR	-	expression tag	UNP Q96HY7
A	37	GLU	-	expression tag	UNP Q96HY7
A	38	ASN	-	expression tag	UNP Q96HY7
A	39	LEU	-	expression tag	UNP Q96HY7
A	40	TYR	-	expression tag	UNP Q96HY7
A	41	PHE	-	expression tag	UNP Q96HY7
A	42	GLN	-	expression tag	UNP Q96HY7
A	43	SER	-	expression tag	UNP Q96HY7
A	44	MET	-	expression tag	UNP Q96HY7
B	22	MET	-	initiating methionine	UNP Q96HY7

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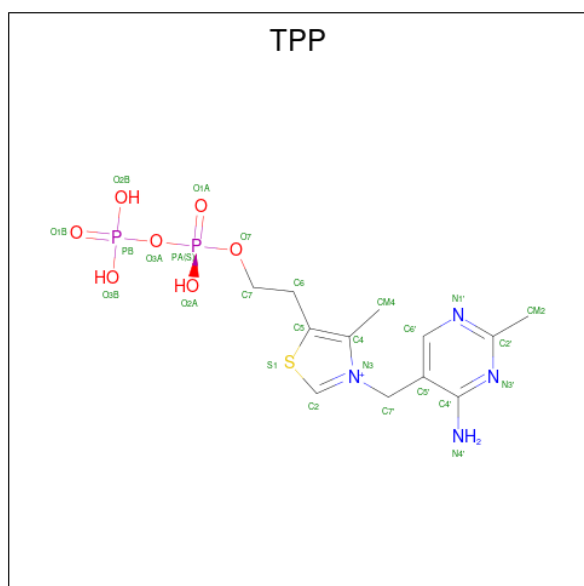
Chain	Residue	Modelled	Actual	Comment	Reference
B	23	HIS	-	expression tag	UNP Q96HY7
B	24	HIS	-	expression tag	UNP Q96HY7
B	25	HIS	-	expression tag	UNP Q96HY7
B	26	HIS	-	expression tag	UNP Q96HY7
B	27	HIS	-	expression tag	UNP Q96HY7
B	28	HIS	-	expression tag	UNP Q96HY7
B	29	SER	-	expression tag	UNP Q96HY7
B	30	SER	-	expression tag	UNP Q96HY7
B	31	GLY	-	expression tag	UNP Q96HY7
B	32	VAL	-	expression tag	UNP Q96HY7
B	33	ASP	-	expression tag	UNP Q96HY7
B	34	LEU	-	expression tag	UNP Q96HY7
B	35	GLY	-	expression tag	UNP Q96HY7
B	36	THR	-	expression tag	UNP Q96HY7
B	37	GLU	-	expression tag	UNP Q96HY7
B	38	ASN	-	expression tag	UNP Q96HY7
B	39	LEU	-	expression tag	UNP Q96HY7
B	40	TYR	-	expression tag	UNP Q96HY7
B	41	PHE	-	expression tag	UNP Q96HY7
B	42	GLN	-	expression tag	UNP Q96HY7
B	43	SER	-	expression tag	UNP Q96HY7
B	44	MET	-	expression tag	UNP Q96HY7

- Molecule 2 is 1-[(2S,4S)-4-fluoro-1-[(2-methyl-1,3-thiazol-4-yl)methyl]pyrrolidin-2-yl]methanamine (three-letter code: WGD) (formula: C₁₀H₁₆FN₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	S	0	0
			15	10	1	3	1		
2	A	1	Total	C	F	N	S	0	0
			15	10	1	3	1		
2	A	1	Total	C	F	N	S	0	0
			15	10	1	3	1		
2	B	1	Total	C	F	N	S	0	0
			15	10	1	3	1		
2	B	1	Total	C	F	N	S	0	0
			15	10	1	3	1		

- Molecule 3 is THIAMINE DIPHOSPHATE (three-letter code: TPP) (formula: C₁₂H₁₉N₄O₇P₂S).



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

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

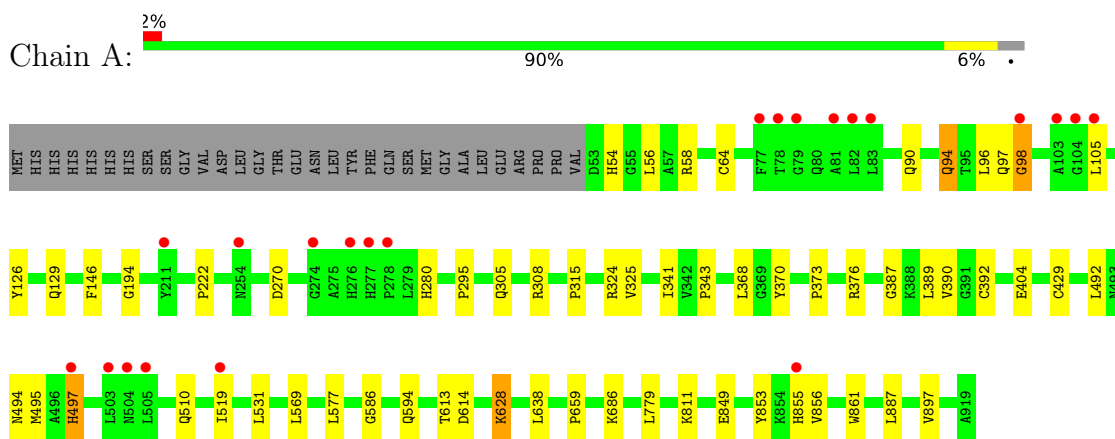
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	999	Total 999	O 999	0	0
5	B	776	Total 776	O 776	0	0

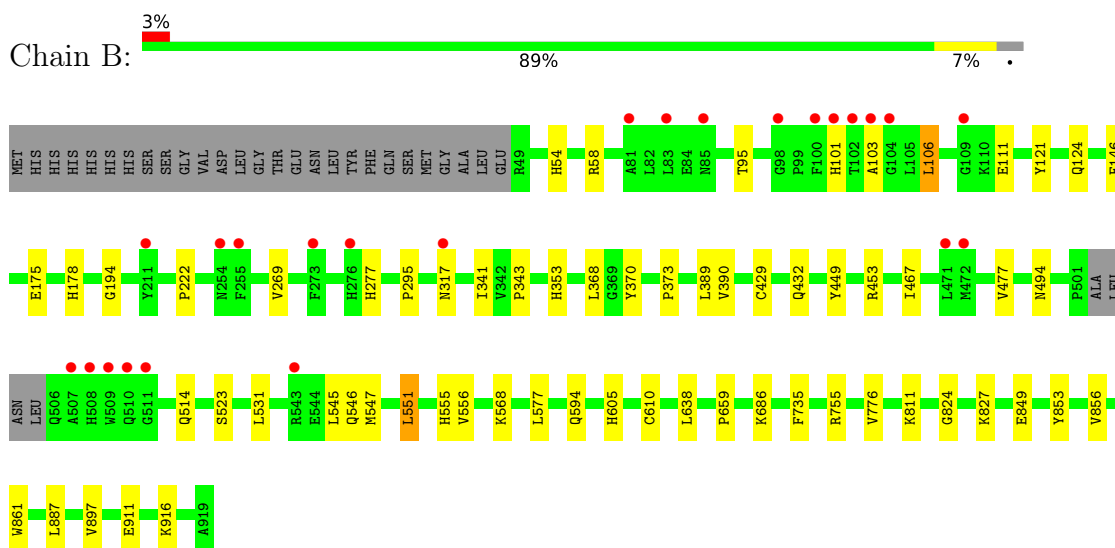
3 Residue-property plots [i](#)

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

- Molecule 1: Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial



- Molecule 1: Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	78.13Å 147.13Å 87.27Å 90.00° 102.91° 90.00°	Depositor
Resolution (Å)	85.07 – 1.67 85.07 – 1.67	Depositor EDS
% Data completeness (in resolution range)	58.7 (85.07-1.67) 58.7 (85.07-1.67)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 1.67Å)	Xtrriage
Refinement program	BUSTER 2.10.3 (20-MAY-2020)	Depositor
R, R_{free}	0.161 , 0.187 0.169 , 0.196	Depositor DCC
R_{free} test set	6392 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	16.9	Xtrriage
Anisotropy	0.098	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 48.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	15420	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TPP, WGD, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.42	0/6959	0.58	0/9439
1	B	0.41	0/6914	0.57	0/9385
All	All	0.42	0/13873	0.58	0/18824

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6775	0	6624	36	0
1	B	6740	0	6571	34	0
2	A	45	0	0	2	0
2	B	30	0	0	0	0
3	A	26	0	16	3	0
3	B	26	0	16	3	0
4	A	1	0	0	0	0
4	B	2	0	0	0	0
5	A	999	0	0	1	0
5	B	776	0	0	1	0
All	All	15420	0	13227	67	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 2.

