



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 5, 2026 – 01:54 PM EDT

PDB ID : 9MRS / pdb_00009mrs
Title : Crystal structure of human MMACHC in complex with MMADHC and B12
Authors : Mascarenhas, R.; Banerjee, R.
Deposited on : 2025-01-08
Resolution : 3.40 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 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

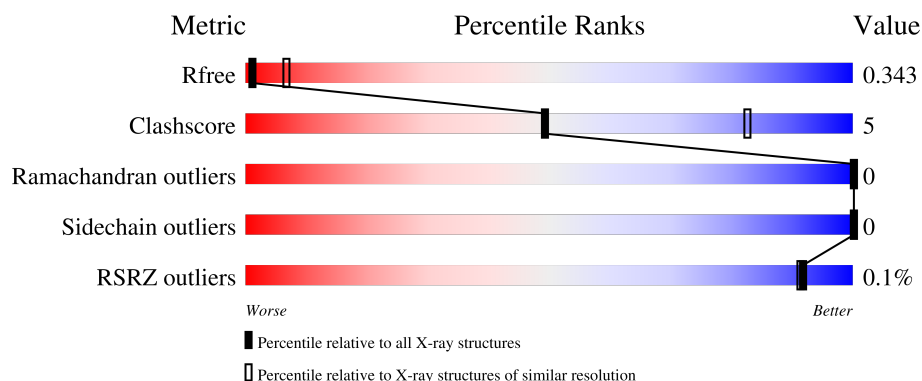
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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.



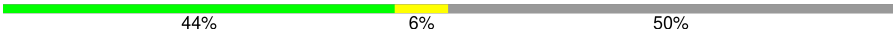
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

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	223	 79% 15% 6%
1	B	223	 77% 18% 5%
1	E	223	 80% 14% 6%
1	G	223	 81% 13% 6%
2	C	296	 44% 51%

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Mol	Chain	Length	Quality of chain
2	D	296	 44% 6% 50%
2	F	296	 44% 5% 51%
2	H	296	 44% 5% 51%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11661 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 Cyanocobalamin reductase / alkylcobalamin dealkylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	209	Total	C	N	O	S	0	1	0
			1653	1071	280	297	5			
1	B	211	Total	C	N	O	S	0	1	0
			1699	1109	287	298	5			
1	E	210	Total	C	N	O	S	0	1	0
			1669	1088	281	295	5			
1	G	210	Total	C	N	O	S	0	1	0
			1694	1099	293	296	6			

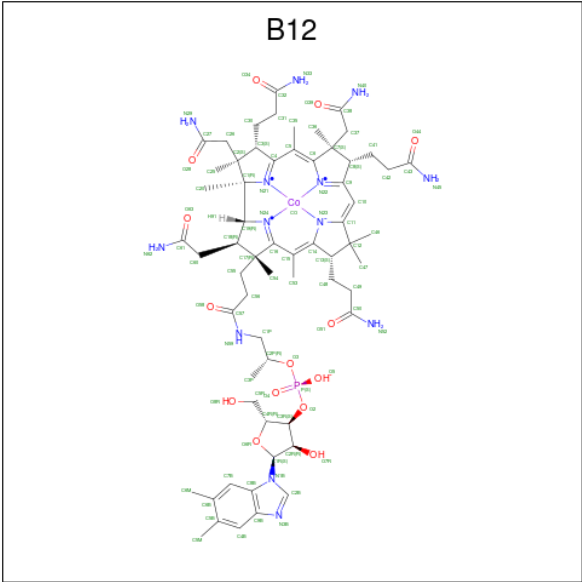
- Molecule 2 is a protein called Cobalamin trafficking protein CblD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	148	Total	C	N	O	S	0	0	0
			1158	742	189	220	7			
2	F	144	Total	C	N	O	S	0	0	0
			1141	731	185	219	6			
2	C	144	Total	C	N	O	S	0	0	0
			1139	729	185	219	6			
2	H	144	Total	C	N	O	S	0	0	0
			1144	733	185	219	7			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	262	SER	CYS	conflict	UNP Q9H3L0
F	262	SER	CYS	conflict	UNP Q9H3L0
C	262	SER	CYS	conflict	UNP Q9H3L0
H	262	SER	CYS	conflict	UNP Q9H3L0

- Molecule 3 is COBALAMIN (CCD ID: B12) (formula: $C_{62}H_{89}CoN_{13}O_{14}P$) (labeled as "Ligand of Interest" by depositor).

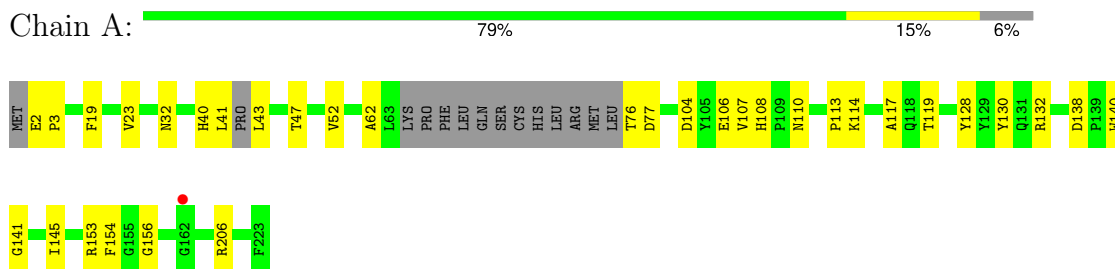


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	Co	N	O	P	0	0
			91	62	1	13	14	1		
3	B	1	Total	C	Co	N	O	P	0	0
			91	62	1	13	14	1		
3	E	1	Total	C	Co	N	O	P	0	0
			91	62	1	13	14	1		
3	G	1	Total	C	Co	N	O	P	0	0
			91	62	1	13	14	1		

