



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 15, 2020 – 02:32 am BST

PDB ID : 3KOW
Title : Crystal Structure of ornithine 4,5 aminomutase backsoaked complex
Authors : Wolthers, K.R.; Levy, C.W.; Scrutton, N.S.; Leys, D.
Deposited on : 2009-11-14
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

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

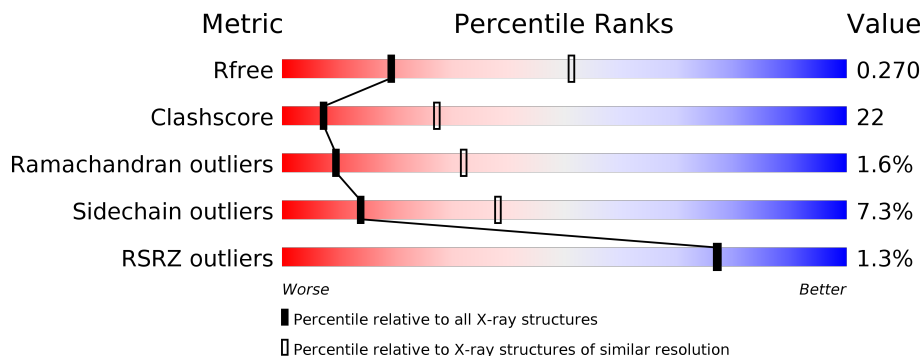
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	763	
1	B	763	
1	C	763	
1	D	763	
2	E	121	
2	F	121	

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Mol	Chain	Length	Quality of chain
2	G	121	
2	H	121	

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
3	B12	A	1801	X	-	X	-
3	B12	B	1801	X	-	X	-
3	B12	C	1801	X	-	X	-
3	B12	D	1801	X	-	-	-
5	5AD	A	1500	X	-	-	-
5	5AD	C	1500	X	-	-	-
5	5AD	D	1500	X	-	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 26527 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 D-ornithine aminomutase E component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	727	Total 5646	C 3558	N 980	O 1074	S 34	0	0	0
1	B	728	Total 5672	C 3579	N 984	O 1075	S 34	0	0	0
1	C	727	Total 5649	C 3567	N 980	O 1068	S 34	0	0	0
1	D	727	Total 5659	C 3572	N 983	O 1070	S 34	0	0	0

There are 104 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ILE	SEE REMARK 999	UNP Q8VPJ5
A	?	-	ASP	SEE REMARK 999	UNP Q8VPJ5
A	?	-	GLY	SEE REMARK 999	UNP Q8VPJ5
A	744	SER	-	EXPRESSION TAG	UNP Q8VPJ5
A	745	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
A	746	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
A	747	PRO	-	EXPRESSION TAG	UNP Q8VPJ5
A	748	ASN	-	EXPRESSION TAG	UNP Q8VPJ5
A	749	SER	-	EXPRESSION TAG	UNP Q8VPJ5
A	750	SER	-	EXPRESSION TAG	UNP Q8VPJ5
A	751	SER	-	EXPRESSION TAG	UNP Q8VPJ5
A	752	VAL	-	EXPRESSION TAG	UNP Q8VPJ5
A	753	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
A	754	LYS	-	EXPRESSION TAG	UNP Q8VPJ5
A	755	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
A	756	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
A	757	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
A	758	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
A	759	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
A	760	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
A	761	HIS	-	EXPRESSION TAG	UNP Q8VPJ5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	762	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
A	763	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
A	764	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
A	765	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
A	766	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	?	-	ILE	SEE REMARK 999	UNP Q8VPJ5
B	?	-	ASP	SEE REMARK 999	UNP Q8VPJ5
B	?	-	GLY	SEE REMARK 999	UNP Q8VPJ5
B	744	SER	-	EXPRESSION TAG	UNP Q8VPJ5
B	745	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
B	746	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
B	747	PRO	-	EXPRESSION TAG	UNP Q8VPJ5
B	748	ASN	-	EXPRESSION TAG	UNP Q8VPJ5
B	749	SER	-	EXPRESSION TAG	UNP Q8VPJ5
B	750	SER	-	EXPRESSION TAG	UNP Q8VPJ5
B	751	SER	-	EXPRESSION TAG	UNP Q8VPJ5
B	752	VAL	-	EXPRESSION TAG	UNP Q8VPJ5
B	753	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
B	754	LYS	-	EXPRESSION TAG	UNP Q8VPJ5
B	755	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
B	756	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
B	757	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
B	758	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
B	759	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
B	760	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
B	761	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	762	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	763	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	764	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	765	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
B	766	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	?	-	ILE	SEE REMARK 999	UNP Q8VPJ5
C	?	-	ASP	SEE REMARK 999	UNP Q8VPJ5
C	?	-	GLY	SEE REMARK 999	UNP Q8VPJ5
C	744	SER	-	EXPRESSION TAG	UNP Q8VPJ5
C	745	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
C	746	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
C	747	PRO	-	EXPRESSION TAG	UNP Q8VPJ5
C	748	ASN	-	EXPRESSION TAG	UNP Q8VPJ5
C	749	SER	-	EXPRESSION TAG	UNP Q8VPJ5
C	750	SER	-	EXPRESSION TAG	UNP Q8VPJ5
C	751	SER	-	EXPRESSION TAG	UNP Q8VPJ5

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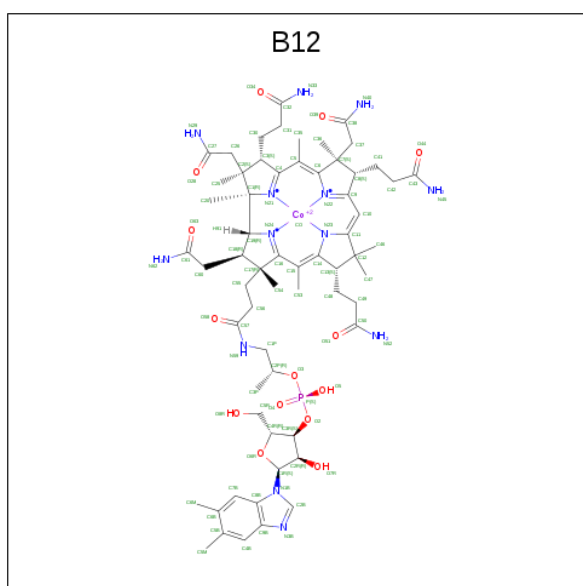
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Chain	Residue	Modelled	Actual	Comment	Reference
C	752	VAL	-	EXPRESSION TAG	UNP Q8VPJ5
C	753	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
C	754	LYS	-	EXPRESSION TAG	UNP Q8VPJ5
C	755	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
C	756	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
C	757	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
C	758	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
C	759	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
C	760	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
C	761	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	762	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	763	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	764	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	765	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
C	766	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	?	-	ILE	SEE REMARK 999	UNP Q8VPJ5
D	?	-	ASP	SEE REMARK 999	UNP Q8VPJ5
D	?	-	GLY	SEE REMARK 999	UNP Q8VPJ5
D	744	SER	-	EXPRESSION TAG	UNP Q8VPJ5
D	745	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
D	746	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
D	747	PRO	-	EXPRESSION TAG	UNP Q8VPJ5
D	748	ASN	-	EXPRESSION TAG	UNP Q8VPJ5
D	749	SER	-	EXPRESSION TAG	UNP Q8VPJ5
D	750	SER	-	EXPRESSION TAG	UNP Q8VPJ5
D	751	SER	-	EXPRESSION TAG	UNP Q8VPJ5
D	752	VAL	-	EXPRESSION TAG	UNP Q8VPJ5
D	753	ASP	-	EXPRESSION TAG	UNP Q8VPJ5
D	754	LYS	-	EXPRESSION TAG	UNP Q8VPJ5
D	755	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
D	756	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
D	757	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
D	758	ALA	-	EXPRESSION TAG	UNP Q8VPJ5
D	759	LEU	-	EXPRESSION TAG	UNP Q8VPJ5
D	760	GLU	-	EXPRESSION TAG	UNP Q8VPJ5
D	761	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	762	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	763	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	764	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	765	HIS	-	EXPRESSION TAG	UNP Q8VPJ5
D	766	HIS	-	EXPRESSION TAG	UNP Q8VPJ5

- Molecule 2 is a protein called D-ornithine aminomutase S component.

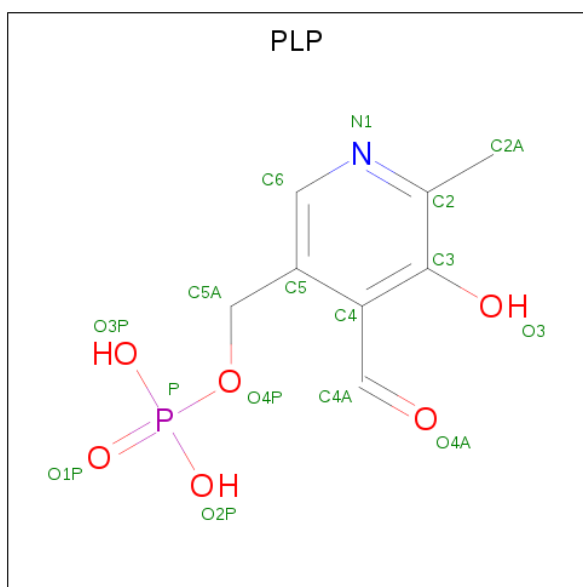
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	E	109	Total 855	538	152	161	4	0	0	0
2	F	109	Total 858	539	152	163	4	0	0	0
2	G	109	Total 855	538	152	161	4	0	0	0
2	H	109	Total 855	538	152	161	4	0	0	0

- Molecule 3 is COBALAMIN (three-letter code: B12) (formula: $C_{62}H_{89}CoN_{13}O_{14}P$).