All (67) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:HIS:CE1	1:B:95:THR:HG22	2.29	0.68
1:A:853:TYR:HA	1:A:855:HIS:CE1	2.30	0.67
1:B:824:GLY:O	1:B:827:LYS:HG2	1.96	0.66
1:A:54:HIS:HE1	1:B:95:THR:HG22	1.59	0.65
1:A:90:GLN:O	1:A:94:GLN:HG2	1.96	0.64
1:B:389:LEU:HD12	1:B:390:VAL:HG13	1.82	0.61
1:A:270:ASP:OD1	1:A:280[B]:HIS:ND1	2.34	0.61
1:A:389:LEU:HD12	1:A:390:VAL:HG13	1.82	0.60
1:A:315:PRO:HD2	2:A:1002:WGD:N3	2.19	0.58
2:A:1001:WGD:N3	5:A:1104:HOH:O	2.32	0.58
1:B:432:GLN:O	1:B:453:ARG:NH1	2.35	0.58
1:A:96:LEU:HD23	1:B:54:HIS:NE2	2.21	0.56
1:B:551:LEU:HD21	1:B:605:HIS:CE1	2.43	0.54
1:A:494:ASN:HA	1:A:497[A]:HIS:CE1	2.42	0.54
1:A:569:LEU:HD21	1:A:779:LEU:HD13	1.89	0.54
1:A:97:GLN:O	1:A:98:GLY:O	2.26	0.53
1:B:853:TYR:HB3	1:B:856:VAL:HG23	1.89	0.53
1:A:853:TYR:HB3	1:A:856:VAL:HG23	1.91	0.53
1:B:368:LEU:HD23	1:B:373:PRO:HA	1.91	0.52
1:B:545:LEU:HG	1:B:610:CYS:HB2	1.90	0.52
1:B:853:TYR:HB3	1:B:856:VAL:CG2	2.40	0.52
1:A:494:ASN:ND2	1:A:497[B]:HIS:CD2	2.78	0.52
1:A:586:GLY:HA2	1:A:628:LYS:HG3	1.92	0.51
1:B:101:HIS:O	1:B:111:GLU:O	2.28	0.51
1:A:376:ARG:NH1	1:B:353:HIS:HD2	2.10	0.50
1:A:194:GLY:O	1:A:429:CYS:HB2	2.12	0.49
1:B:194:GLY:O	1:B:429:CYS:HB2	2.12	0.49
3:A:1004:TPP:HN42	3:A:1004:TPP:H2	1.77	0.49
1:A:594:GLN:OE1	3:B:1003:TPP:H6'	2.13	0.48
1:B:547:MET:SD	1:B:556:VAL:HG21	2.53	0.48
1:A:387:GLY:O	1:A:392[B]:CYS:HB2	2.14	0.48
1:A:64:CYS:HG	1:A:126:TYR:HH	1.59	0.47
1:A:343:PRO:HB3	1:A:389:LEU:HD21	1.97	0.47
1:A:492:LEU:HD12	1:A:495:MET:HE2	1.96	0.47
3:A:1004:TPP:HN42	3:A:1004:TPP:C2	2.28	0.47
1:A:853:TYR:HB3	1:A:856:VAL:CG2	2.45	0.47
1:A:531:LEU:HD22	1:A:577:LEU:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:735:PHE:CE2	1:B:755:ARG:NH2	2.84	0.45
1:B:551:LEU:HD13	1:B:555:HIS:HB3	1.97	0.45
1:A:368:LEU:HD23	1:A:373:PRO:HA	1.98	0.45
1:B:449:TYR:HD2	1:B:453:ARG:NH1	2.15	0.45
1:A:897:VAL:HG11	1:B:686:LYS:HG3	1.98	0.44
1:A:96:LEU:HD23	1:B:54:HIS:CE1	2.53	0.44
1:B:343:PRO:HB3	1:B:389:LEU:HD21	1.98	0.44
3:B:1003:TPP:HN42	3:B:1003:TPP:H2	1.82	0.44
3:A:1004:TPP:H6'	1:B:594:GLN:OE1	2.18	0.43
1:B:175:GLU:OE2	1:B:178[B]:HIS:HD2	2.02	0.43
1:B:531:LEU:HD22	1:B:577:LEU:HB3	2.00	0.43
1:B:54:HIS:O	1:B:58:ARG:HG3	2.19	0.43
1:B:106:LEU:HG	1:B:121:TYR:CE2	2.54	0.42
1:A:376:ARG:NH1	1:B:353:HIS:CD2	2.87	0.42
1:A:861:TRP:HB2	1:A:887:LEU:HD13	2.01	0.42
1:B:467:ILE:HD11	1:B:477:VAL:HG21	2.01	0.42
1:A:54:HIS:O	1:A:58:ARG:HG3	2.19	0.42
1:A:129:GLN:HB2	1:A:404:GLU:HG3	2.02	0.41
1:A:308:ARG:O	1:A:324:ARG:NH2	2.51	0.41
1:A:295:PRO:HG3	1:A:341:ILE:HD11	2.03	0.41
1:A:613:THR:O	1:A:614:ASP:HB2	2.20	0.41
1:B:295:PRO:HG3	1:B:341:ILE:HD11	2.03	0.41
1:A:56:LEU:HD23	1:A:105:LEU:HD12	2.02	0.41
1:B:861:TRP:HB2	1:B:887:LEU:HD13	2.03	0.41
1:A:686:LYS:HG3	1:B:897:VAL:HG11	2.01	0.41
3:B:1003:TPP:HN42	3:B:1003:TPP:C2	2.34	0.41
1:B:514:GLN:NE2	5:B:1138:HOH:O	2.55	0.40
1:B:568:LYS:HA	1:B:776:VAL:HB	2.04	0.40
1:A:305:GLN:HG2	1:A:325:VAL:HB	2.03	0.40
1:B:916:LYS:HE3	1:B:916:LYS:HB2	1.83	0.40

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	870/898 (97%)	838 (96%)	28 (3%)	4 (0%)	29	12
1	B	865/898 (96%)	832 (96%)	29 (3%)	4 (0%)	29	12
All	All	1735/1796 (97%)	1670 (96%)	57 (3%)	8 (0%)	29	12

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	98	GLY
1	A	222	PRO
1	A	510	GLN
1	B	222	PRO
1	B	103	ALA
1	B	277	HIS
1	A	659	PRO
1	B	659	PRO

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	729/776 (94%)	719 (99%)	10 (1%)	67	51
1	B	723/776 (93%)	709 (98%)	14 (2%)	57	38
All	All	1452/1552 (94%)	1428 (98%)	24 (2%)	62	43