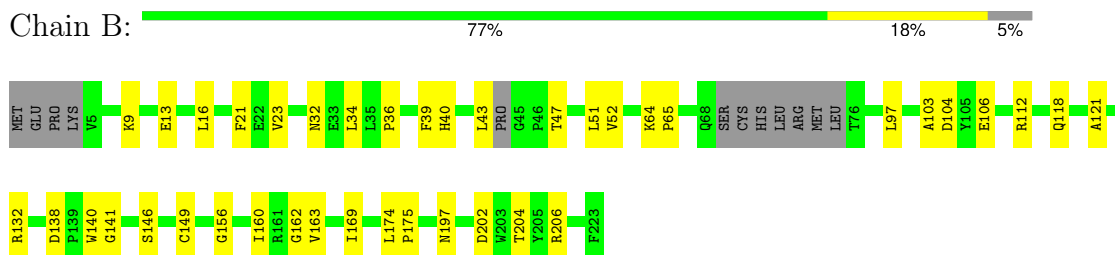
3 Residue-property plots [i](#)

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.

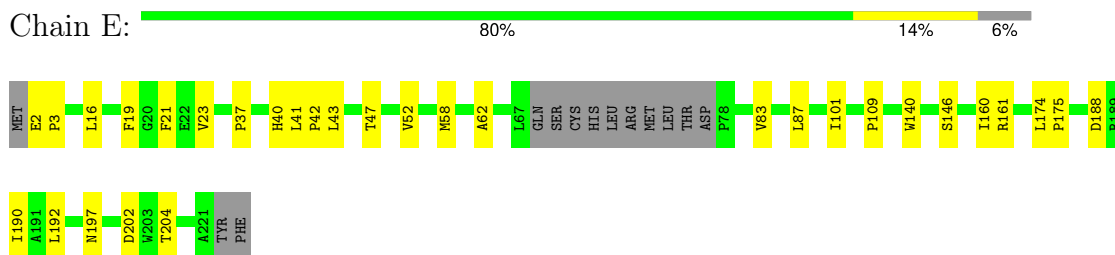
- Molecule 1: Cyanocobalamin reductase / alkylcobalamin dealkylase



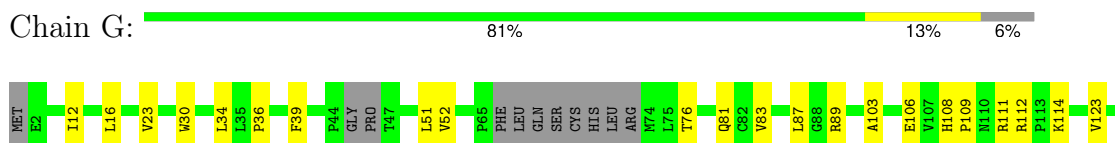
- Molecule 1: Cyanocobalamin reductase / alkylcobalamin dealkylase



- Molecule 1: Cyanocobalamin reductase / alkylcobalamin dealkylase



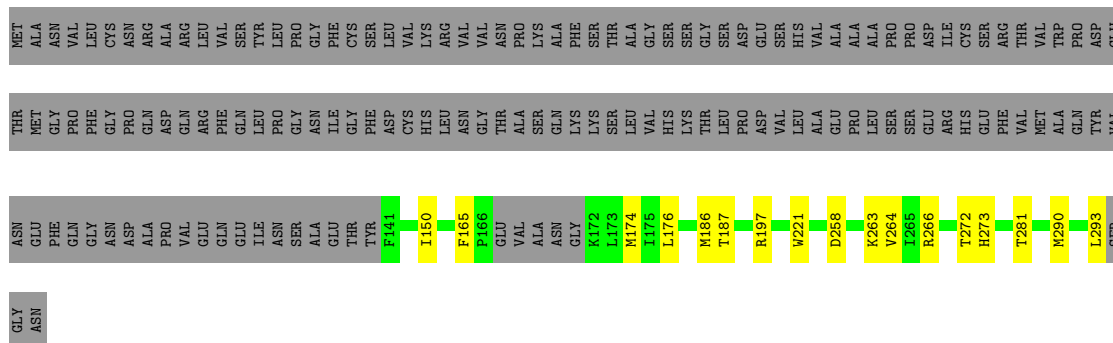
- Molecule 1: Cyanocobalamin reductase / alkylcobalamin dealkylase





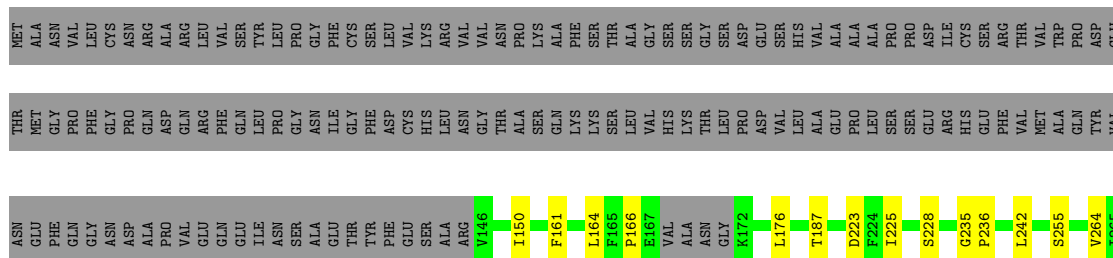
- Molecule 2: Cobalamin trafficking protein CblD

