



wwPDB X-ray Structure Validation Summary Report

Jun 15, 2020 – 02:15 am BST

PDB ID : 3IQF
Title : Structure of F420 dependent methylene-tetrahydromethanopterin dehydrogenase in complex with methenyl-tetrahydromethanopterin
Authors : Ceh, K.E.; Demmer, U.; Warkentin, E.; Moll, J.; Thauer, R.K.; Shima, S.; Ermler, U.
Deposited on : 2009-08-20
Resolution : 2.10 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

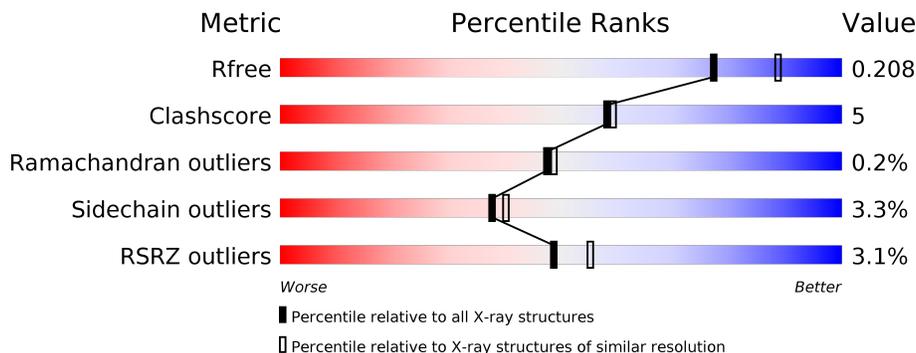
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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.



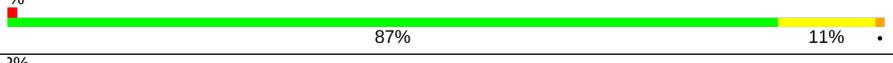
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	283	
1	B	283	
1	C	283	
1	D	283	
1	E	283	
1	F	283	

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Mol	Chain	Length	Quality of chain
1	G	283	 4% 88% 11% •
1	H	283	 3% 85% 14% •
1	I	283	 2% 85% 12% •
1	J	283	 6% 88% 11% •
1	K	283	 % 87% 11% •
1	L	283	 2% 84% 13% ••

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 27835 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 F420-dependent methylenetetrahydromethanopterin dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	282	2182	1369	357	437	19	0	0	0
1	B	282	2182	1369	357	437	19	0	0	0
1	C	282	2187	1373	357	437	20	0	1	0
1	D	282	2182	1369	357	437	19	0	0	0
1	E	282	2182	1369	357	437	19	0	0	0
1	F	282	2182	1369	357	437	19	0	0	0
1	G	282	2187	1373	357	437	20	0	1	0
1	H	282	2187	1372	357	439	19	0	1	0
1	I	282	2187	1373	357	437	20	0	1	0
1	J	282	2182	1369	357	437	19	0	0	0
1	K	282	2194	1378	358	439	19	0	2	0
1	L	282	2185	1371	357	438	19	0	1	0

- Molecule 2 is 1-{4-[(6S,6aR,7R)-3-amino-6,7-dimethyl-1-oxo-1,2,5,6,6a,7-hexahydro-8H-imidazo[1,5-f]pteridin-10-ium-8-yl]phenyl}-1-deoxy-5-O-{5-O-[(S)-{(1S)-1,3-dicarboxypropyl}oxy}(hydroxy)phosphoryl]-alpha-D-ribofuranosyl}-D-ribitol (three-letter code: E4M) (formula: C₃₁H₄₄N₆O₁₆P).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	J	1	Total Ca 1 1	0	0
3	K	2	Total Ca 2 2	0	0
3	E	1	Total Ca 1 1	0	0
3	B	1	Total Ca 1 1	0	0
3	I	1	Total Ca 1 1	0	0
3	L	1	Total Ca 1 1	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	F	1	Total Na 1 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	55	Total O 55 55	0	0
5	B	110	Total O 110 110	0	0
5	C	95	Total O 95 95	0	0
5	D	78	Total O 78 78	0	0
5	E	88	Total O 88 88	0	0
5	F	99	Total O 99 99	0	0
5	G	74	Total O 74 74	0	0
5	H	108	Total O 108 108	0	0
5	I	116	Total O 116 116	0	0
5	J	62	Total O 62 62	0	0
5	K	88	Total O 88 88	0	0

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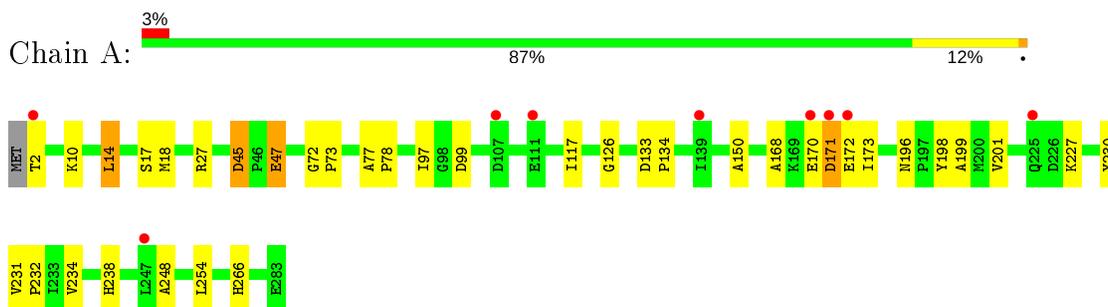
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	95	Total	O	0	0
			95	95		