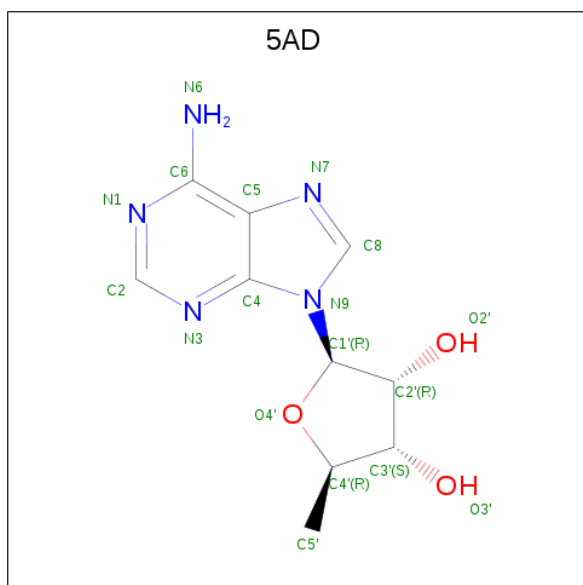
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	Co	N	O			P
3	A	1	Total 91	62	1	13	14	1	0	0
3	B	1	Total 91	62	1	13	14	1	0	0
3	C	1	Total 91	62	1	13	14	1	0	0
3	D	1	Total 91	62	1	13	14	1	0	0

- Molecule 4 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: $C_8H_{10}NO_6P$).

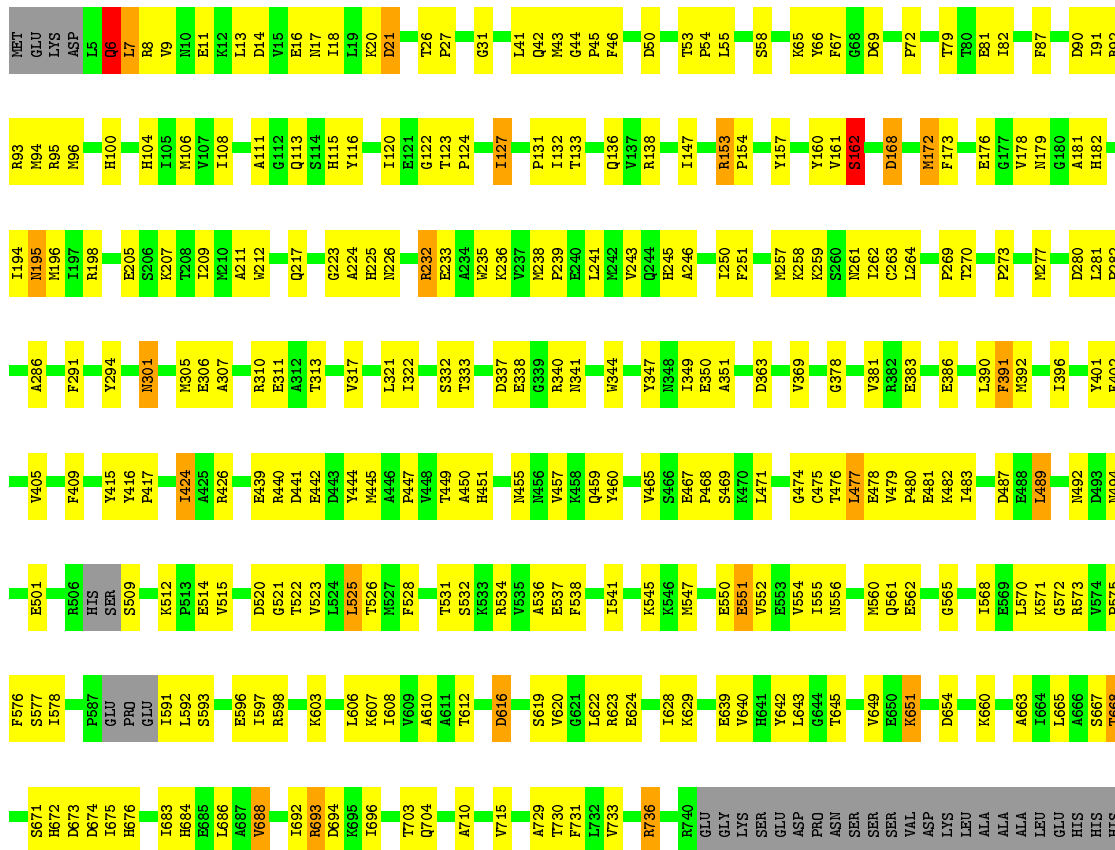


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
4	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
4	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
4	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 5 is 5'-DEOXYADENOSINE (three-letter code: 5AD) (formula: $C_{10}H_{13}N_5O_3$).

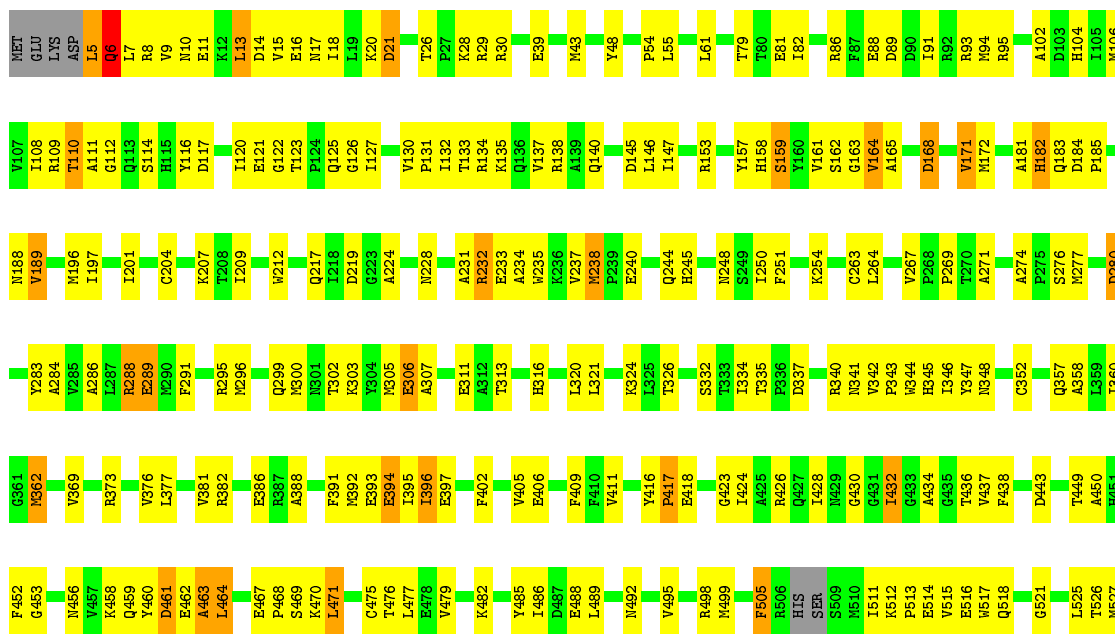


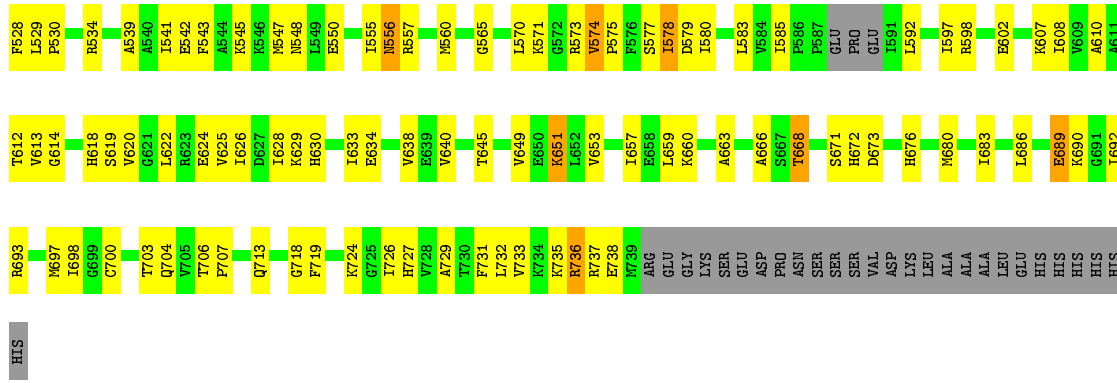
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total 18	C 10	N 5	O 3	0	0
5	C	1	Total 18	C 10	N 5	O 3	0	0
5	D	1	Total 18	C 10	N 5	O 3	0	0