Chain D: 44% 6% 50%



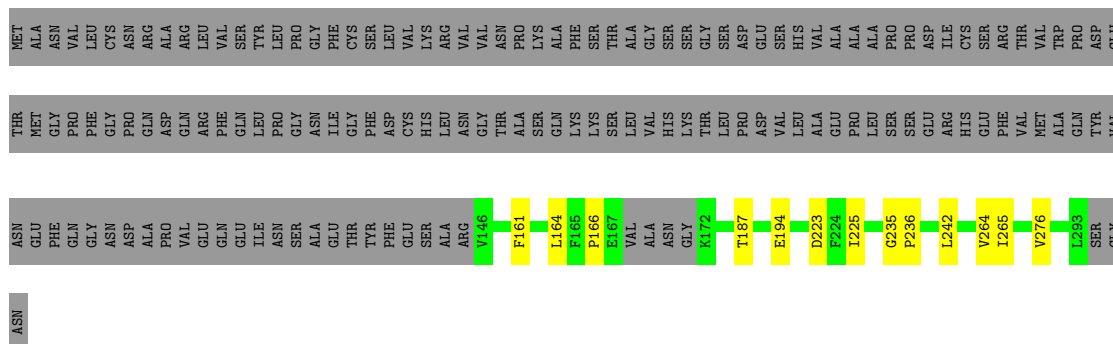
- Molecule 2: Cobalamin trafficking protein CblD

Chain F: 44% 5% 51%



- Molecule 2: Cobalamin trafficking protein CblD

Chain C: 44% 5% 51%



- Molecule 2: Cobalamin trafficking protein CblD

Chain H: 44% 5% 51%

V264	ASN	THR	MET	ALA	MET
L293	GLU	GLY	GLY	ASN	GLY
SER	PHE	GLN	PRO	VAL	PHE
GLY	GLY	GLY	PHE	LEU	GLY
ASN	ASN	PRO	GLY	CYS	PRO
ASP	ASP	ASN	GLN	ARG	GLN
PRO	ALA	GLN	ASP	ALA	ASP
VAL	VAL	GLN	GLN	ARG	GLN
GLU	GLU	ARG	PHE	LEU	VAL
GLN	GLN	GLN	GLN	SER	SER
	GLU	GLN	PHE	TYR	LEU
	ILE	PRO	LEU	LEU	PRO
	ASN	GLY	GLY	PRO	GLY
	SER	ASN	ASN	GLY	PRO
	ALA	ILE	GLY	PHE	PHE
	GLU	GLY	GLY	CYS	ASP
	THR	CYS	LEU	VAL	VAL
	TYR	HIS	LYS	ARG	LYS
	PHE	LEU	ARG	VAL	ARG
	GLU	ASN	VAL	VAL	VAL
	ARG	THR	ASN	ASN	VAL
	V146	ALA	THR	ASN	VAL
	I150	SER	LYS	PRO	LYS
	P166	GLN	ALA	LYS	ALA
	E167	LYS	PHE	PHE	PHE
	VAL	LYS	SER	SER	SER
	ALA	SER	THR	THR	THR
	ASN	LEU	ALA	ALA	ALA
	GLY	VAL	GLY	GLY	GLY
	K172	HIS	SER	SER	SER
	L176	LYS	SER	SER	SER
	M186	THR	GLY	GLY	GLY
	T187	LEU	SER	SER	SER
	R197	PRO	ASP	GLU	GLU
	R216	VAL	SER	SER	SER
	L225	LEU	VAL	VAL	VAL
	S228	LEU	LEU	VAL	VAL
	F234	ALA	ALA	ALA	ALA
	G235	PRO	PRO	ALA	ALA
	P236	SER	SER	PRO	PRO
	L242	ILE	ASP	PRO	PRO
	R250	ARG	GLU	ASP	ASP
	V256	CYS	HIS	CYS	CYS
		SER	GLY	SER	SER
		PHE	PHE	ARG	ARG
		VAL	VAL	THR	THR
		MET	MET	VAL	VAL
		ALA	ALA	TRP	TRP
		GLN	GLN	PRO	PRO
		TYR	TYR	ASN	ASN
		VAL	VAL	GLU	GLU

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	72.76Å 67.98Å 192.66Å 90.00° 99.38° 90.00°	Depositor
Resolution (Å)	41.24 – 3.40 41.24 – 3.40	Depositor EDS
% Data completeness (in resolution range)	53.2 (41.24-3.40) 53.6 (41.24-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.69 (at 3.41Å)	Xtriage
Refinement program	PHENIX (1.15.2_3472: ???)	Depositor
R, R_{free}	0.300 , 0.357 0.306 , 0.343	Depositor DCC
R_{free} test set	673 reflections (2.60%)	wwPDB-VP
Wilson B-factor (Å ²)	81.5	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 122.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.077 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	11661	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% 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

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	0.09	0/1709	0.24	0/2340
1	B	0.08	0/1759	0.24	0/2407
1	E	0.09	0/1729	0.25	0/2370
1	G	0.09	0/1750	0.26	0/2390
2	C	0.07	0/1163	0.20	0/1574
2	D	0.07	0/1182	0.21	0/1600
2	F	0.07	0/1165	0.21	0/1577
2	H	0.07	0/1168	0.21	0/1580
All	All	0.08	0/11625	0.23	0/15838

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	1653	0	1569	20	0
1	B	1699	0	1635	25	0
1	E	1669	0	1604	21	0
1	G	1694	0	1644	19	0
2	C	1139	0	1102	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1158	0	1124	9	0
2	F	1141	0	1109	8	0
2	H	1144	0	1116	11	0
3	A	91	0	88	7	0
3	B	91	0	88	8	0
3	E	91	0	88	4	0
3	G	91	0	88	2	0
All	All	11661	0	11255	124	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 5.