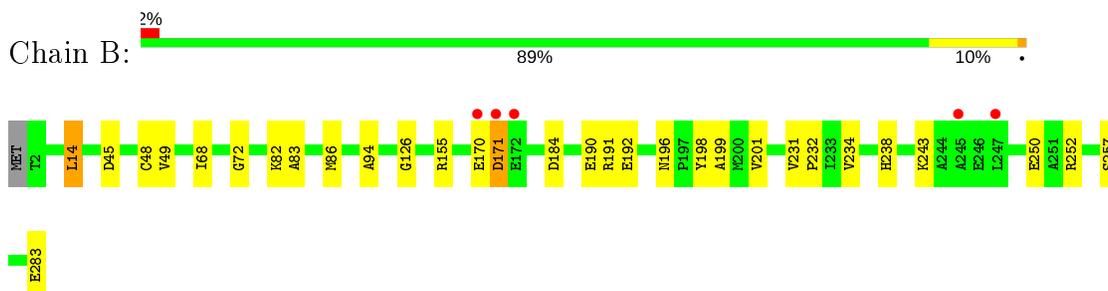
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

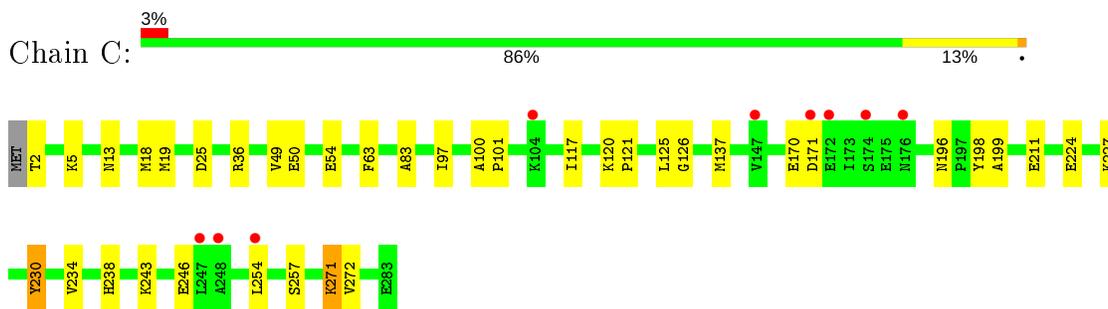
- Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase



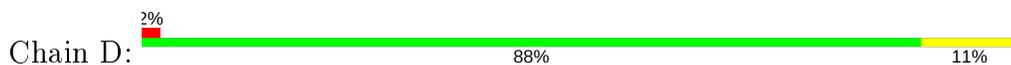
- Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase



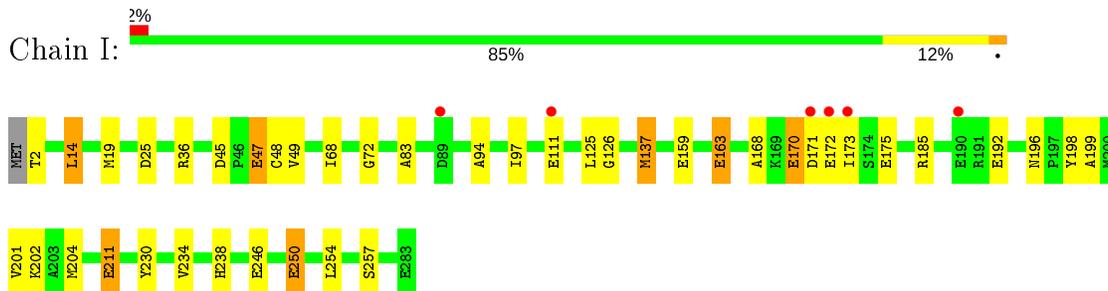
- Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase



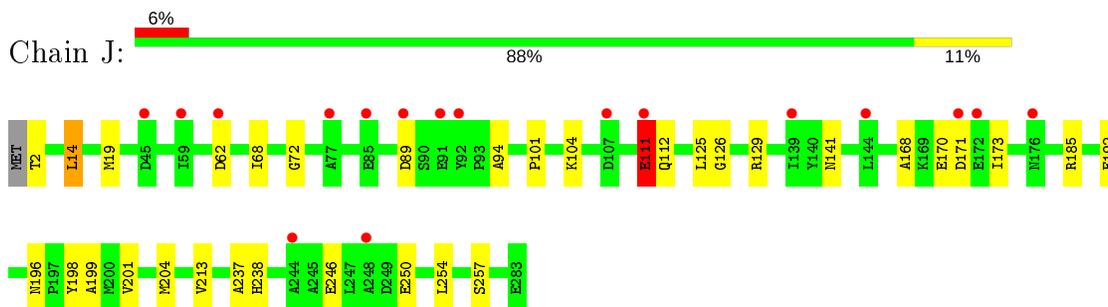
- Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase