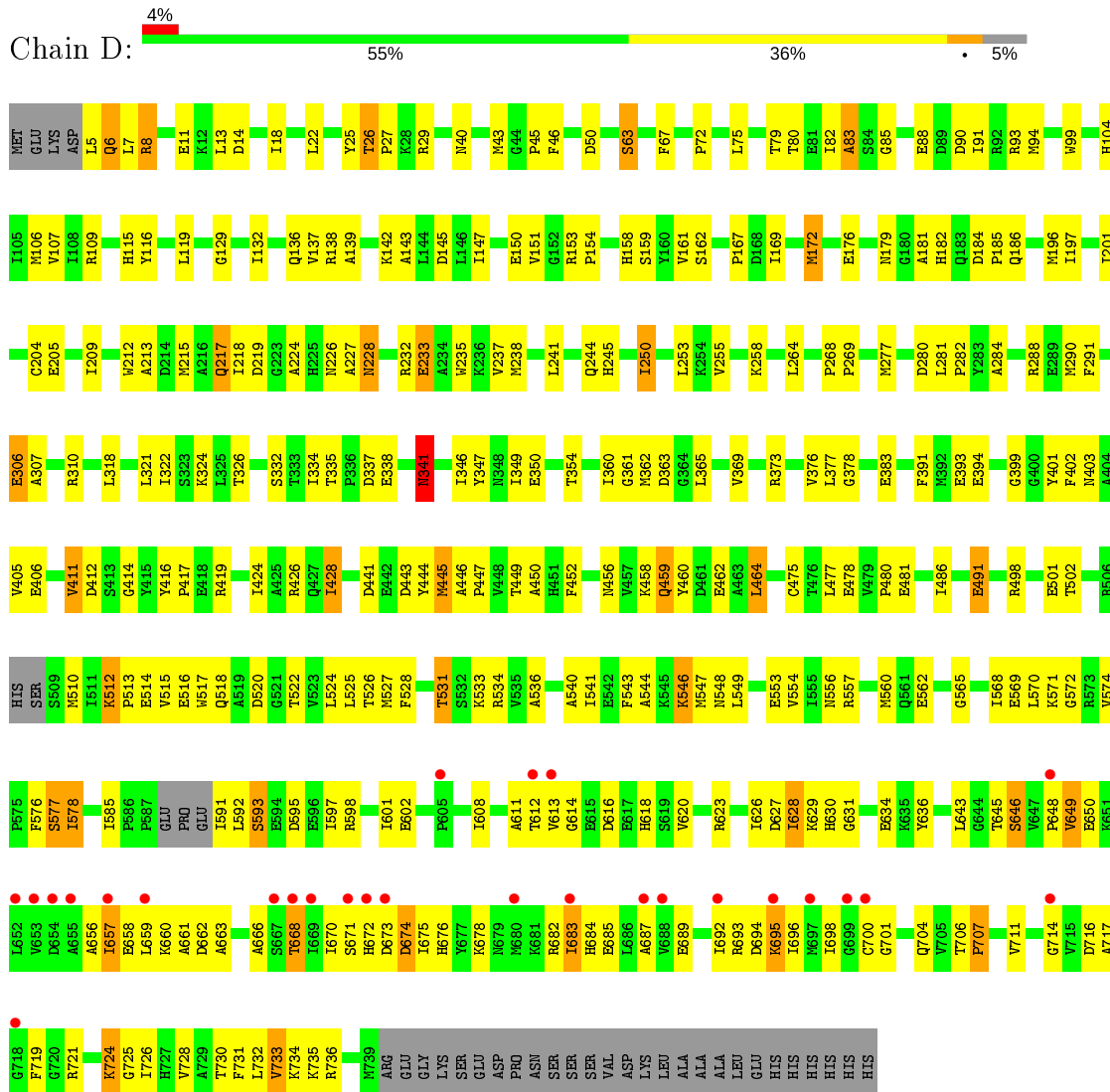
HIS
HIS
HIS

• Molecule 1: D-ornithine aminomutase E component



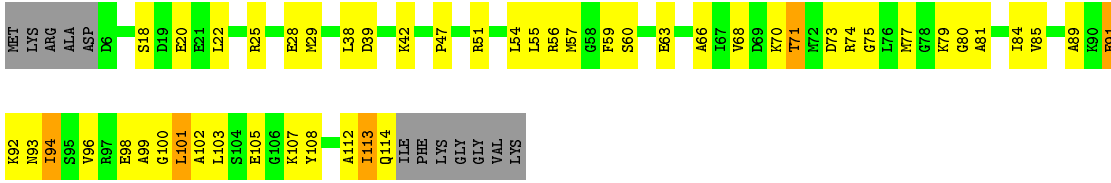


• Molecule 1: D-ornithine aminomutase E component

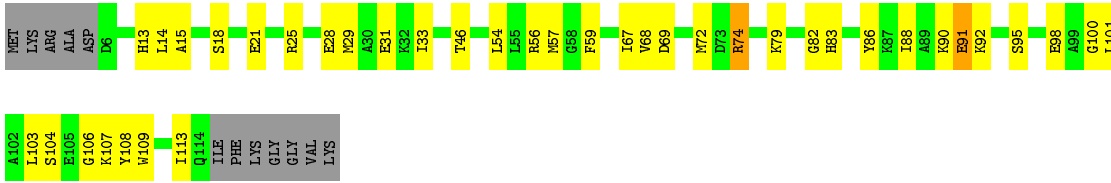


• Molecule 2: D-ornithine aminomutase S component

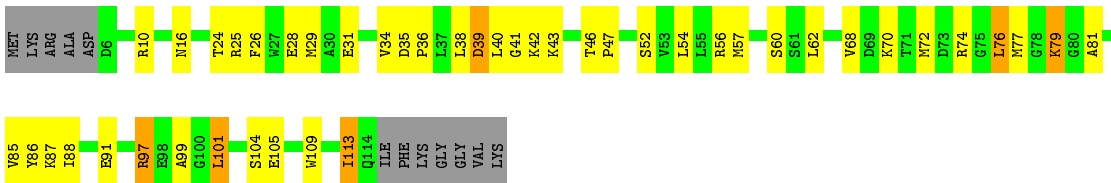




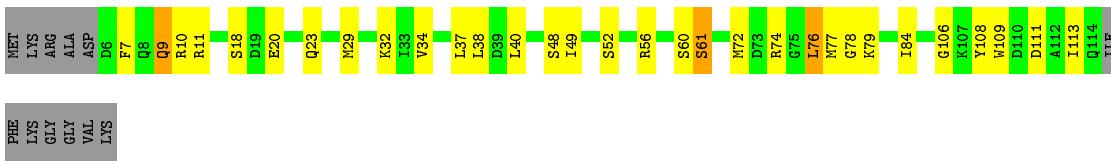
• Molecule 2: D-ornithine aminomutase S component



• Molecule 2: D-ornithine aminomutase S component



• Molecule 2: D-ornithine aminomutase S component



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.18Å 229.01Å 123.92Å 90.00° 102.76° 90.00°	Depositor
Resolution (Å)	120.86 – 2.90 62.21 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.9 (120.86-2.90) 97.9 (62.21-2.90)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.91Å)	Xtrriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.191 , 0.279 0.181 , 0.270	Depositor DCC
R_{free} test set	3837 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	41.7	Xtrriage
Anisotropy	0.555	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.038 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	26527	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.35% 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: B12, 5AD, PLP

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	0.45	0/5751	0.60	0/7787
1	B	0.50	0/5777	0.63	0/7818
1	C	0.45	0/5754	0.59	0/7789
1	D	0.48	0/5764	0.62	0/7801
2	E	0.46	0/867	0.58	0/1163
2	F	0.53	0/870	0.64	0/1167
2	G	0.47	0/867	0.56	0/1163
2	H	0.50	0/867	0.60	0/1163
All	All	0.47	0/26517	0.61	0/35851

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 [i](#)

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	5646	0	5580	256	0
1	B	5672	0	5642	242	0
1	C	5649	0	5616	282	0
1	D	5659	0	5632	260	0
2	E	855	0	863	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	858	0	865	38	0
2	G	855	0	863	44	0
2	H	855	0	863	24	0
3	A	91	0	87	25	0
3	B	91	0	87	27	0
3	C	91	0	87	29	0
3	D	91	0	87	18	0
4	A	15	0	6	2	0
4	B	15	0	7	2	0
4	C	15	0	7	0	0
4	D	15	0	6	2	0
5	A	18	0	9	3	0
5	C	18	0	9	2	0
5	D	18	0	10	2	0
All	All	26527	0	26326	1183	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 22.