The worst 5 of 124 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:149:CYS:H	3:B:301:B12:H332	1.40	0.67
2:F:255:SER:HB2	2:F:266:ARG:HB2	1.78	0.65
2:D:290:MET:HA	2:D:293:LEU:HD23	1.79	0.64
1:E:160:ILE:O	3:E:301:B12:N29	2.32	0.62
1:B:118:GLN:HE21	3:B:301:B12:H331	1.48	0.61

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	204/223 (92%)	195 (96%)	9 (4%)	0	100	100
1	B	206/223 (92%)	200 (97%)	6 (3%)	0	100	100
1	E	207/223 (93%)	197 (95%)	10 (5%)	0	100	100
1	G	203/223 (91%)	194 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	140/296 (47%)	138 (99%)	2 (1%)	0	100	100
2	D	144/296 (49%)	136 (94%)	8 (6%)	0	100	100
2	F	140/296 (47%)	134 (96%)	6 (4%)	0	100	100
2	H	140/296 (47%)	136 (97%)	4 (3%)	0	100	100
All	All	1384/2076 (67%)	1330 (96%)	54 (4%)	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	169/192 (88%)	169 (100%)	0	100	100
1	B	176/192 (92%)	176 (100%)	0	100	100
1	E	172/192 (90%)	172 (100%)	0	100	100
1	G	176/192 (92%)	176 (100%)	0	100	100
2	C	125/256 (49%)	125 (100%)	0	100	100
2	D	126/256 (49%)	126 (100%)	0	100	100
2	F	126/256 (49%)	126 (100%)	0	100	100
2	H	127/256 (50%)	127 (100%)	0	100	100
All	All	1197/1792 (67%)	1197 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	F	288	HIS
1	G	131	GLN
2	C	288	HIS
2	H	251	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	G	301	-	94,101,101	1.03	6 (6%)	149,166,166	1.68	26 (17%)
3	B12	B	301	-	94,101,101	1.04	5 (5%)	149,166,166	1.69	28 (18%)
3	B12	E	301	-	94,101,101	1.04	5 (5%)	149,166,166	1.73	27 (18%)
3	B12	A	401	-	94,101,101	1.04	4 (4%)	149,166,166	1.72	27 (18%)

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	G	301	-	-	25/56/223/223	0/3/11/11
3	B12	B	301	-	-	26/56/223/223	0/3/11/11
3	B12	E	301	-	-	17/56/223/223	0/3/11/11
3	B12	A	401	-	-	18/56/223/223	0/3/11/11

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	301	B12	C54-C17	2.78	1.59	1.54
3	G	301	B12	C54-C17	2.75	1.59	1.54
3	E	301	B12	C14-N23	2.73	1.38	1.35
3	E	301	B12	C54-C17	2.72	1.59	1.54
3	A	401	B12	C54-C17	2.69	1.59	1.54

The worst 5 of 108 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	B12	C19-N24-C16	7.71	115.72	107.29
3	E	301	B12	C19-N24-C16	7.32	115.29	107.29
3	B	301	B12	C19-N24-C16	7.13	115.08	107.29
3	G	301	B12	C19-N24-C16	6.63	114.54	107.29
3	B	301	B12	C9-N22-C6	5.36	111.73	105.28

There are no chirality outliers.

5 of 86 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	401	B12	C38-C37-C7-C6
3	A	401	B12	C38-C37-C7-C36
3	A	401	B12	C38-C37-C7-C8
3	A	401	B12	C42-C41-C8-C9
3	A	401	B12	C14-C13-C48-C49