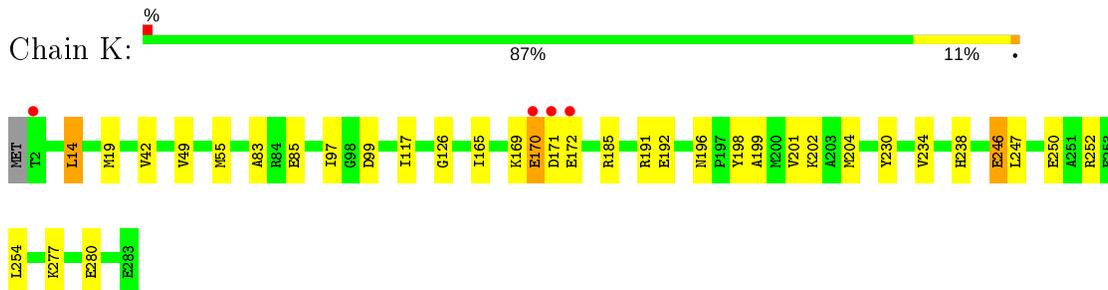
- Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase



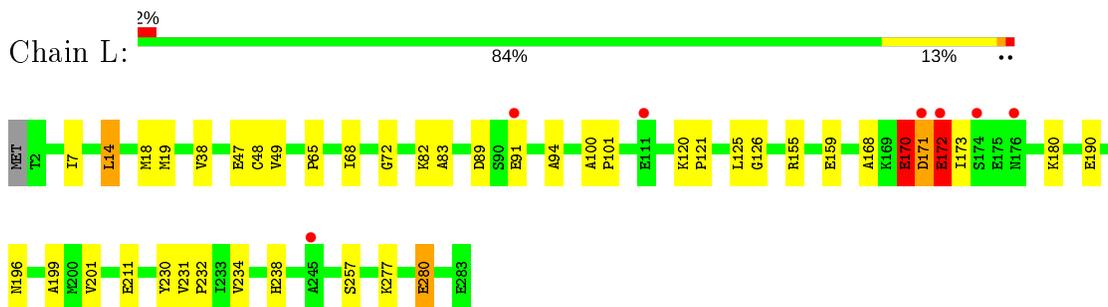
- Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase



- Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase



- Molecule 1: F420-dependent methylenetetrahydromethanopterin dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	103.40Å 167.10Å 122.50Å 90.00° 113.60° 90.00°	Depositor
Resolution (Å)	112.50 – 2.10 48.02 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.2 (112.50-2.10) 99.2 (48.02-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.67 (at 2.10Å)	Xtrriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.160 , 0.200 0.172 , 0.208	Depositor DCC
R_{free} test set	11021 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	30.9	Xtrriage
Anisotropy	0.255	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	27835	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 63.47 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.6236e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: NA, CA, E4M

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	0.75	0/2215	0.77	1/2989 (0.0%)
1	B	0.89	1/2215 (0.0%)	0.91	8/2989 (0.3%)
1	C	0.84	1/2223 (0.0%)	0.82	2/2999 (0.1%)
1	D	0.78	1/2215 (0.0%)	0.77	1/2989 (0.0%)
1	E	0.78	0/2215	0.85	3/2989 (0.1%)
1	F	0.85	0/2215	0.81	1/2989 (0.0%)
1	G	0.80	2/2223 (0.1%)	0.77	2/2999 (0.1%)
1	H	0.83	0/2223	0.86	4/3001 (0.1%)
1	I	0.91	4/2223 (0.2%)	0.83	0/2999
1	J	0.79	2/2215 (0.1%)	0.78	1/2989 (0.0%)
1	K	0.89	0/2233	0.93	6/3012 (0.2%)
1	L	0.88	2/2221 (0.1%)	0.86	4/2997 (0.1%)
All	All	0.83	13/26636 (0.0%)	0.83	33/35941 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	D	0	1
1	F	0	2
1	J	0	2
1	L	0	3
All	All	0	9

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	250	GLU	CB-CG	-8.83	1.35	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	111	GLU	CB-CG	7.78	1.67	1.52
1	J	111	GLU	CG-CD	7.24	1.62	1.51
1	B	250	GLU	CB-CG	-6.12	1.40	1.52
1	I	211	GLU	CB-CG	-5.90	1.41	1.52

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	191	ARG	NE-CZ-NH2	-15.43	112.58	120.30
1	B	191	ARG	NE-CZ-NH2	-15.14	112.73	120.30
1	E	191	ARG	NE-CZ-NH2	-12.79	113.90	120.30
1	K	191	ARG	NE-CZ-NH1	11.80	126.20	120.30
1	H	191	ARG	NE-CZ-NH2	-10.61	115.00	120.30

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	170	GLU	Peptide
1	D	170	GLU	Peptide
1	F	170	GLU	Peptide
1	F	171	ASP	Peptide
1	J	111	GLU	Mainchain