The worst 5 of 1183 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)
2:F:74:ARG:HH11	2:F:74:ARG:HG3	0.95	1.08
1:A:82:ILE:HG12	1:A:93:ARG:HD2	1.39	1.05
1:B:528:PHE:HE1	1:B:560:MET:HG3	1.22	1.04
1:A:120:ILE:HG13	1:A:133:THR:HG22	1.48	0.96
2:F:74:ARG:CG	2:F:74:ARG:HH11	1.78	0.95

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	721/763 (94%)	633 (88%)	75 (10%)	13 (2%)	8	29
1	B	722/763 (95%)	658 (91%)	56 (8%)	8 (1%)	14	42
1	C	721/763 (94%)	629 (87%)	79 (11%)	13 (2%)	8	29
1	D	721/763 (94%)	643 (89%)	64 (9%)	14 (2%)	8	28
2	E	107/121 (88%)	93 (87%)	11 (10%)	3 (3%)	5	19
2	F	107/121 (88%)	95 (89%)	11 (10%)	1 (1%)	17	48
2	G	107/121 (88%)	97 (91%)	9 (8%)	1 (1%)	17	48
2	H	107/121 (88%)	102 (95%)	5 (5%)	0	100	100
All	All	3313/3536 (94%)	2950 (89%)	310 (9%)	53 (2%)	9	32

5 of 53 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	12	LYS
1	A	69	ASP
1	B	162	SER
1	D	6	GLN

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	598/644 (93%)	547 (92%)	51 (8%)	10	31
1	B	604/644 (94%)	561 (93%)	43 (7%)	14	40
1	C	600/644 (93%)	562 (94%)	38 (6%)	18	46
1	D	602/644 (94%)	557 (92%)	45 (8%)	13	37
2	E	89/100 (89%)	84 (94%)	5 (6%)	21	52
2	F	90/100 (90%)	86 (96%)	4 (4%)	28	61
2	G	89/100 (89%)	79 (89%)	10 (11%)	6	18
2	H	89/100 (89%)	84 (94%)	5 (6%)	21	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2761/2976 (93%)	2560 (93%)	201 (7%)	14 38

5 of 201 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	628	ILE
1	C	171	VAL
1	D	578	ILE
1	B	674	ASP
2	F	101	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	217	GLN
1	C	492	ASN
1	D	518	GLN
1	C	459	GLN
1	C	518	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

11 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	B12	C	1801	1,5	80,101,101	1.13	5 (6%)	101,166,166	2.24	23 (22%)
5	5AD	D	1500	3	17,20,20	2.13	6 (35%)	15,30,30	4.36	8 (53%)
4	PLP	D	1802	1	15,15,16	1.43	1 (6%)	20,22,23	1.37	3 (15%)
5	5AD	C	1500	3	17,20,20	2.13	6 (35%)	15,30,30	4.30	8 (53%)
3	B12	A	1801	1,5	80,101,101	1.14	4 (5%)	101,166,166	2.12	24 (23%)
4	PLP	B	1802	1	15,15,16	1.75	3 (20%)	20,22,23	1.96	7 (35%)
4	PLP	C	1802	1	15,15,16	1.75	3 (20%)	20,22,23	1.66	2 (10%)
3	B12	B	1801	1,5	80,101,101	1.18	7 (8%)	101,166,166	2.11	24 (23%)
4	PLP	A	1802	1	15,15,16	2.00	3 (20%)	20,22,23	1.64	2 (10%)
3	B12	D	1801	1	80,101,101	1.13	4 (5%)	101,166,166	1.99	20 (19%)
5	5AD	A	1500	3	17,20,20	2.19	6 (35%)	15,30,30	3.99	8 (53%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	B12	C	1801	1,5	1/1/36/38	11/51/223/223	0/3/11/11
4	PLP	A	1802	1	-	0/6/6/8	0/1/1/1
4	PLP	D	1802	1	-	0/6/6/8	0/1/1/1
5	5AD	C	1500	3	3/3/4/4	0/0/20/20	0/3/3/3
3	B12	A	1801	1,5	1/1/36/38	12/51/223/223	0/3/11/11
4	PLP	B	1802	1	-	0/6/6/8	0/1/1/1
4	PLP	C	1802	1	-	0/6/6/8	0/1/1/1
3	B12	B	1801	1,5	1/1/36/38	3/51/223/223	0/3/11/11
5	5AD	D	1500	3	3/3/4/4	0/0/20/20	0/3/3/3
3	B12	D	1801	1	1/1/36/38	19/51/223/223	0/3/11/11
5	5AD	A	1500	3	3/3/4/4	0/0/20/20	0/3/3/3

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1802	PLP	C6-N1	4.93	1.44	1.34
3	D	1801	B12	C11-C10	-4.85	1.32	1.40
3	B	1801	B12	C11-C10	-4.84	1.32	1.40
4	A	1802	PLP	C6-N1	4.62	1.44	1.34
4	D	1802	PLP	C6-N1	4.59	1.44	1.34

The worst 5 of 129 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	1500	5AD	C5'-C4'-C3'	10.91	127.15	115.70
5	D	1500	5AD	C5'-C4'-C3'	10.72	126.96	115.70
5	A	1500	5AD	C5'-C4'-C3'	8.83	124.97	115.70
3	C	1801	B12	C1-C19-N24	8.73	116.06	106.24
3	A	1801	B12	C1-C19-N24	8.60	115.91	106.24

5 of 13 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	C	1801	B12	C19
5	D	1500	5AD	C2'
5	D	1500	5AD	C4'
5	D	1500	5AD	C3'
5	C	1500	5AD	C2'

5 of 45 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	1801	B12	C38-C37-C7-C36
3	C	1801	B12	C38-C37-C7-C8
3	C	1801	B12	C42-C41-C8-C7
3	C	1801	B12	C42-C41-C8-C9
3	C	1801	B12	C16-C17-C55-C56

There are no ring outliers.

10 monomers are involved in 105 short contacts:

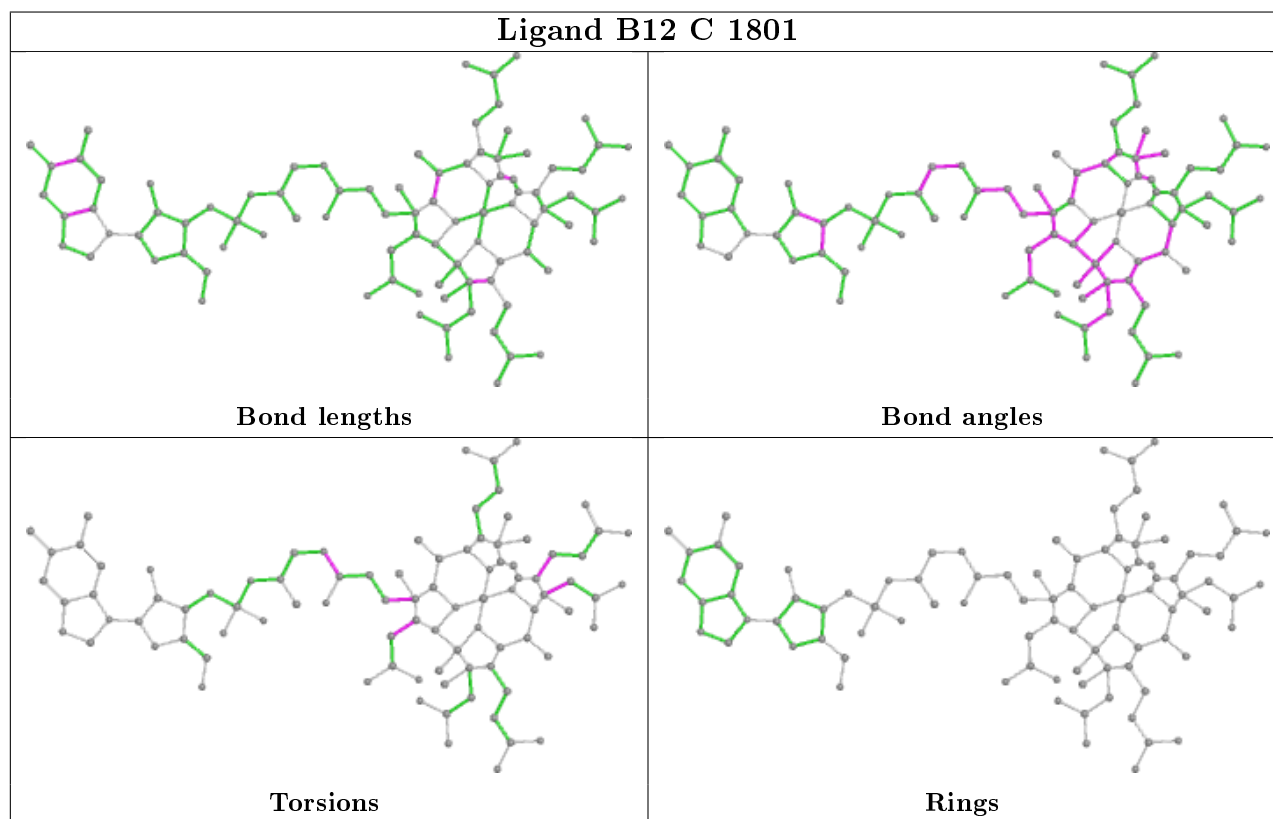
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1801	B12	29	0
5	D	1500	5AD	2	0
4	D	1802	PLP	2	0
5	C	1500	5AD	2	0
3	A	1801	B12	25	0