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	GLN
1	A	146	PHE
1	A	370	TYR
1	A	497[A]	HIS
1	A	497[B]	HIS

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Mol	Chain	Res	Type
1	A	519	ILE
1	A	628	LYS
1	A	638	LEU
1	A	811	LYS
1	A	849	GLU
1	B	106	LEU
1	B	124	GLN
1	B	146	PHE
1	B	269	VAL
1	B	317	ASN
1	B	370	TYR
1	B	494	ASN
1	B	523	SER
1	B	546	GLN
1	B	551	LEU
1	B	638	LEU
1	B	811	LYS
1	B	849	GLU
1	B	911	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	129	GLN
1	A	317	ASN
1	A	418	GLN
1	A	494	ASN
1	B	280	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 10 ligands modelled in this entry, 3 are monoatomic - leaving 7 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
2	WGD	A	1003	-	12,16,16	0.52	0	12,22,22	1.14	2 (16%)
2	WGD	A	1001	-	12,16,16	0.52	0	12,22,22	1.24	2 (16%)
3	TPP	A	1004	4	22,27,27	0.60	0	29,40,40	0.83	1 (3%)
2	WGD	B	1002	-	12,16,16	0.54	0	12,22,22	1.09	1 (8%)
3	TPP	B	1003	4	22,27,27	0.65	0	29,40,40	0.88	1 (3%)
2	WGD	B	1001	-	12,16,16	0.48	0	12,22,22	1.04	1 (8%)
2	WGD	A	1002	-	12,16,16	0.48	0	12,22,22	1.21	1 (8%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	WGD	A	1003	-	1/1/3/3	4/6/18/18	0/2/2/2
2	WGD	A	1001	-	-	1/6/18/18	0/2/2/2
3	TPP	A	1004	4	-	4/16/17/17	0/2/2/2
2	WGD	B	1002	-	1/1/3/3	1/6/18/18	0/2/2/2
3	TPP	B	1003	4	-	2/16/17/17	0/2/2/2
2	WGD	B	1001	-	-	2/6/18/18	0/2/2/2
2	WGD	A	1002	-	1/1/3/3	2/6/18/18	0/2/2/2

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1003	TPP	C7'-N3-C2	-2.97	119.98	125.35
2	A	1001	WGD	C4-C3-C10	-2.81	125.39	129.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1004	TPP	C7'-N3-C2	-2.63	120.60	125.35
2	A	1002	WGD	C5-N2-C8	2.44	109.73	105.34
2	B	1001	WGD	C4-C3-C10	-2.43	125.96	129.62
2	A	1001	WGD	C4-N2-C5	2.42	116.41	113.16
2	A	1003	WGD	C4-C3-C10	-2.28	126.19	129.62
2	B	1002	WGD	C3-C4-N2	2.06	116.97	112.30
2	A	1003	WGD	C5-N2-C8	2.00	108.94	105.34

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1002	WGD	C8
2	A	1003	WGD	C6
2	B	1002	WGD	C6

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1002	WGD	C3-C4-N2-C5
2	A	1002	WGD	C3-C4-N2-C8
2	A	1003	WGD	C10-C3-C4-N2
2	A	1003	WGD	C3-C4-N2-C5
2	A	1003	WGD	C3-C4-N2-C8
2	B	1001	WGD	N1-C3-C4-N2
2	B	1001	WGD	C10-C3-C4-N2
3	A	1004	TPP	PA-O3A-PB-O2B
3	A	1004	TPP	PA-O3A-PB-O3B
2	B	1002	WGD	C3-C4-N2-C8
2	A	1001	WGD	C10-C3-C4-N2
3	A	1004	TPP	C4-C5-C6-C7
3	B	1003	TPP	C4-C5-C6-C7
2	A	1003	WGD	N1-C3-C4-N2
3	B	1003	TPP	PA-O3A-PB-O3B
3	A	1004	TPP	PA-O3A-PB-O1B

There are no ring outliers.

4 monomers are involved in 8 short contacts:

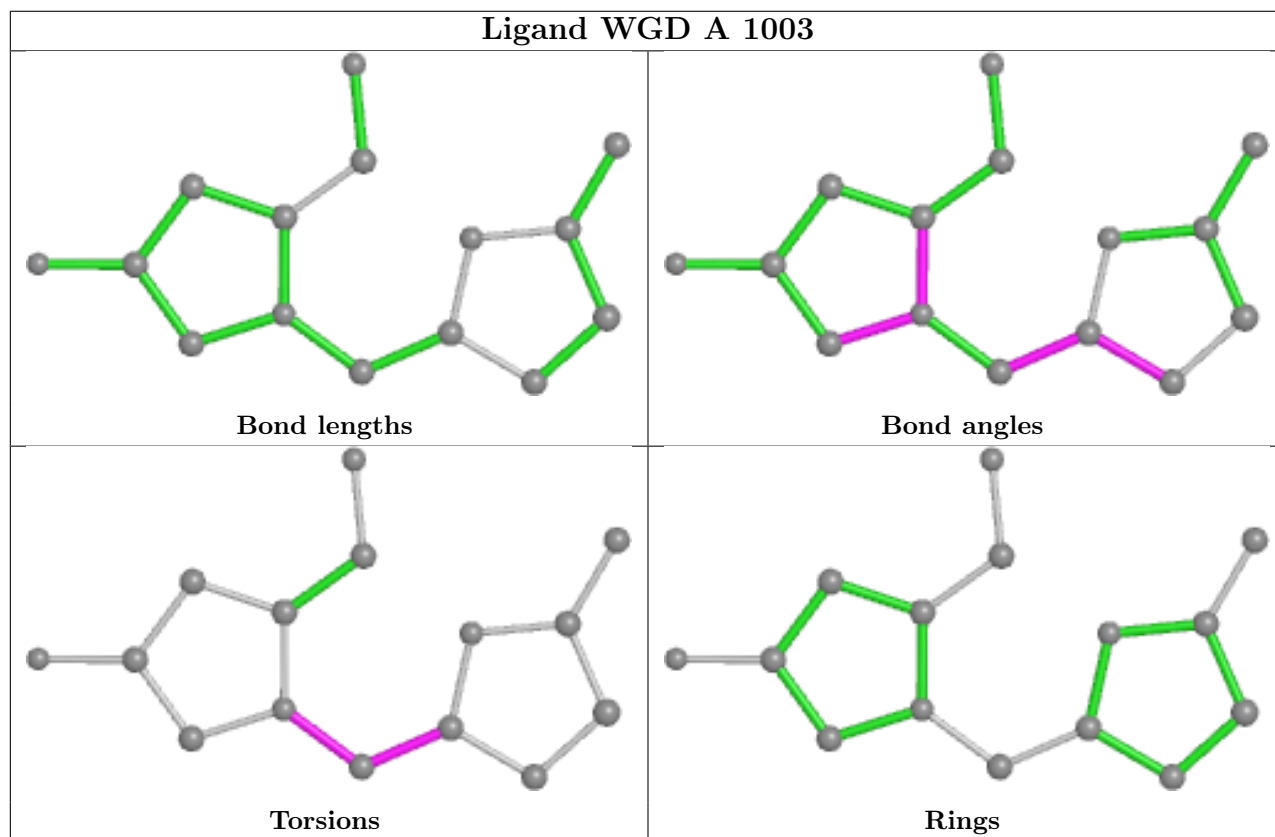
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	WGD	1	0
3	A	1004	TPP	3	0