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	2182	0	2157	22	0
1	B	2182	0	2157	16	0
1	C	2187	0	2166	26	0
1	D	2182	0	2157	15	0
1	E	2182	0	2157	29	1
1	F	2182	0	2157	20	0
1	G	2187	0	2166	20	0
1	H	2187	0	2161	24	0
1	I	2187	0	2166	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	2182	0	2157	26	0
1	K	2194	0	2176	21	1
1	L	2185	0	2162	25	0
2	A	45	0	36	0	0
2	B	45	0	36	1	0
2	C	45	0	36	3	0
2	D	45	0	36	0	0
2	E	45	0	36	0	0
2	F	45	0	36	1	0
2	G	45	0	36	1	0
2	H	45	0	36	2	0
2	I	45	0	36	4	0
2	J	45	0	36	3	0
2	K	45	0	36	1	0
2	L	45	0	36	0	0
3	B	1	0	0	0	0
3	E	1	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
3	K	2	0	0	1	0
3	L	1	0	0	0	0
4	F	1	0	0	0	0
5	A	55	0	0	0	0
5	B	110	0	0	0	0
5	C	95	0	0	2	0
5	D	78	0	0	0	0
5	E	88	0	0	1	0
5	F	99	0	0	2	0
5	G	74	0	0	0	0
5	H	108	0	0	4	0
5	I	116	0	0	6	0
5	J	62	0	0	2	0
5	K	88	0	0	3	0
5	L	95	0	0	3	0
All	All	27835	0	26371	255	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 5.

The worst 5 of 255 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:I:48:CYS:SG	5:K:482:HOH:O	2.12	1.06
1:B:48:CYS:SG	5:F:779:HOH:O	2.13	1.05
5:H:1201:HOH:O	1:L:48:CYS:SG	2.20	0.99
1:H:126:GLY:H	1:H:238:HIS:HE1	1.08	0.96
1:I:137[A]:MET:HE2	2:I:284:E4M:HN8	1.34	0.93

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:2:THR:N	1:K:172:GLU:OE2[1_554]	1.92	0.28

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	280/283 (99%)	269 (96%)	10 (4%)	1 (0%)	34	32
1	B	280/283 (99%)	272 (97%)	7 (2%)	1 (0%)	34	32
1	C	281/283 (99%)	275 (98%)	6 (2%)	0	100	100
1	D	280/283 (99%)	274 (98%)	5 (2%)	1 (0%)	34	32
1	E	280/283 (99%)	272 (97%)	7 (2%)	1 (0%)	34	32
1	F	280/283 (99%)	272 (97%)	6 (2%)	2 (1%)	22	18
1	G	281/283 (99%)	270 (96%)	10 (4%)	1 (0%)	34	32
1	H	281/283 (99%)	273 (97%)	7 (2%)	1 (0%)	34	32
1	I	281/283 (99%)	273 (97%)	8 (3%)	0	100	100
1	J	280/283 (99%)	270 (96%)	10 (4%)	0	100	100
1	K	282/283 (100%)	273 (97%)	9 (3%)	0	100	100
1	L	281/283 (99%)	271 (96%)	10 (4%)	0	100	100
All	All	3367/3396 (99%)	3264 (97%)	95 (3%)	8 (0%)	47	49

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	171	ASP
1	D	171	ASP
1	F	171	ASP
1	H	171	ASP
1	E	171	ASP

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	233/234 (100%)	227 (97%)	6 (3%)	46	50
1	B	233/234 (100%)	229 (98%)	4 (2%)	60	67
1	C	234/234 (100%)	228 (97%)	6 (3%)	46	50
1	D	233/234 (100%)	222 (95%)	11 (5%)	26	25
1	E	233/234 (100%)	222 (95%)	11 (5%)	26	25
1	F	233/234 (100%)	225 (97%)	8 (3%)	37	39
1	G	234/234 (100%)	227 (97%)	7 (3%)	41	44
1	H	234/234 (100%)	228 (97%)	6 (3%)	46	50
1	I	234/234 (100%)	223 (95%)	11 (5%)	26	25
1	J	233/234 (100%)	224 (96%)	9 (4%)	32	33
1	K	235/234 (100%)	228 (97%)	7 (3%)	41	44
1	L	234/234 (100%)	226 (97%)	8 (3%)	37	39
All	All	2803/2808 (100%)	2709 (97%)	94 (3%)	38	39

5 of 94 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	190	GLU
1	G	230	TYR
1	L	14	LEU
1	F	230	TYR

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Mol	Chain	Res	Type
1	G	89	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	238	HIS
1	G	196	ASN
1	L	196	ASN
1	F	196	ASN
1	F	212	ASN

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](#)

Of 20 ligands modelled in this entry, 8 are monoatomic - leaving 12 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	E4M	K	284	-	45,49,58	1.79	4 (8%)	60,74,86	1.92	11 (18%)
2	E4M	I	284	-	45,49,58	1.71	4 (8%)	60,74,86	2.16	15 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	E4M	G	284	-	45,49,58	1.60	3 (6%)	60,74,86	2.15	12 (20%)
2	E4M	E	284	-	45,49,58	1.76	4 (8%)	60,74,86	1.96	14 (23%)
2	E4M	C	284	-	45,49,58	1.89	4 (8%)	60,74,86	1.91	14 (23%)
2	E4M	A	284	-	45,49,58	1.61	3 (6%)	60,74,86	1.90	14 (23%)
2	E4M	L	284	-	45,49,58	1.80	3 (6%)	60,74,86	1.98	14 (23%)
2	E4M	J	284	-	45,49,58	1.72	3 (6%)	60,74,86	1.85	13 (21%)
2	E4M	H	284	-	45,49,58	1.75	3 (6%)	60,74,86	1.99	13 (21%)
2	E4M	F	284	-	45,49,58	1.70	5 (11%)	60,74,86	2.02	10 (16%)
2	E4M	D	284	-	45,49,58	1.70	2 (4%)	60,74,86	2.04	14 (23%)
2	E4M	B	284	-	45,49,58	1.77	5 (11%)	60,74,86	2.19	13 (21%)