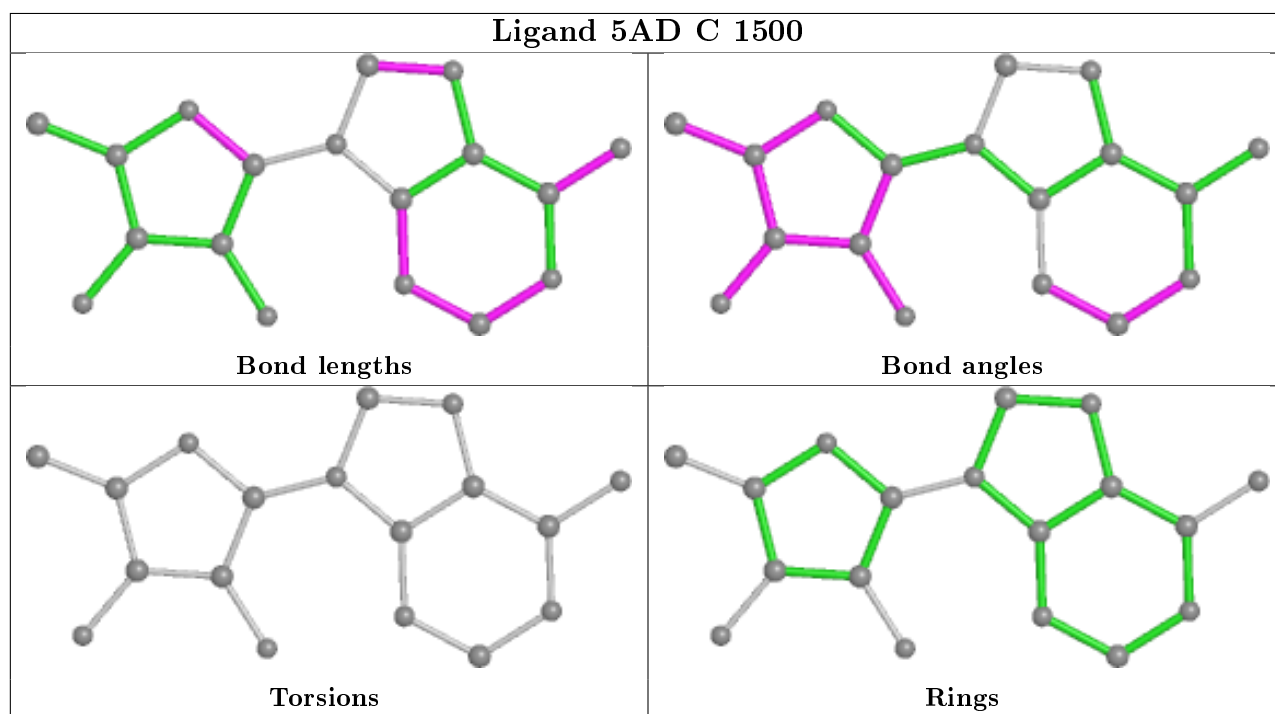
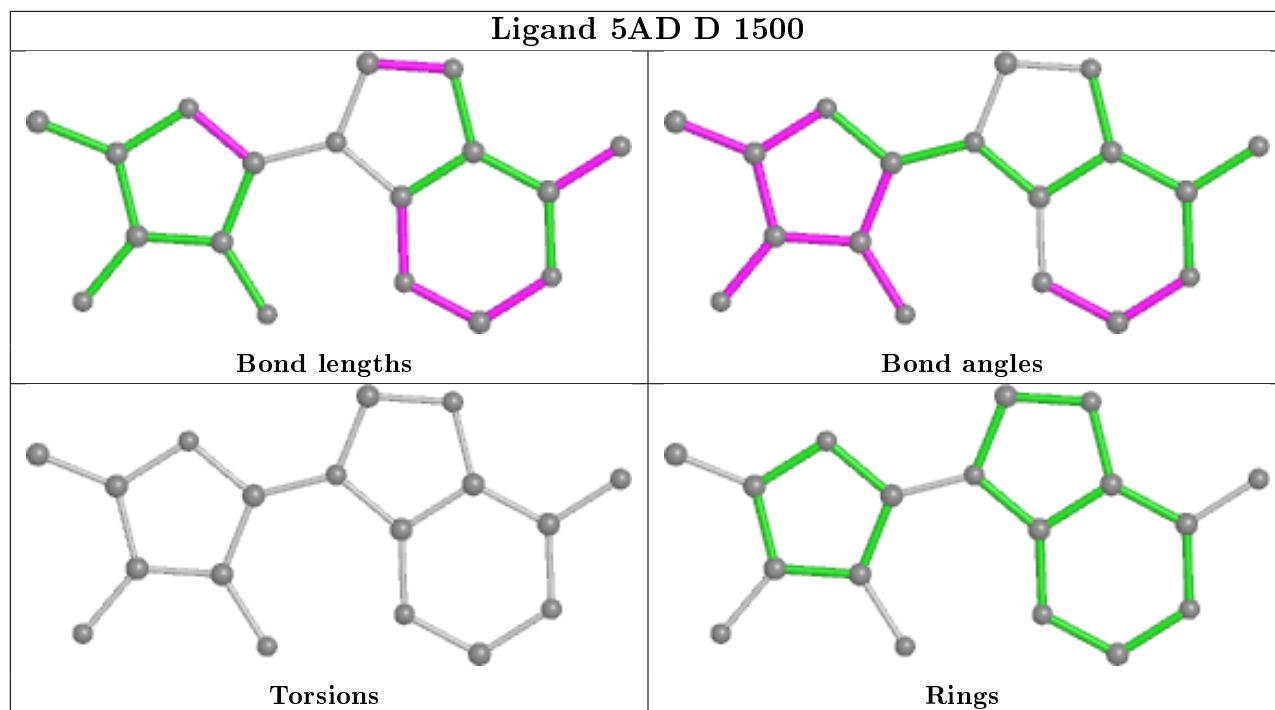
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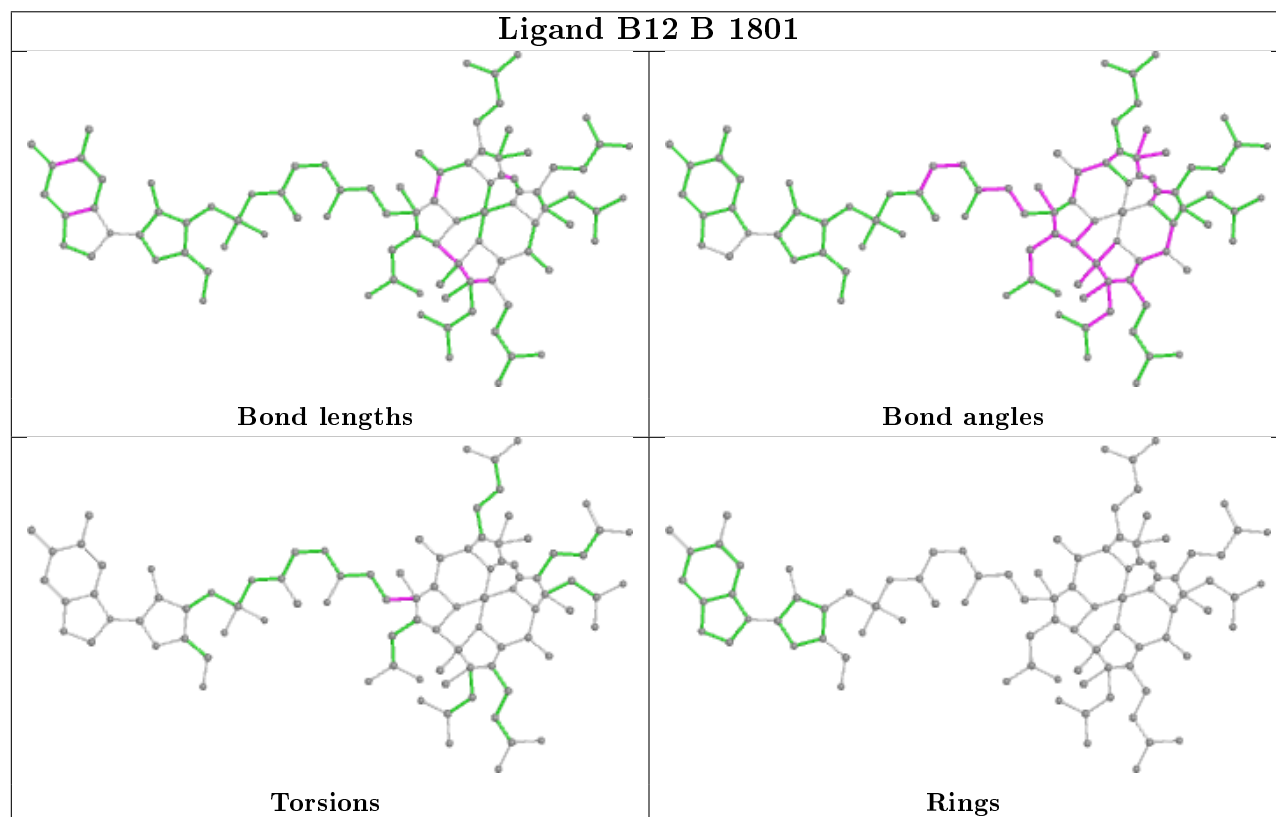
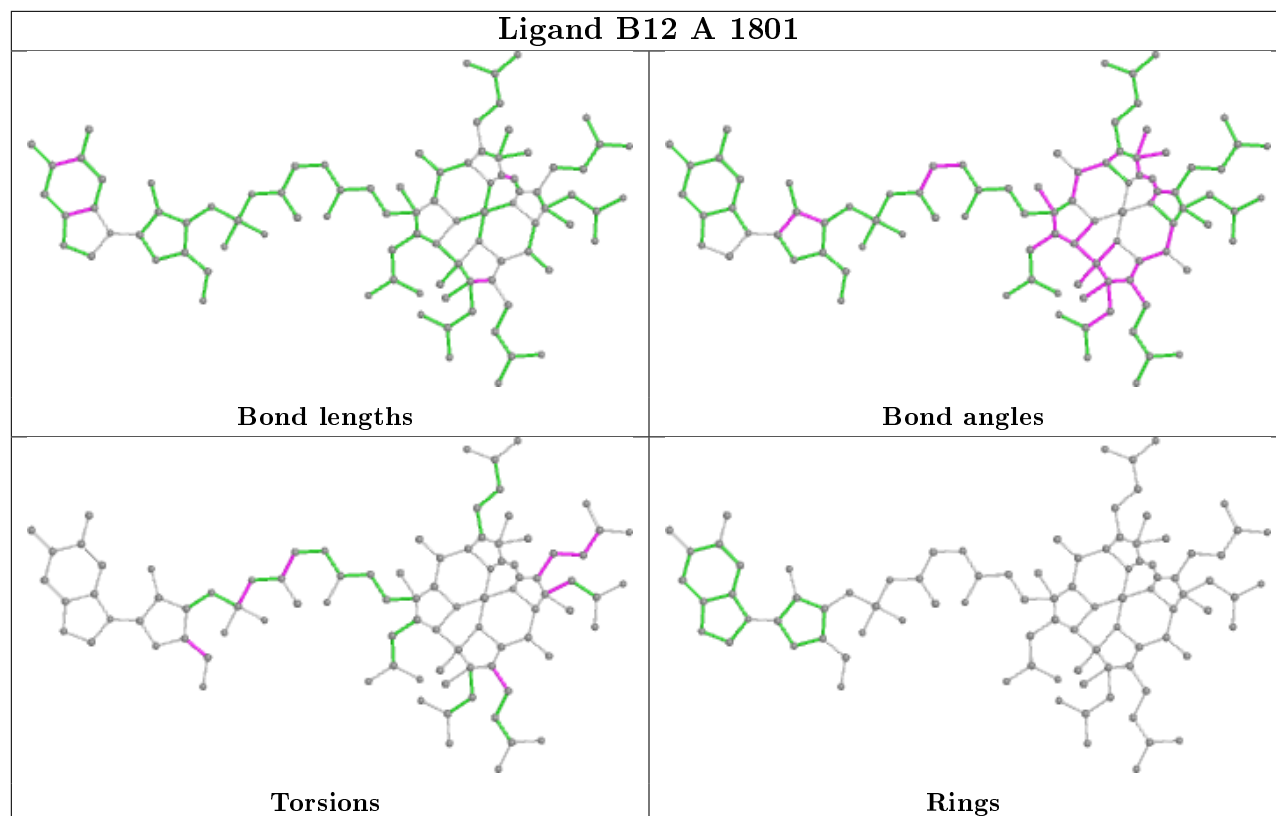