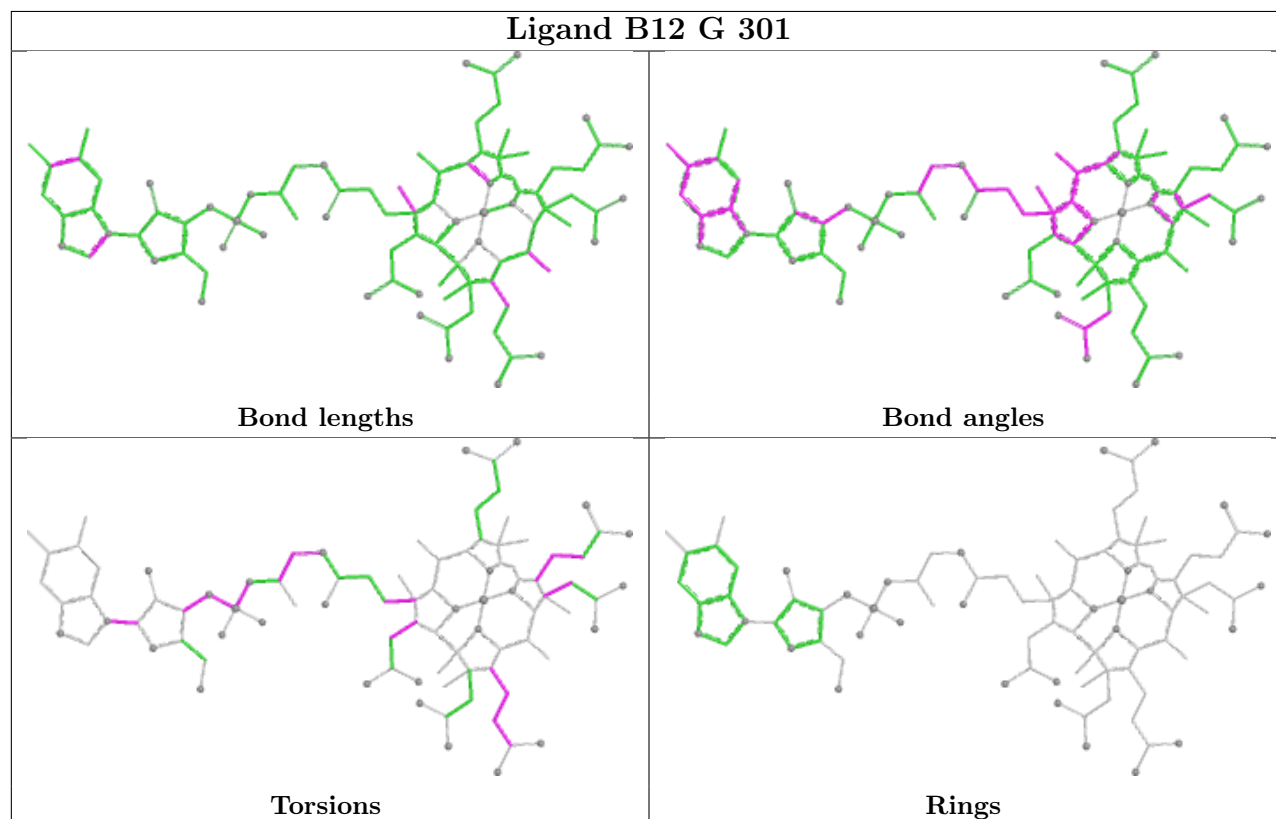
There are no ring outliers.