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
2	E4M	K	284	-	-	5/27/71/85	0/5/5/5
2	E4M	I	284	-	-	2/27/71/85	0/5/5/5
2	E4M	G	284	-	-	5/27/71/85	0/5/5/5
2	E4M	E	284	-	-	9/27/71/85	0/5/5/5
2	E4M	C	284	-	-	5/27/71/85	0/5/5/5
2	E4M	A	284	-	-	10/27/71/85	0/5/5/5
2	E4M	L	284	-	-	5/27/71/85	0/5/5/5
2	E4M	J	284	-	-	5/27/71/85	0/5/5/5
2	E4M	H	284	-	-	5/27/71/85	0/5/5/5
2	E4M	F	284	-	-	2/27/71/85	0/5/5/5
2	E4M	D	284	-	-	2/27/71/85	0/5/5/5
2	E4M	B	284	-	-	5/27/71/85	0/5/5/5

The worst 5 of 43 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	284	E4M	C10-N5	9.65	1.46	1.32
2	L	284	E4M	C10-N5	9.52	1.45	1.32
2	J	284	E4M	C10-N5	9.26	1.45	1.32
2	B	284	E4M	C10-N5	9.19	1.45	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	284	E4M	C10-N5	9.06	1.45	1.32

The worst 5 of 157 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	284	E4M	C4-C4A-C8A	9.38	120.67	114.53
2	B	284	E4M	C4-C4A-C8A	8.88	120.34	114.53
2	G	284	E4M	O4J-C1J-OX5	-8.53	102.59	111.95
2	H	284	E4M	C4-C4A-C8A	8.46	120.06	114.53
2	I	284	E4M	C4-C4A-C8A	7.99	119.75	114.53

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	K	284	E4M	C5J-O5J-PA-O2A
2	K	284	E4M	C5J-O5J-PA-O1A
2	K	284	E4M	C5J-O5J-PA-O3A
2	K	284	E4M	C2J-C1J-OX5-CX5
2	K	284	E4M	O4J-C1J-OX5-CX5

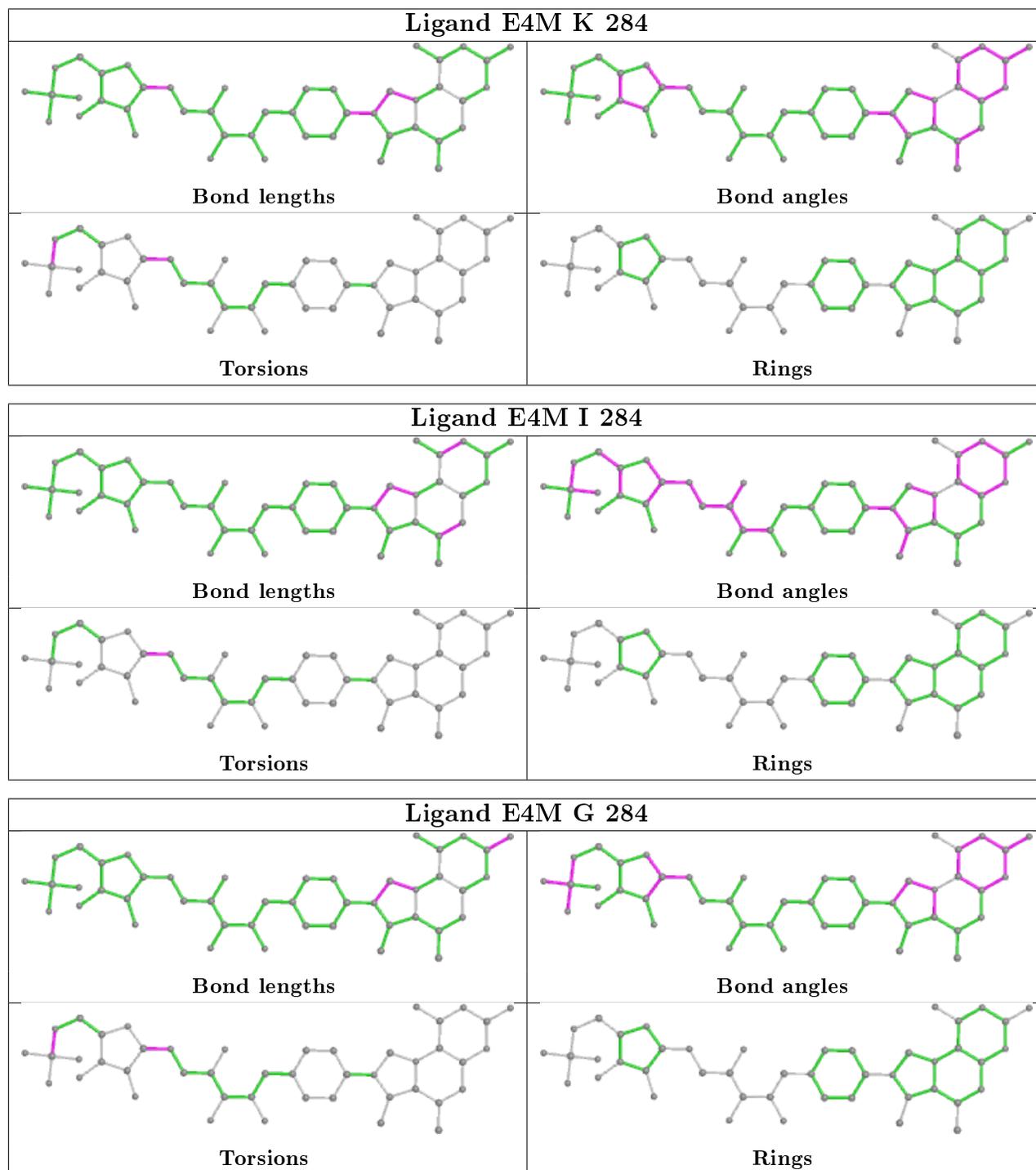
There are no ring outliers.