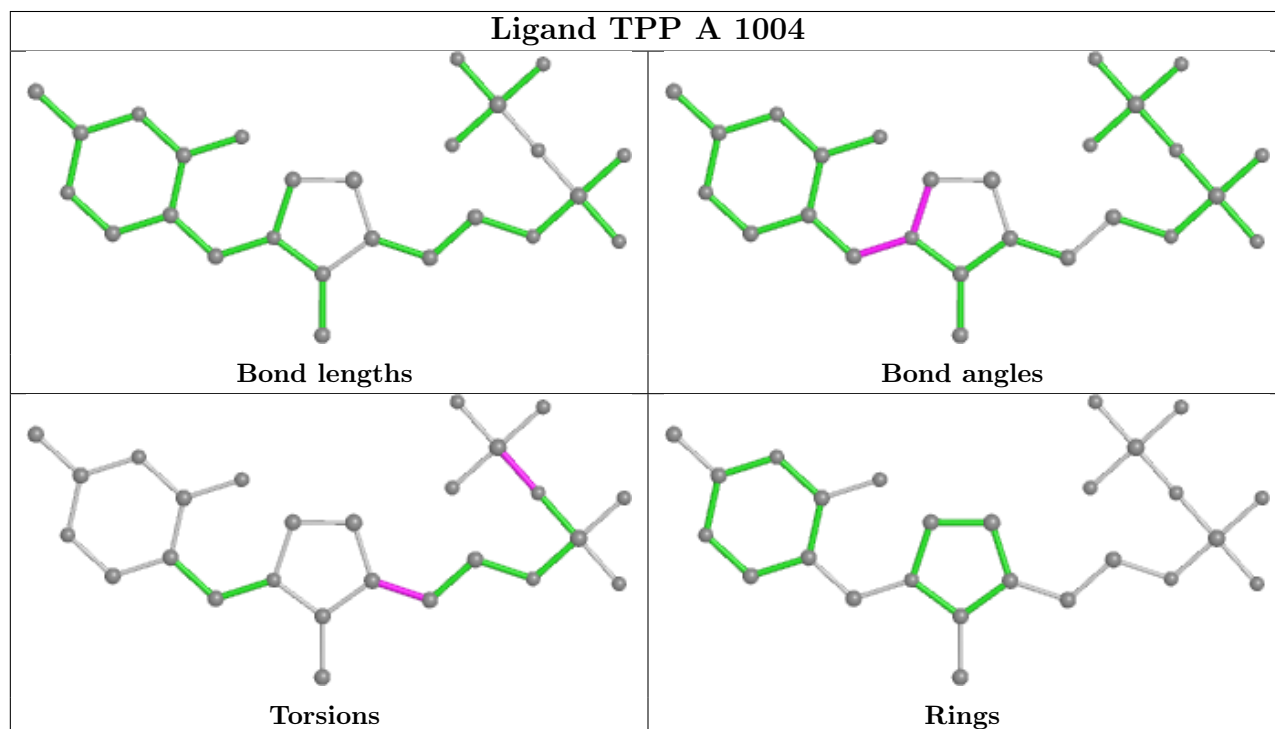
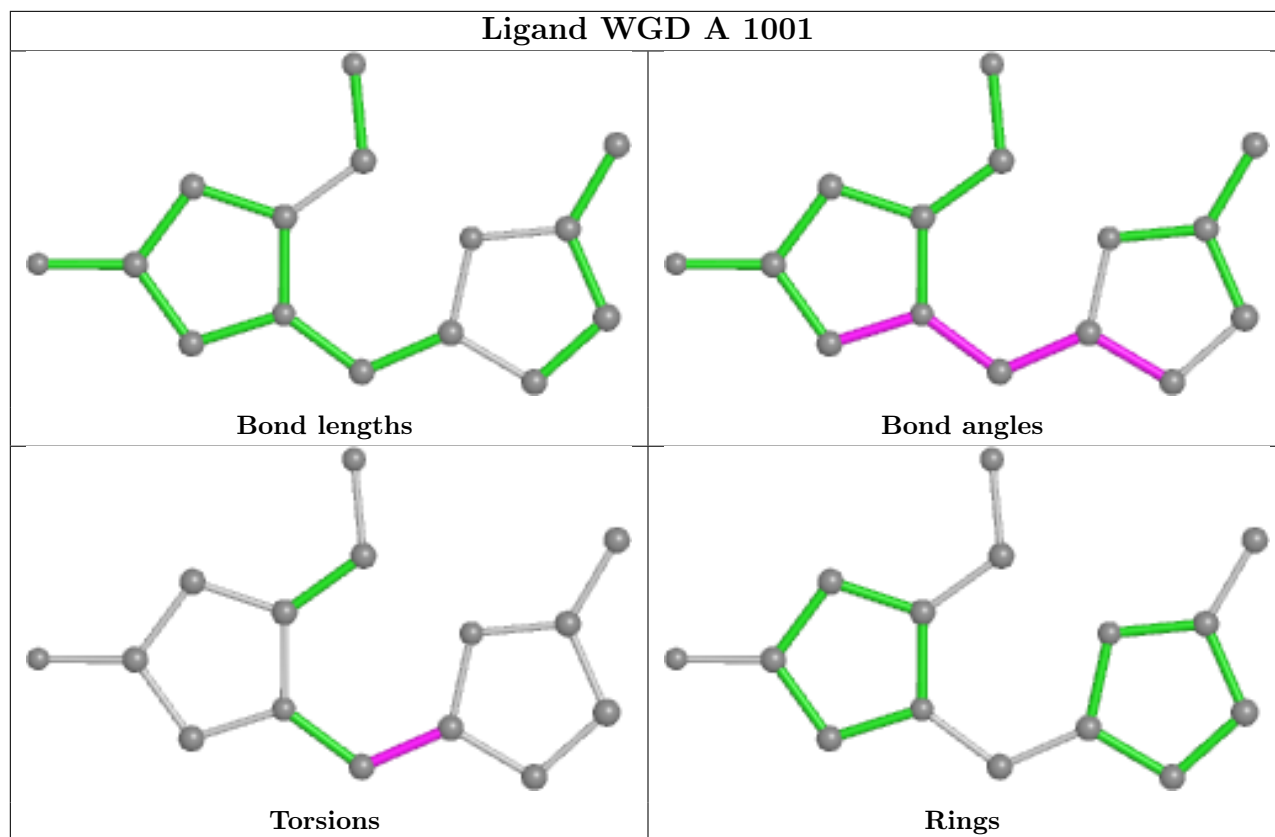
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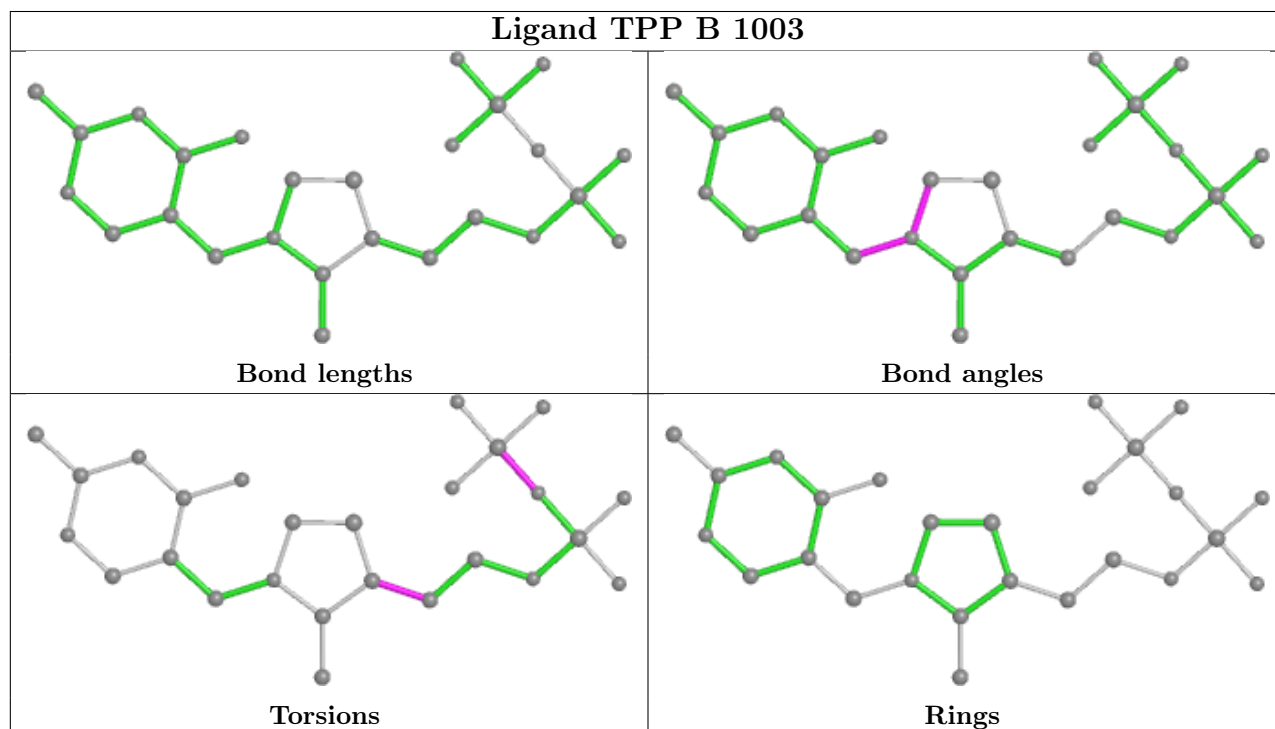
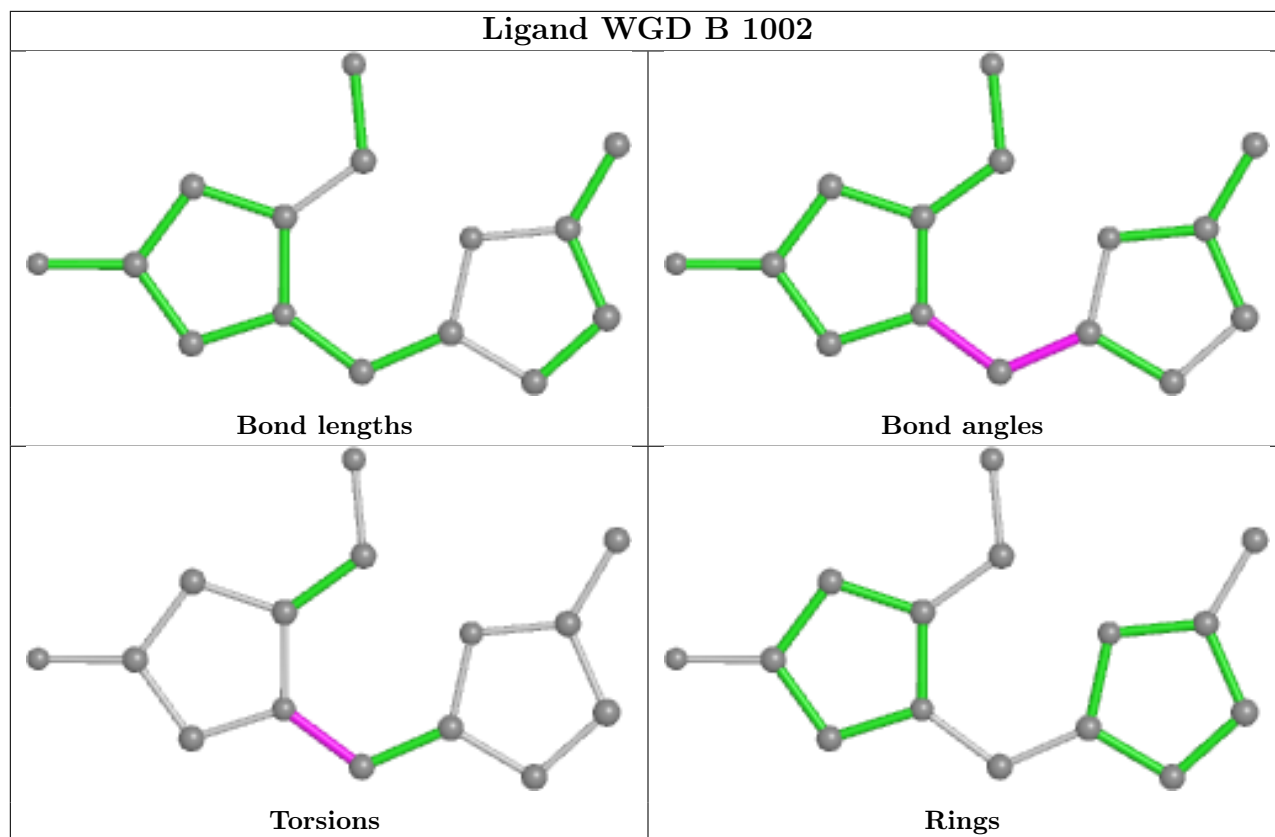
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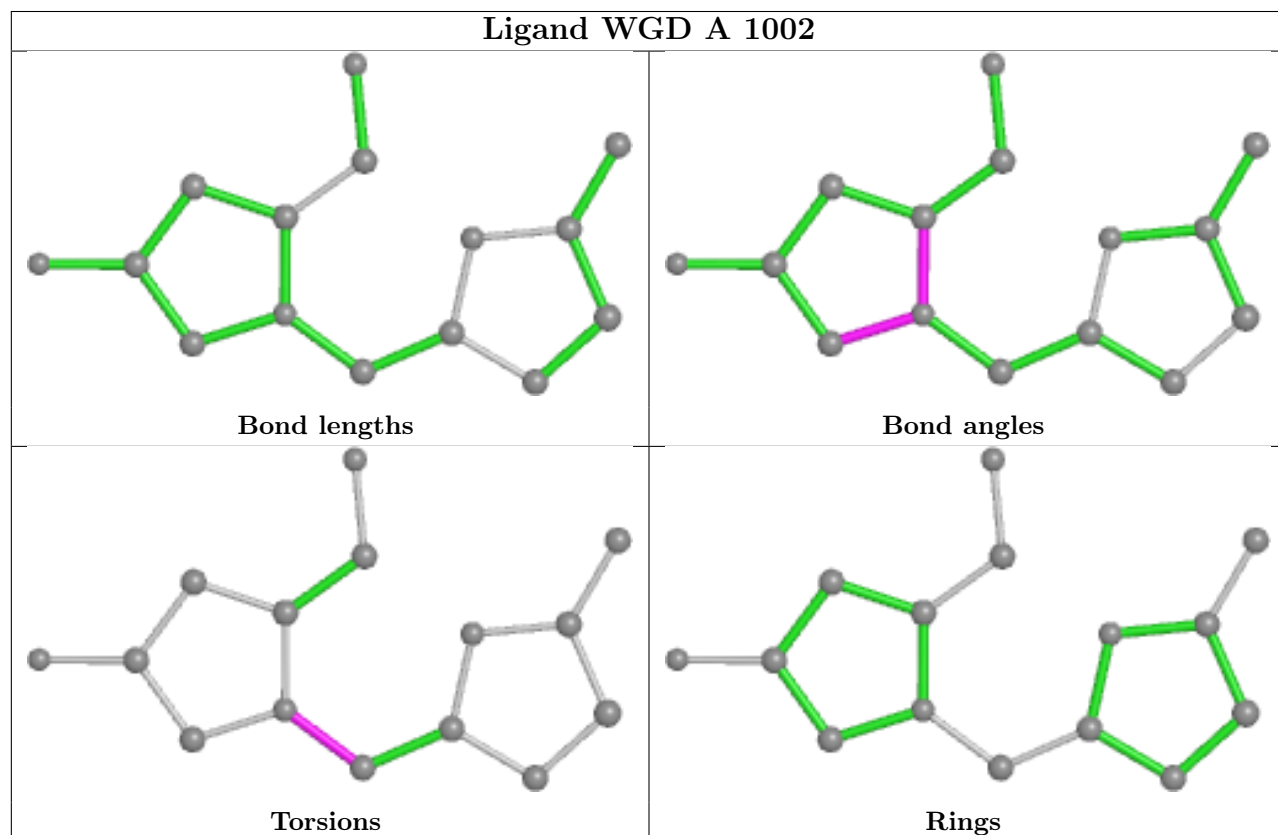
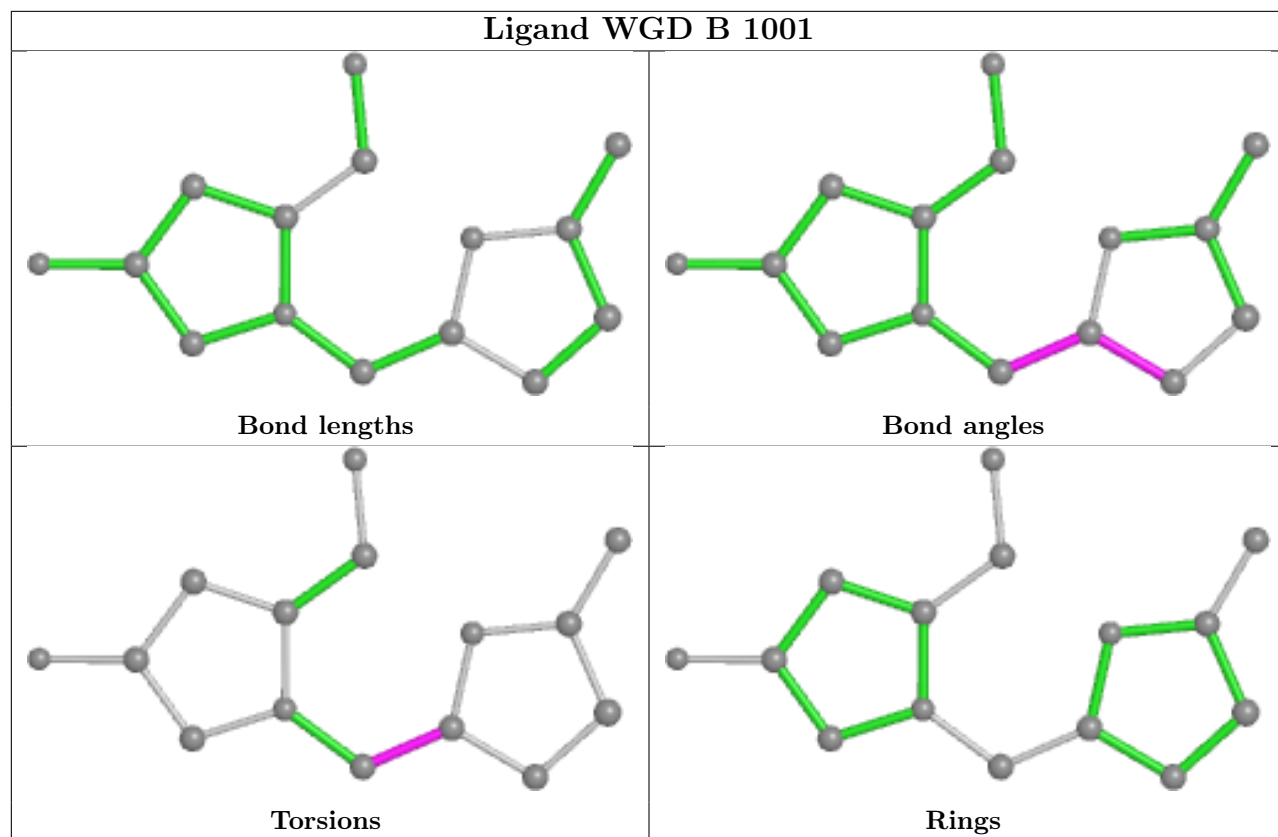
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1003	TPP	3	0
2	A	1002	WGD	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	867/898 (96%)	-0.38	22 (2%) 57 60	8, 19, 42, 58	0