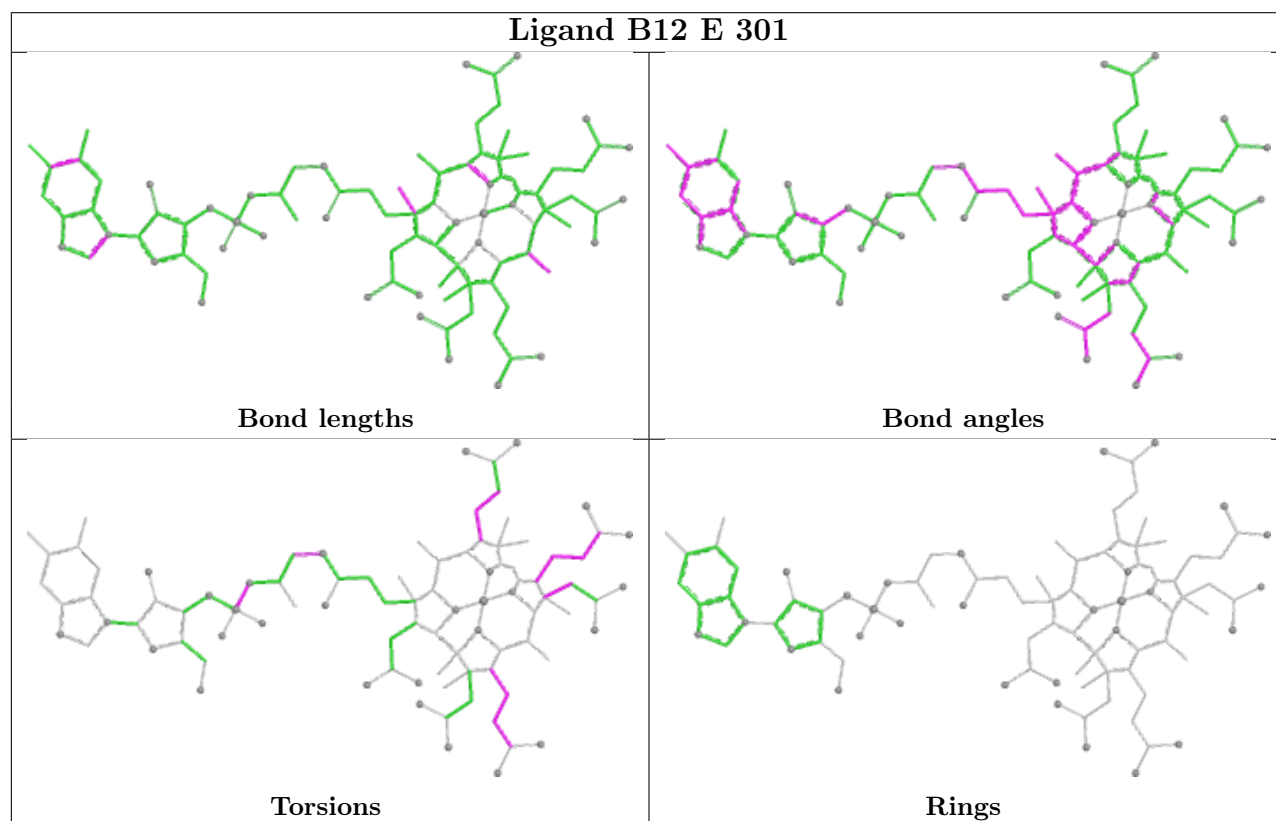
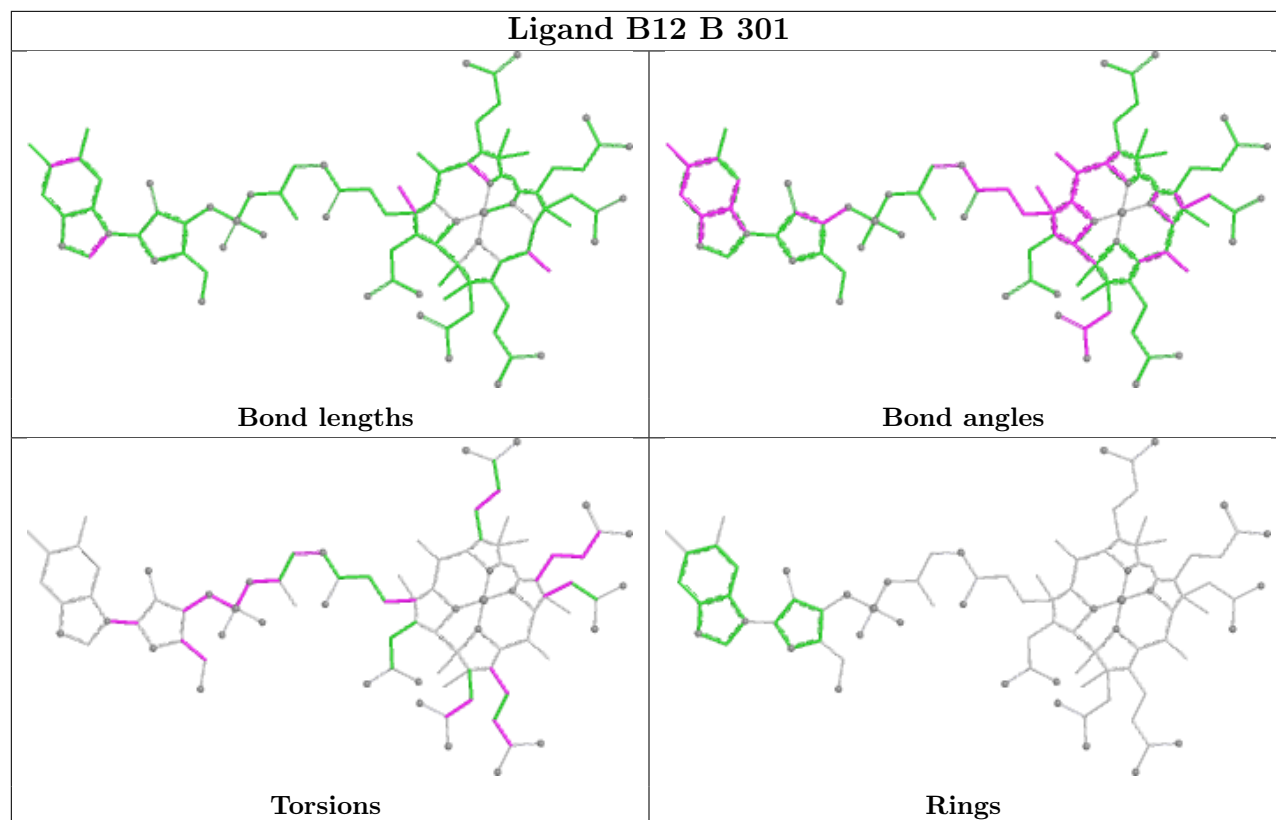
4 monomers are involved in 21 short contacts:

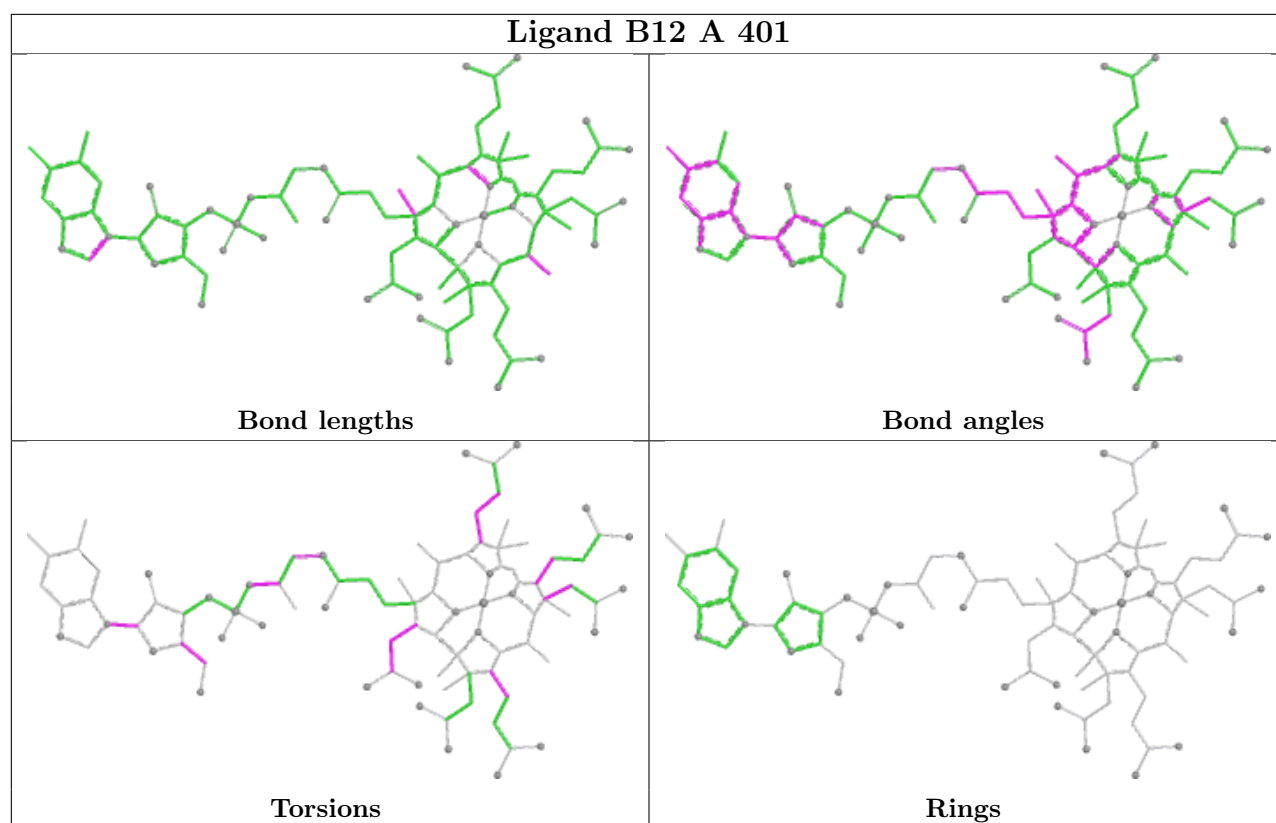
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	301	B12	2	0
3	B	301	B12	8	0
3	E	301	B12	4	0
3	A	401	B12	7	0

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	209/223 (93%)	-1.23	1 (0%) 87 78	43, 60, 63, 64	1 (0%)
1	B	211/223 (94%)	-1.23	0 100 100	47, 64, 69, 74	1 (0%)
1	E	210/223 (94%)	-1.14	0 100 100	40, 71, 79, 83	1 (0%)
1	G	210/223 (94%)	-1.07	0 100 100	53, 86, 94, 100	1 (0%)
2	C	144/296 (48%)	-1.23	0 100 100	61, 68, 74, 78	0
2	D	148/296 (50%)	-1.23	0 100 100	58, 62, 68, 71	0
2	F	144/296 (48%)	-1.19	0 100 100	72, 76, 83, 86	0
2	H	144/296 (48%)	-1.06	0 100 100	79, 88, 93, 94	0
All	All	1420/2076 (68%)	-1.17	1 (0%) 92 91	40, 69, 92, 100	4 (0%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	162	GLY	2.4

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

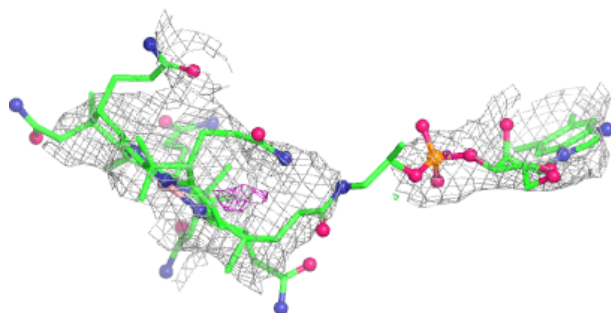
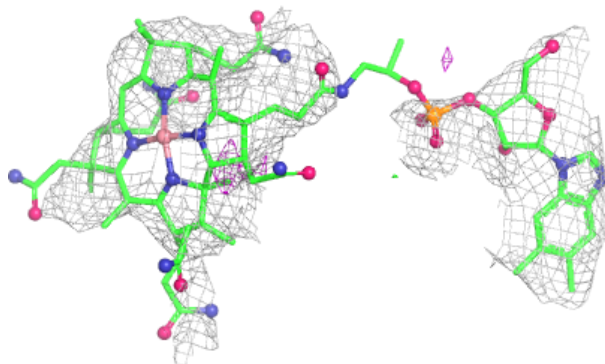
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	B12	G	301	91/91	0.98	0.06	84,91,93,94	0
3	B12	B	301	91/91	0.99	0.05	58,63,64,65	0
3	B12	E	301	91/91	0.99	0.05	70,74,75,75	0
3	B12	A	401	91/91	0.99	0.04	56,59,59,60	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.