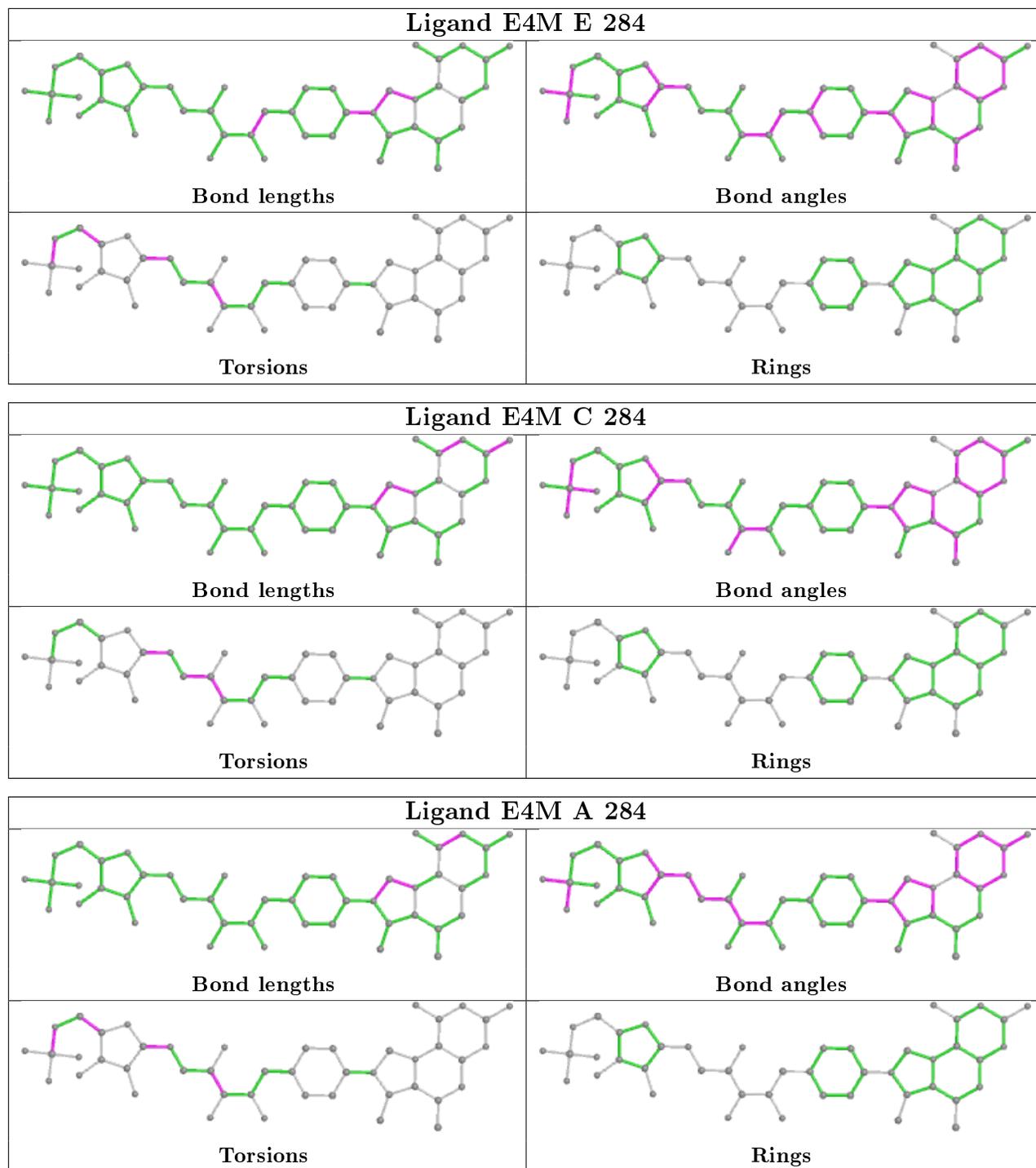
8 monomers are involved in 16 short contacts:

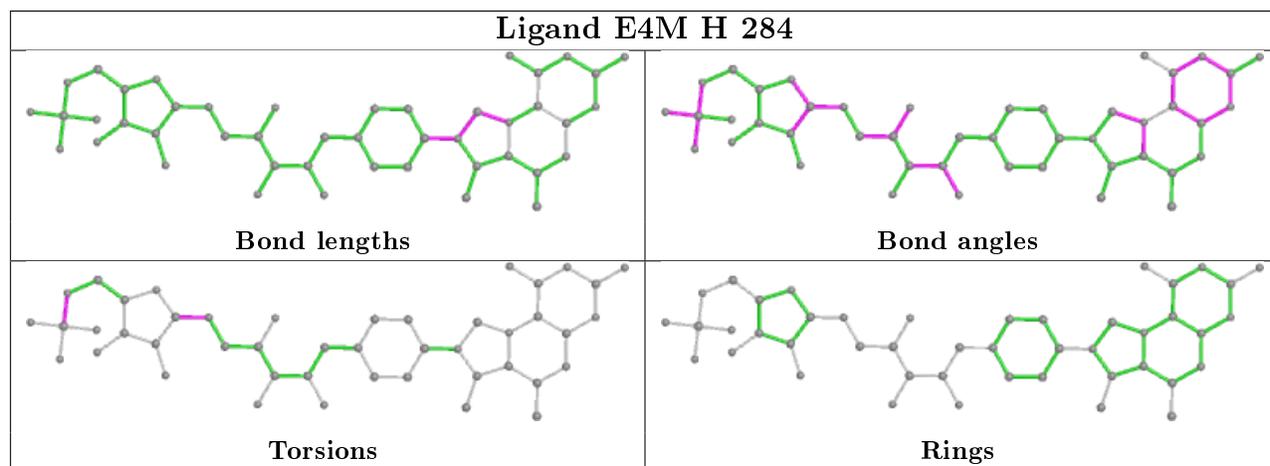
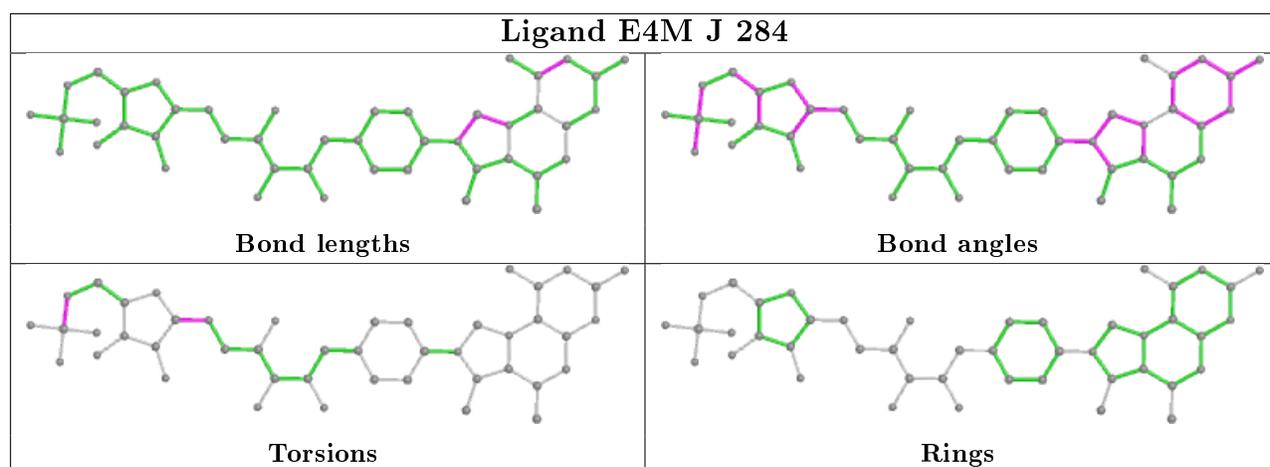
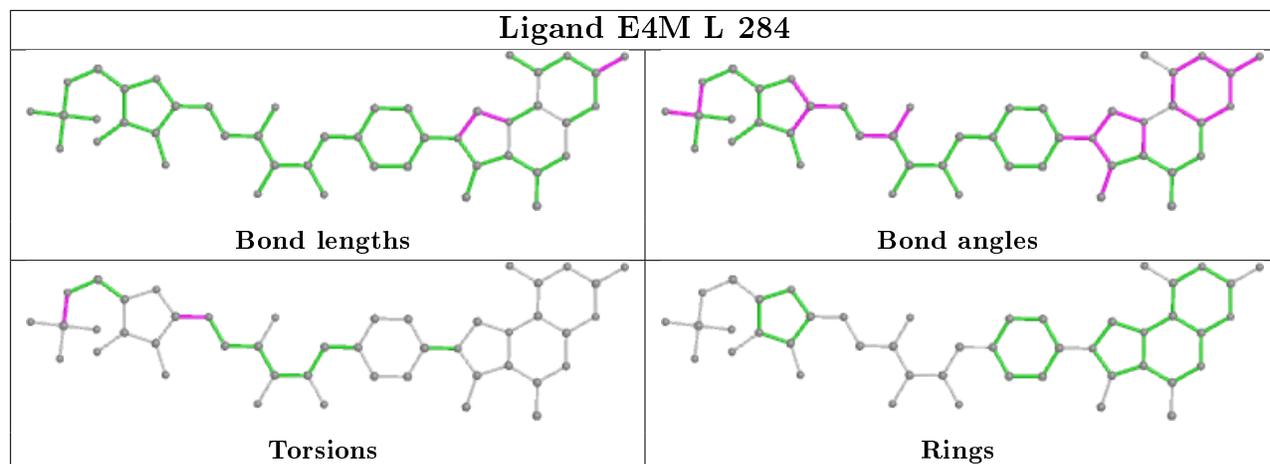
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	K	284	E4M	1	0
2	I	284	E4M	4	0
2	G	284	E4M	1	0
2	C	284	E4M	3	0
2	J	284	E4M	3	0
2	H	284	E4M	2	0
2	F	284	E4M	1	0
2	B	284	E4M	1	0