1	B	867/898 (96%)	-0.29	24 (2%) 53 55	9, 23, 51, 72	0
All	All	1734/1796 (96%)	-0.34	46 (2%) 54 57	8, 20, 49, 72	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	82	LEU	13.1
1	A	104	GLY	7.3
1	A	276	HIS	6.2
1	A	505	LEU	5.6
1	A	83	LEU	5.6
1	A	103	ALA	5.6
1	A	98	GLY	5.2
1	A	81	ALA	5.1
1	A	503	LEU	4.9
1	B	276	HIS	4.5
1	B	101	HIS	4.4
1	B	103	ALA	4.0
1	B	98	GLY	3.9
1	A	277	HIS	3.7
1	B	508	HIS	3.7
1	B	109	GLY	3.6
1	B	509	TRP	3.6
1	B	511	GLY	3.4
1	A	278	PRO	3.2
1	B	211	TYR	3.2
1	A	79	GLY	3.2
1	A	105	LEU	3.2
1	B	83	LEU	3.2
1	B	510	GLN	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	317	ASN	3.0
1	A	78	THR	2.9
1	B	102	THR	2.9
1	B	81	ALA	2.6
1	A	504	ASN	2.6
1	A	211	TYR	2.5
1	B	254	ASN	2.5
1	B	471	LEU	2.5
1	A	77	PHE	2.4
1	B	507	ALA	2.3
1	B	543	ARG	2.3
1	B	85	ASN	2.3
1	B	273	PHE	2.3
1	A	519	ILE	2.2
1	B	255	PHE	2.2
1	A	497[A]	HIS	2.2
1	A	274	GLY	2.2
1	B	472	MET	2.1
1	B	104	GLY	2.1
1	A	855	HIS	2.1
1	B	100	PHE	2.0
1	A	254	ASN	2.0