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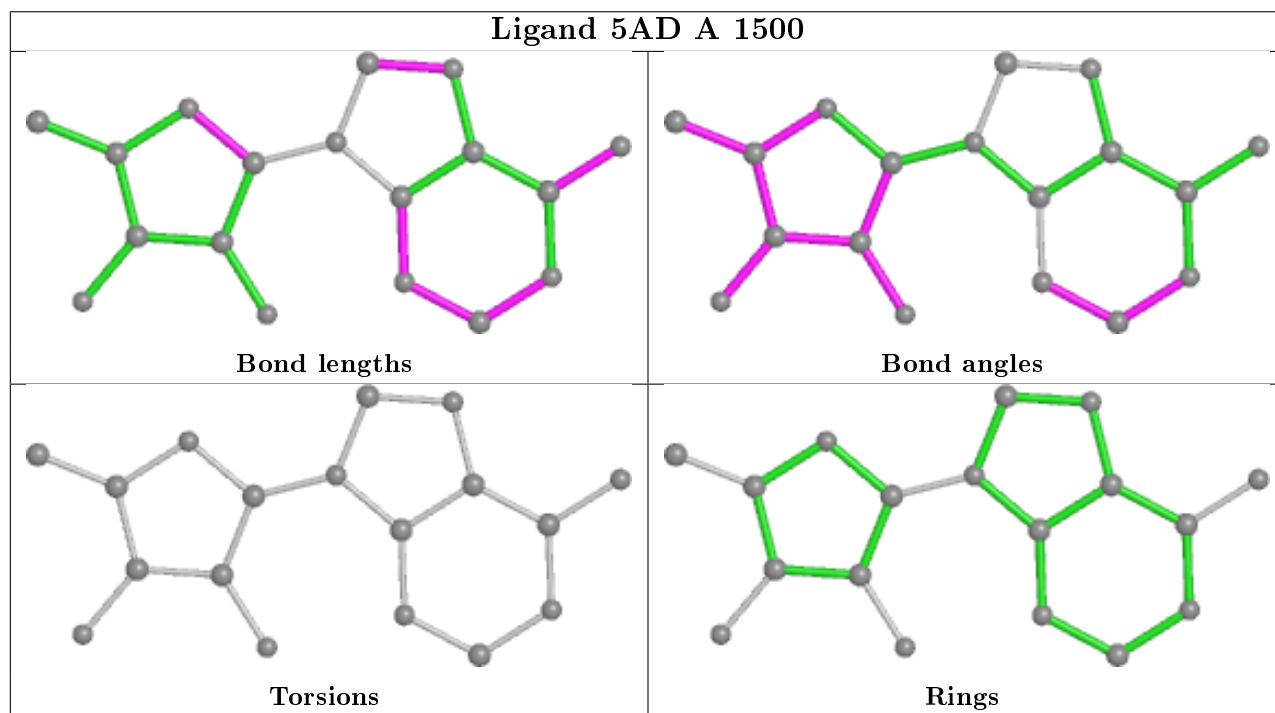
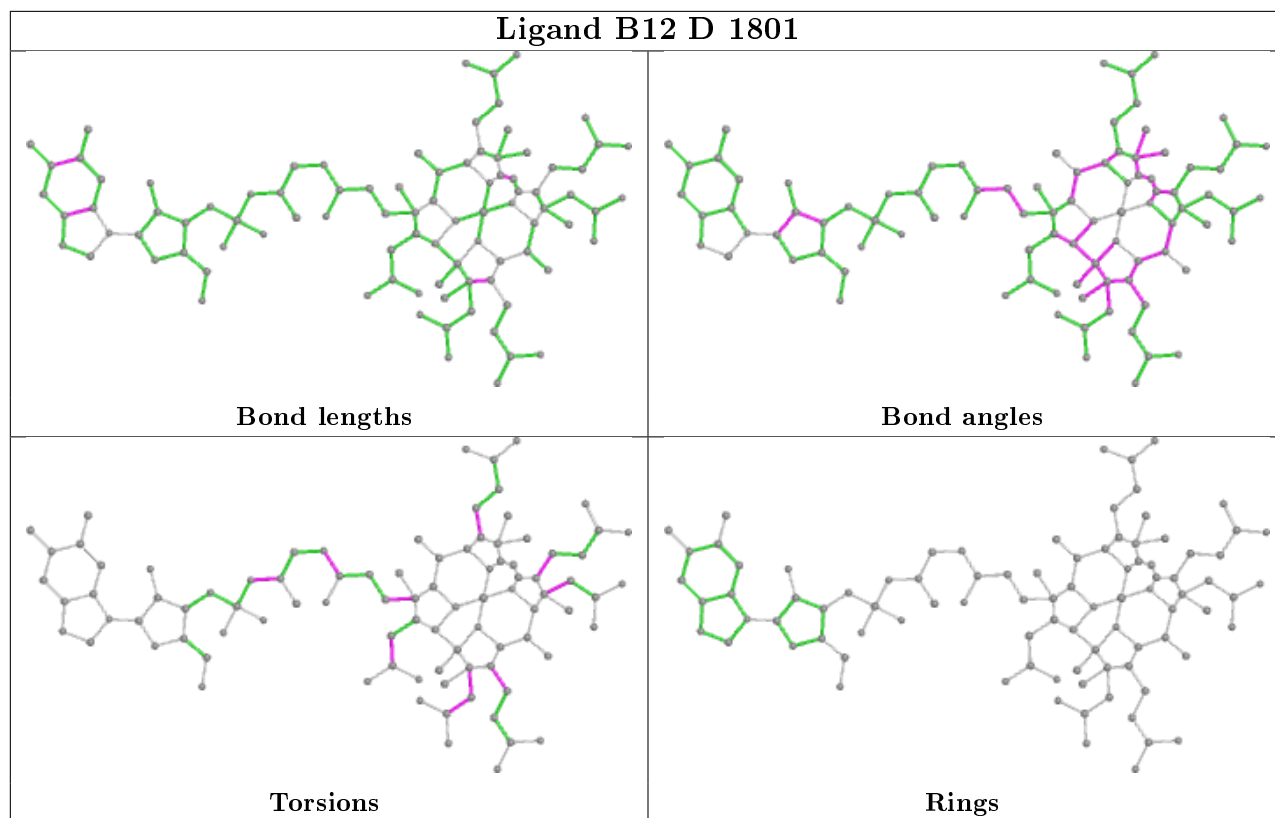
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1802	PLP	2	0
3	B	1801	B12	27	0
4	A	1802	PLP	2	0
3	D	1801	B12	18	0
5	A	1500	5AD	3	0