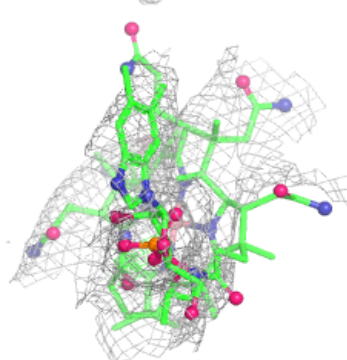
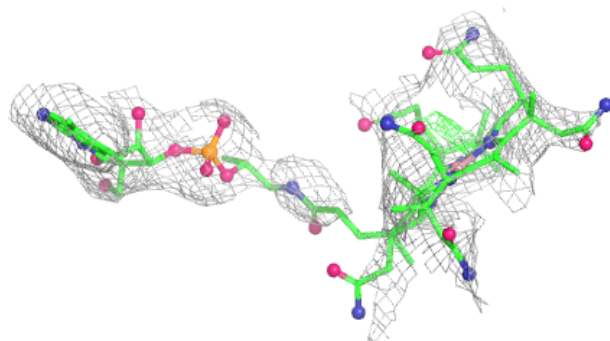
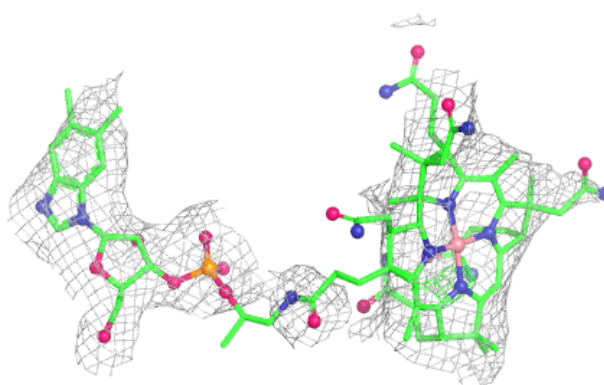
Electron density around B12 G 301:

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

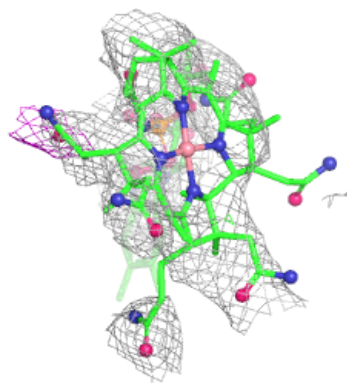
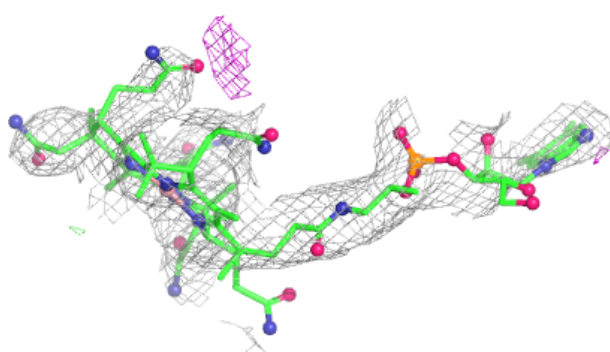
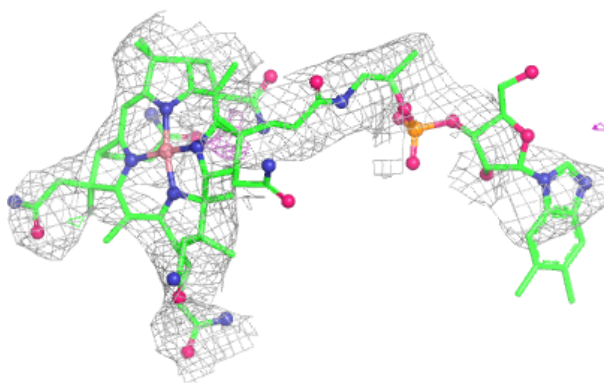


Electron density around B12 B 301:

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

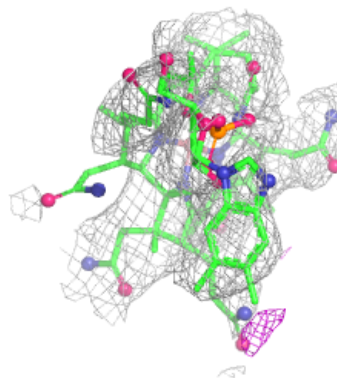
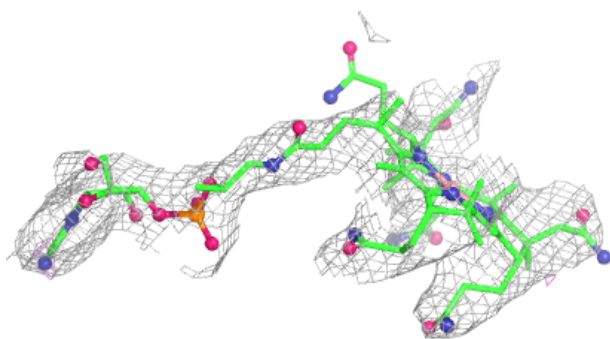
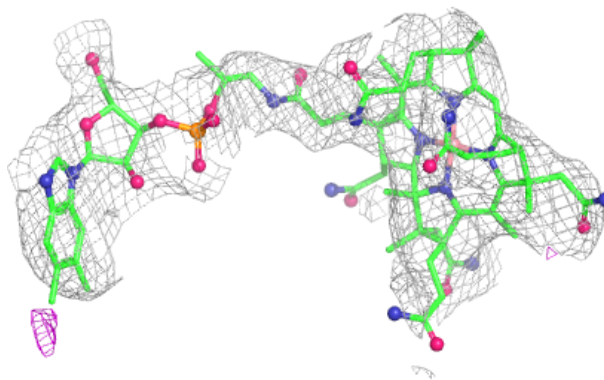
**Electron density around B12 E 301:**

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



Electron density around B12 A 401:

$2mF_o-DF_c$ (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.