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

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

6.3 Carbohydrates [\(i\)](#)

There are no 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.

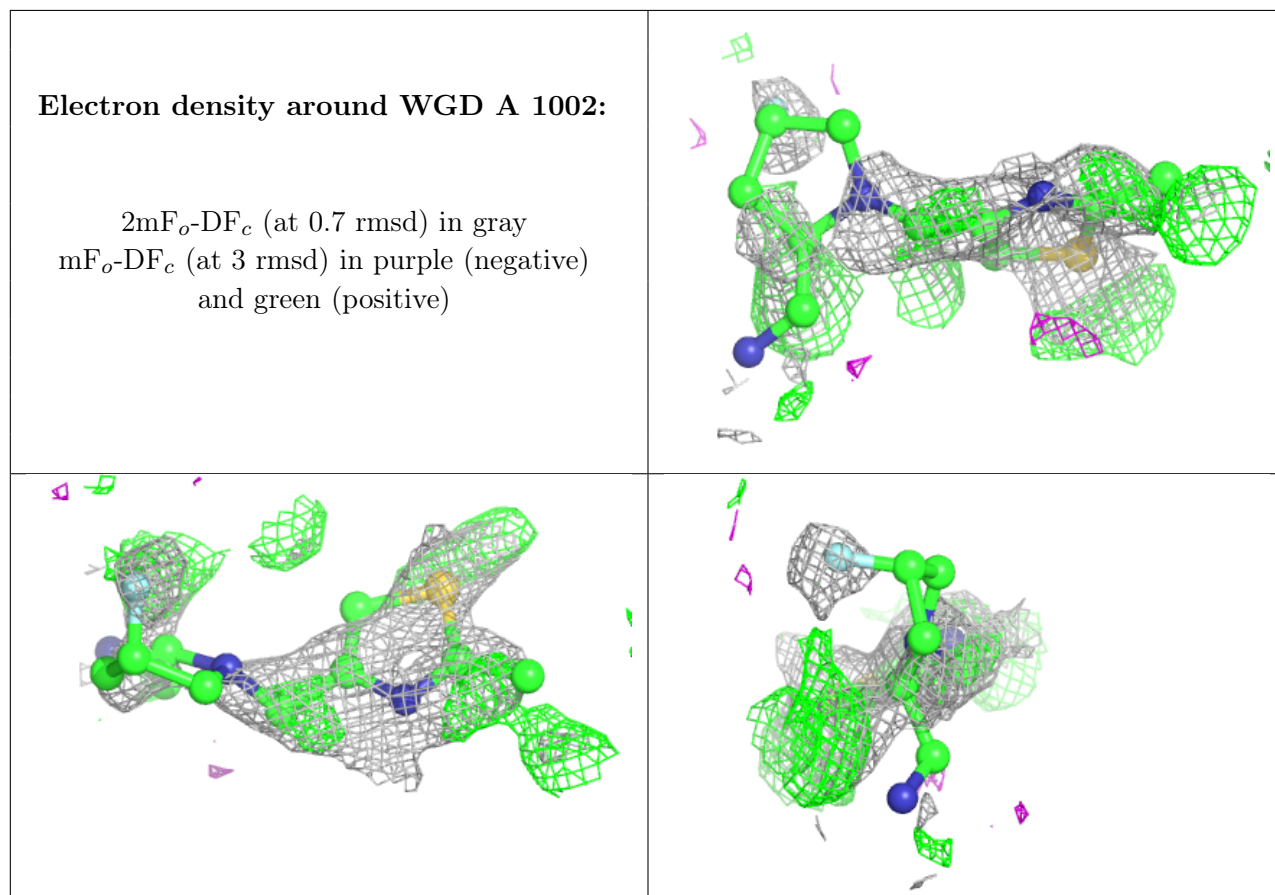
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	WGD	A	1002	15/15	0.61	0.36	56,56,56,57	15

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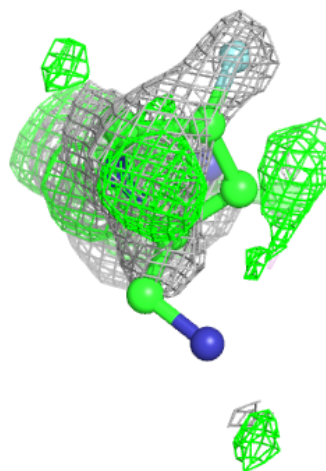
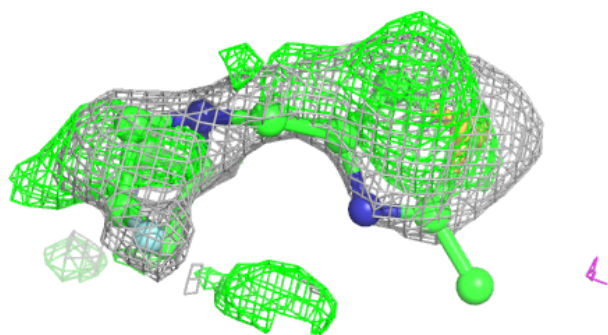
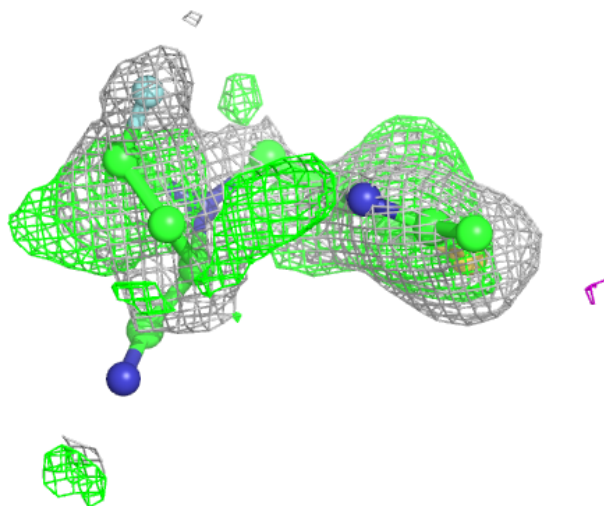
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	WGD	B	1002	15/15	0.80	0.37	33,35,37,38	15
2	WGD	B	1001	15/15	0.83	0.17	30,32,33,33	15
2	WGD	A	1003	15/15	0.83	0.21	34,35,37,38	15
2	WGD	A	1001	15/15	0.93	0.16	16,17,18,19	15
3	TPP	B	1003	26/26	0.98	0.07	12,14,15,16	0
3	TPP	A	1004	26/26	0.99	0.06	10,12,13,14	0
4	MG	A	1005	1/1	0.99	0.04	13,13,13,13	0
4	MG	B	1004	1/1	0.99	0.04	15,15,15,15	0
4	MG	B	1005	1/1	1.00	0.04	10,10,10,10	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.



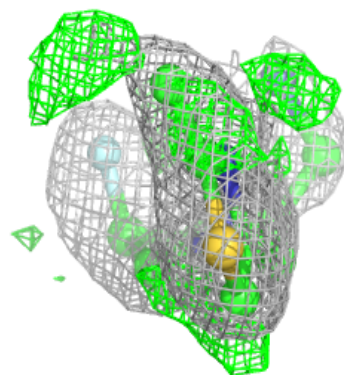
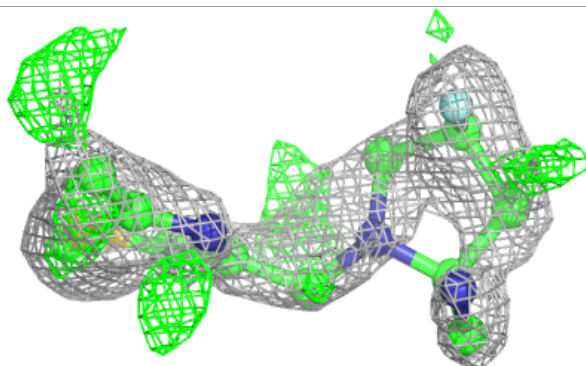
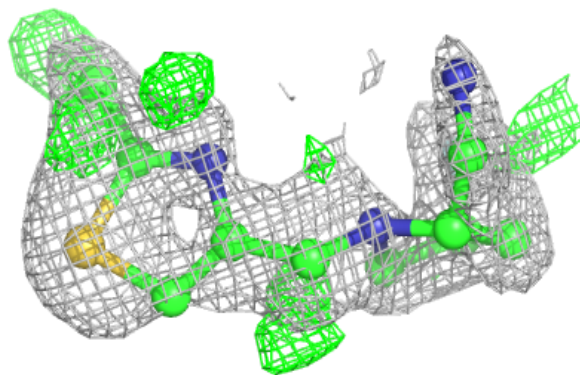
Electron density around WGD B 1002:

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



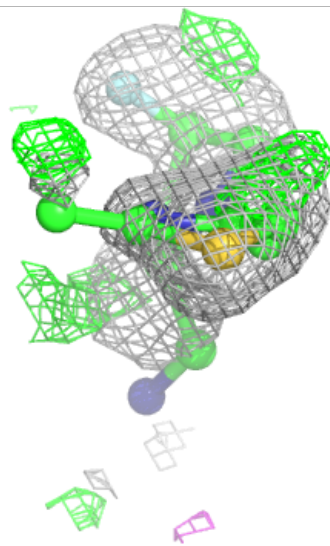
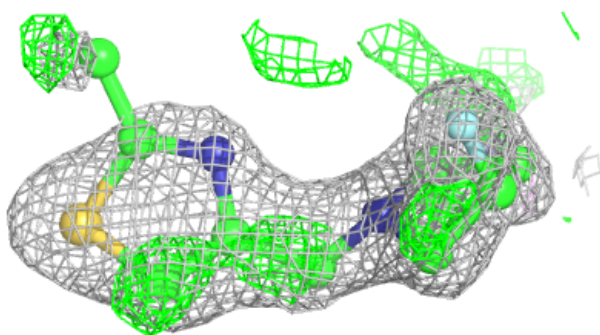
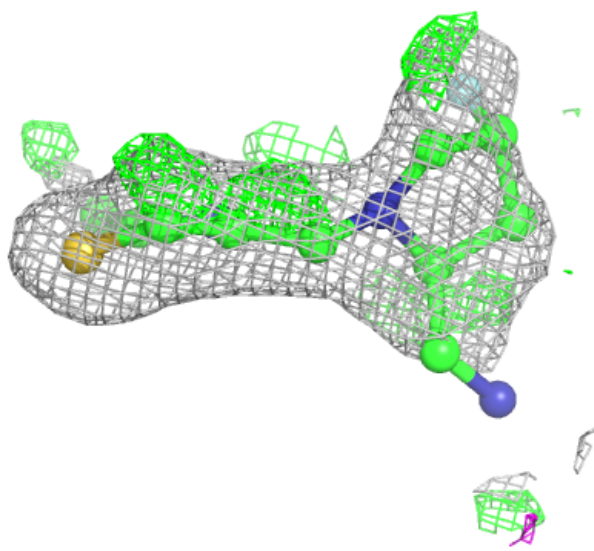
Electron density around WGD B 1001:

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



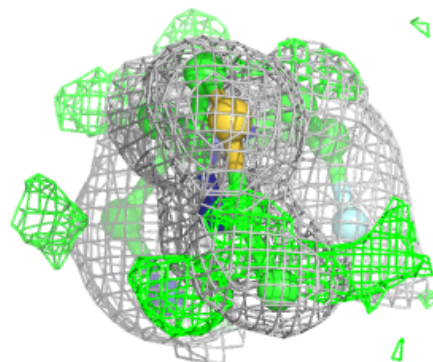
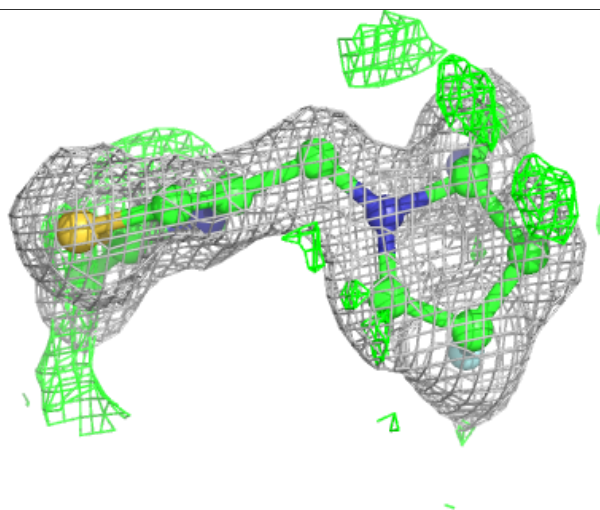
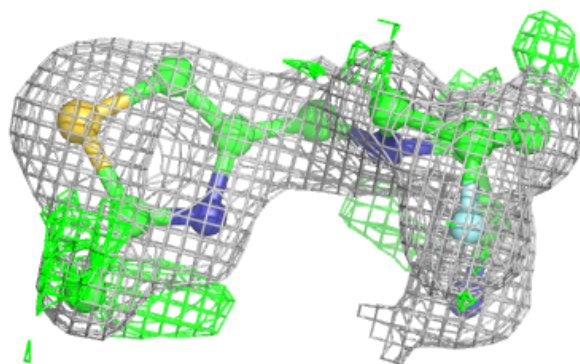
Electron density around WGD A 1003:

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



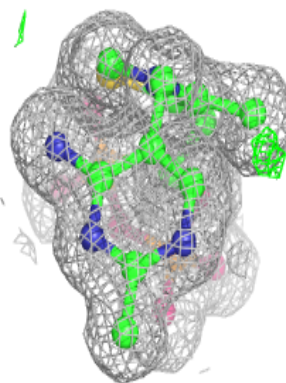
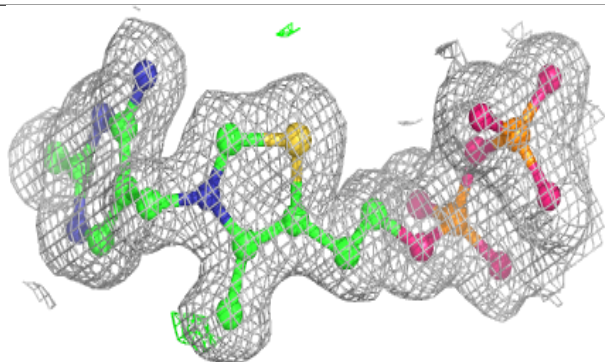
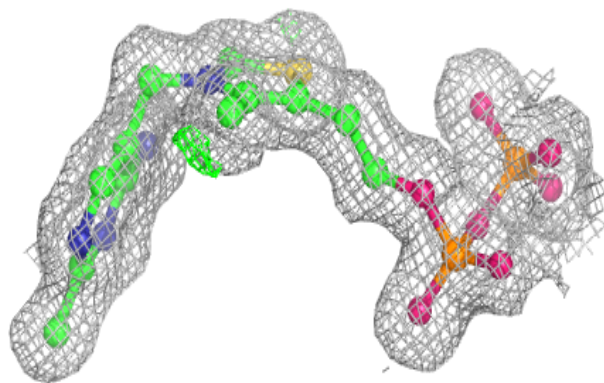
Electron density around WGD A 1001:

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

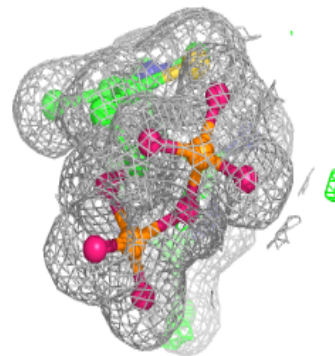
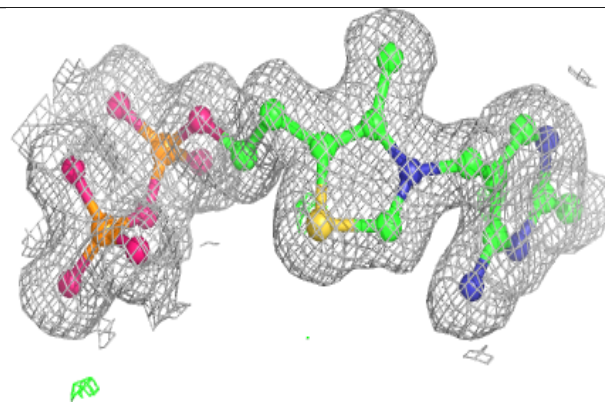
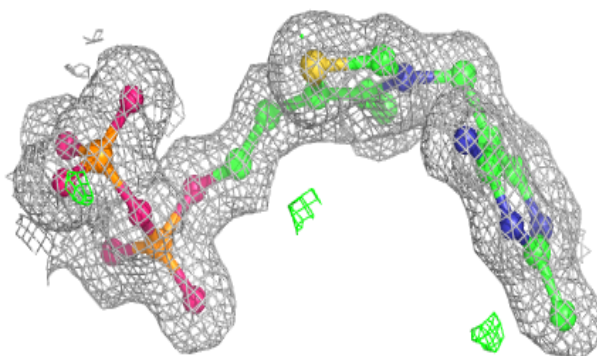


Electron density around TPP B 1003:

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

**Electron density around TPP A 1004:**

$2mF_o-DF_c$ (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.