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









5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å ²)	Q < 0.9
1	A	727/763 (95%)	-0.15	18 (2%) 57 55	16, 37, 90, 105	0
1	B	728/763 (95%)	-0.38	0 100 100	15, 32, 54, 72	0
1	C	727/763 (95%)	-0.29	0 100 100	17, 38, 65, 84	0
1	D	727/763 (95%)	-0.14	27 (3%) 41 37	15, 30, 93, 118	0
2	E	109/121 (90%)	-0.32	0 100 100	22, 39, 59, 75	0
2	F	109/121 (90%)	-0.33	0 100 100	19, 32, 53, 69	0
2	G	109/121 (90%)	-0.22	0 100 100	25, 44, 62, 68	0
2	H	109/121 (90%)	-0.18	0 100 100	15, 31, 55, 72	0
All	All	3345/3536 (94%)	-0.24	45 (1%) 77 77	15, 35, 79, 118	0

The worst 5 of 45 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	692	ILE	5.0
1	D	652	LEU	3.6
1	D	688	VAL	3.4
1	D	671	SER	3.2
1	A	680	MET	3.2

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](#)

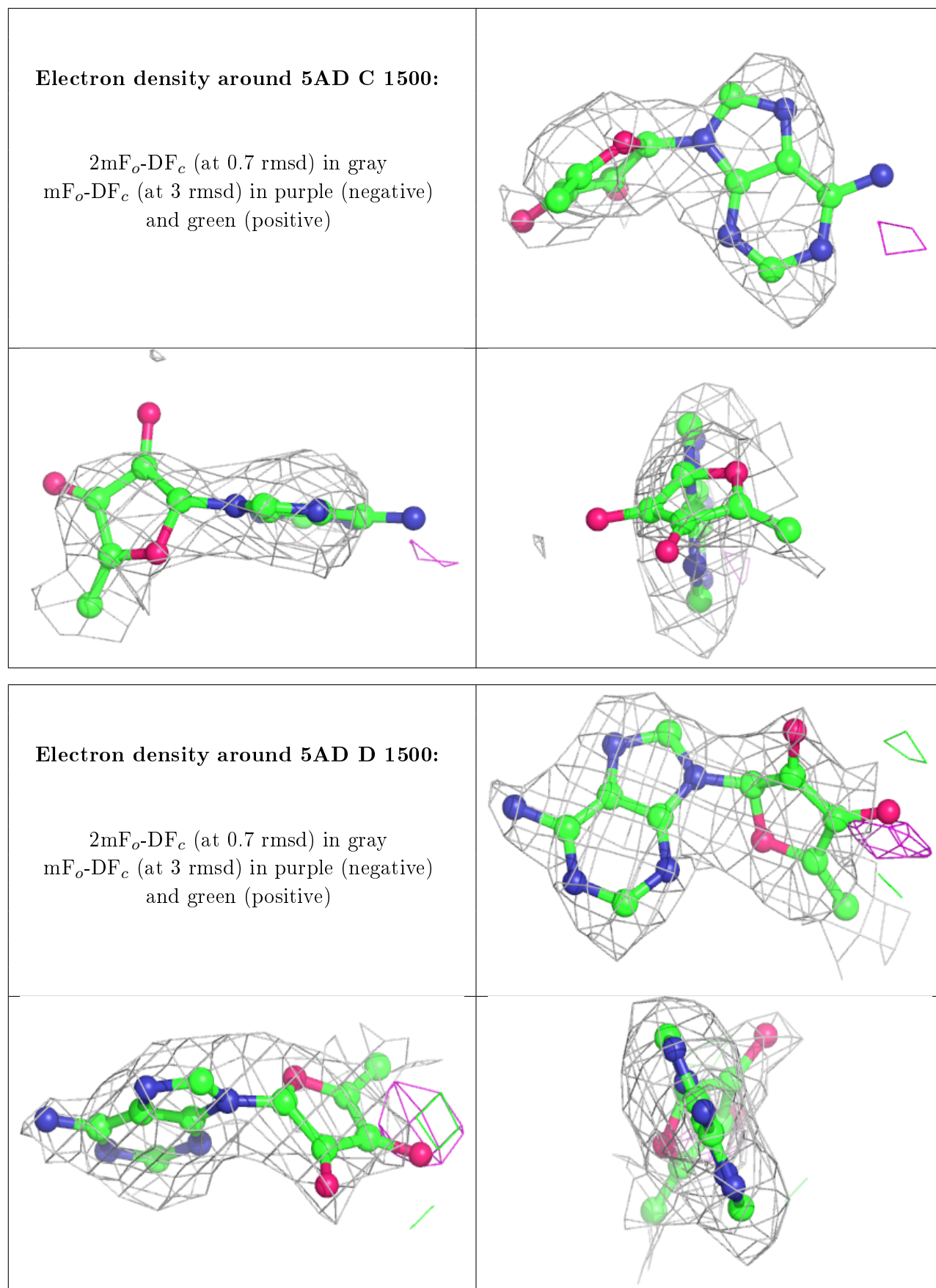
There are no carbohydrates in this entry.

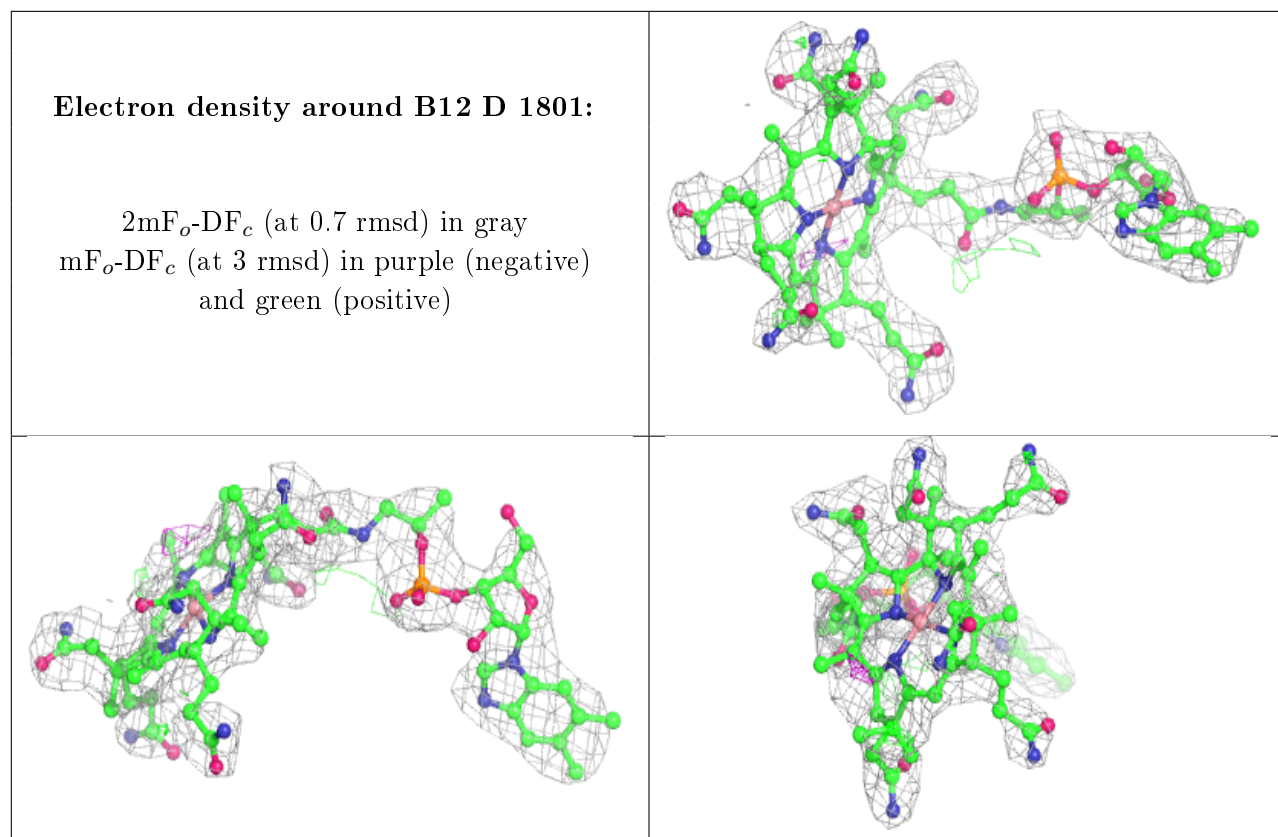
6.4 Ligands

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	5AD	C	1500	18/18	0.85	0.28	68,80,83,86	0
5	5AD	D	1500	18/18	0.93	0.19	27,44,50,51	0
3	B12	D	1801	91/91	0.94	0.24	37,56,69,77	0
5	5AD	A	1500	18/18	0.94	0.23	37,56,61,65	0
3	B12	A	1801	91/91	0.95	0.20	41,65,75,82	0
4	PLP	C	1802	15/16	0.97	0.14	27,29,36,37	0
3	B12	B	1801	91/91	0.97	0.16	16,28,35,38	0
4	PLP	A	1802	15/16	0.97	0.15	30,37,49,52	0
3	B12	C	1801	91/91	0.97	0.17	17,35,43,50	0
4	PLP	D	1802	15/16	0.97	0.12	25,32,38,43	0
4	PLP	B	1802	15/16	0.98	0.13	18,27,36,37	0

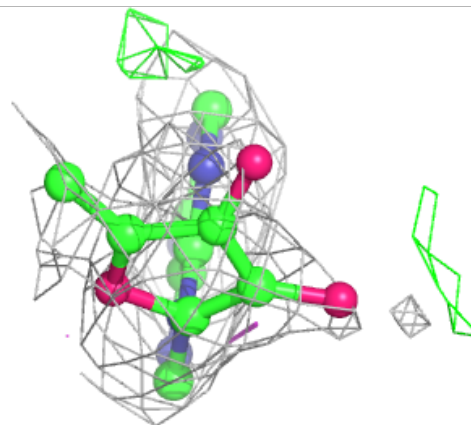
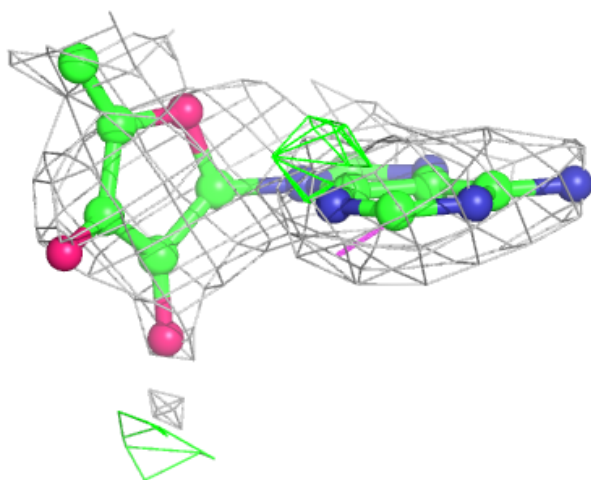
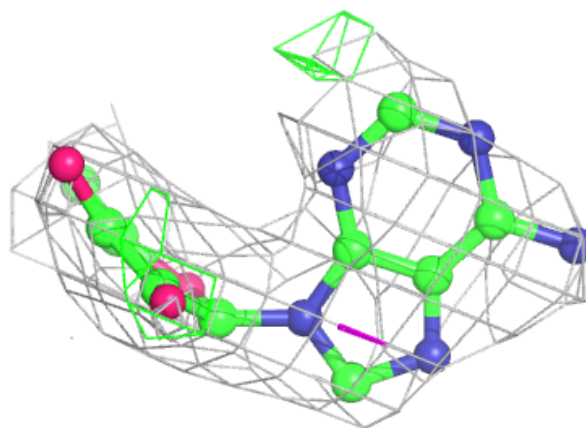
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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





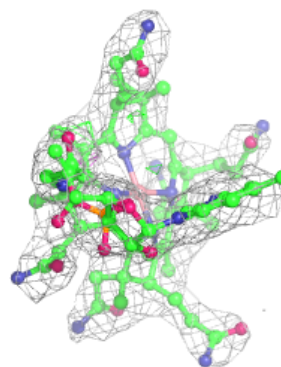
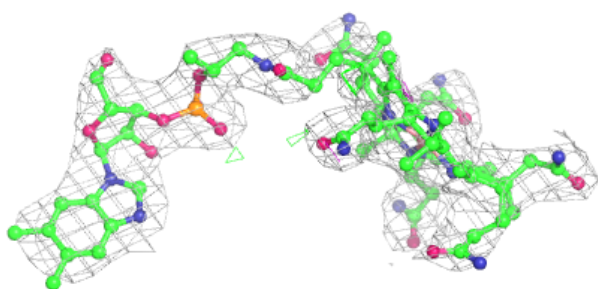
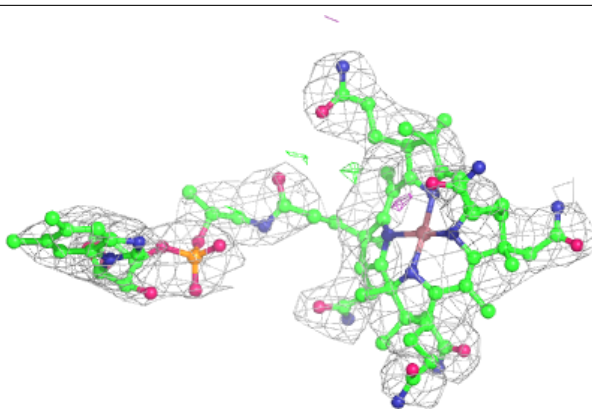
Electron density around 5AD A 1500:

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

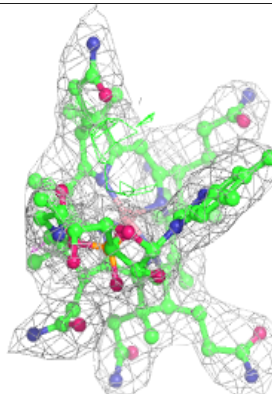
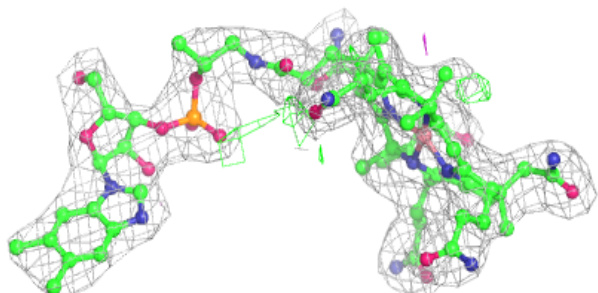
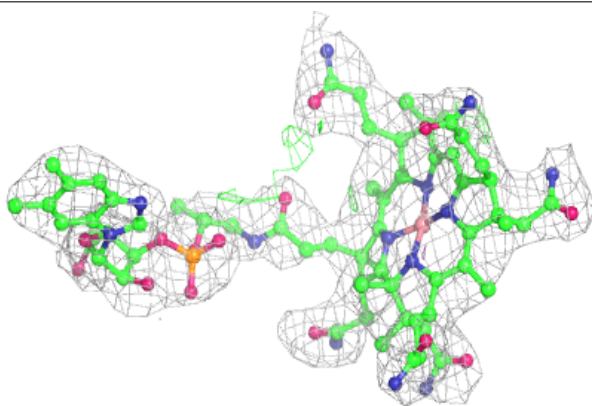


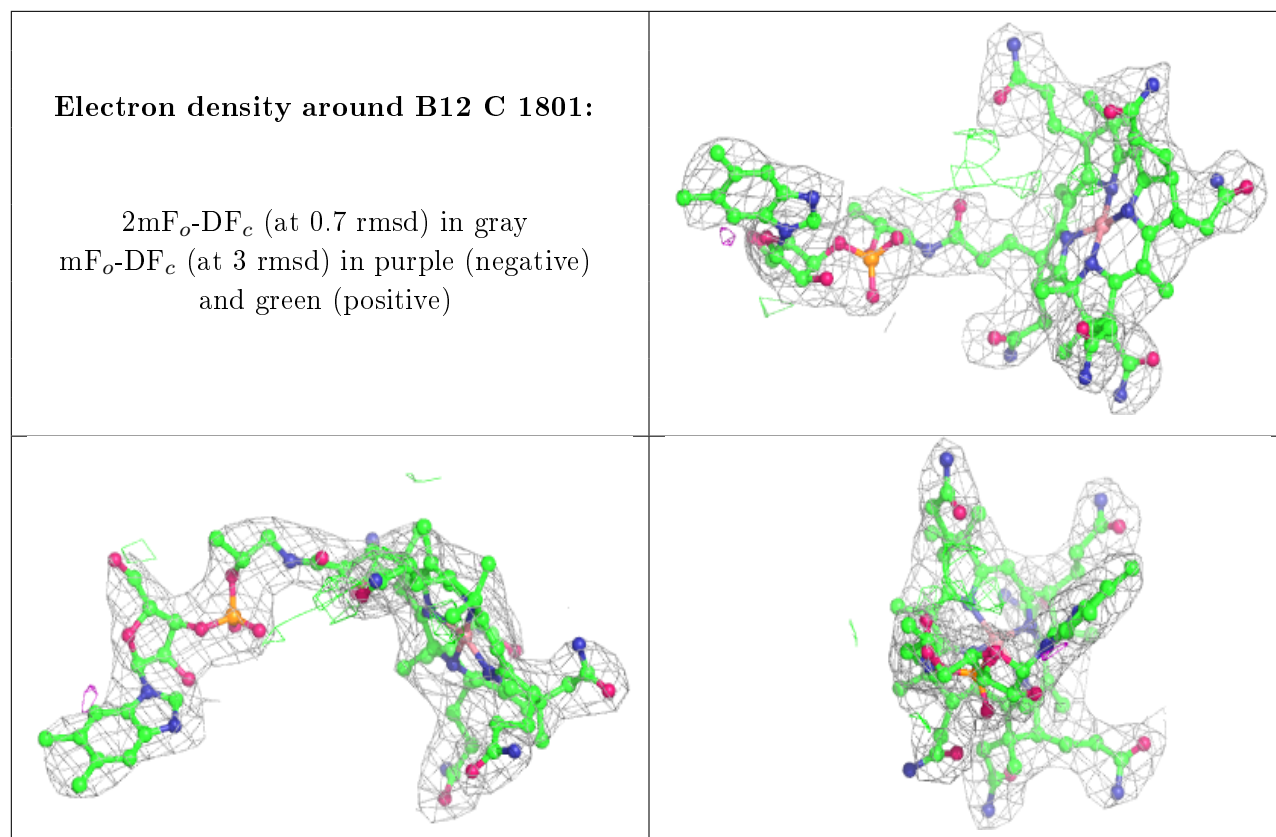
Electron density around B12 A 1801:

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

**Electron density around B12 B 1801:**

$2mF_o-DF_c$ (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.