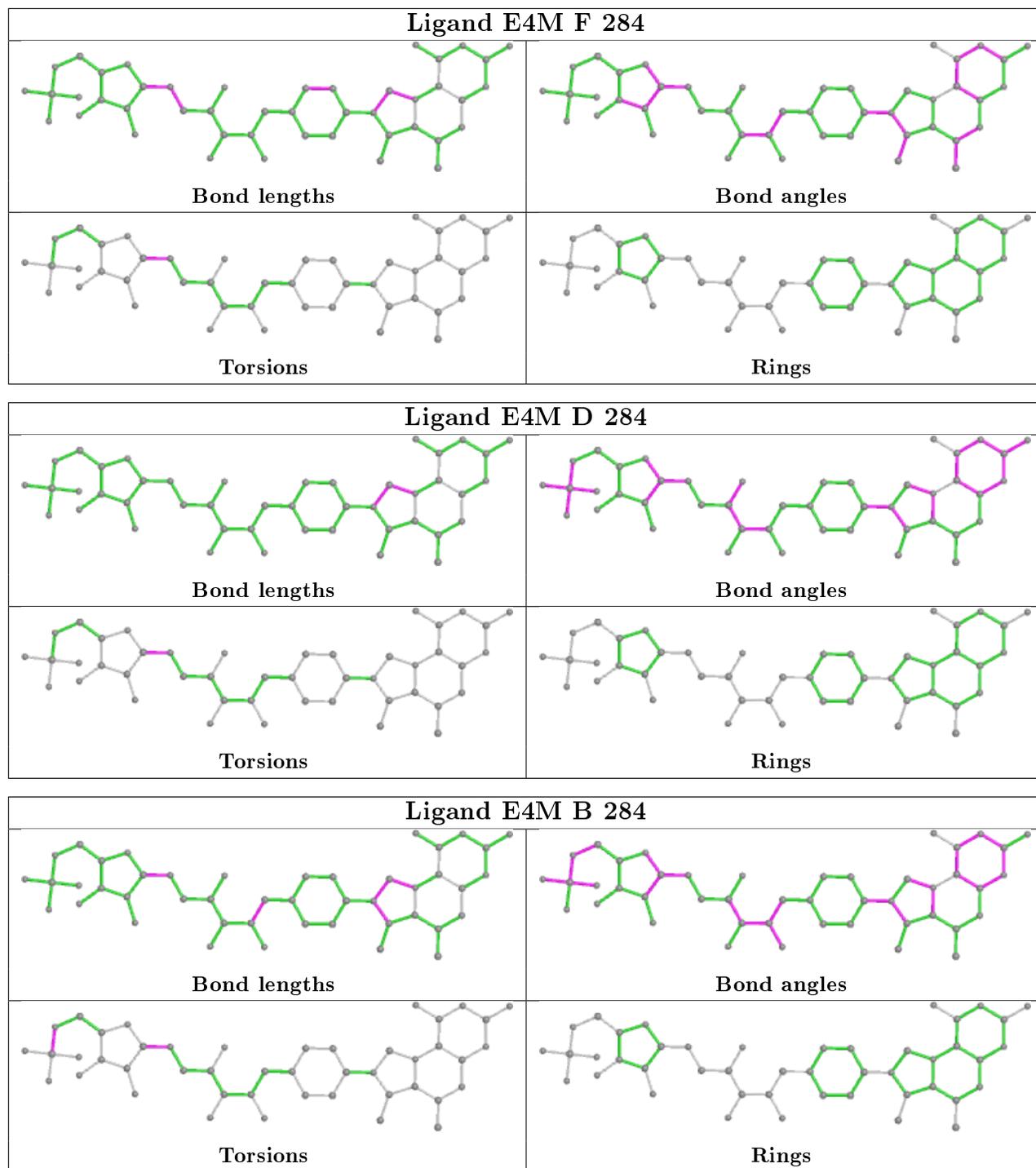
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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	282/283 (99%)	0.11	9 (3%) 47 54	22, 27, 36, 54	0
1	B	282/283 (99%)	-0.13	5 (1%) 68 72	21, 27, 37, 54	1 (0%)
1	C	282/283 (99%)	-0.01	9 (3%) 47 54	21, 27, 36, 54	1 (0%)
1	D	282/283 (99%)	0.07	7 (2%) 57 62	21, 27, 37, 54	0
1	E	282/283 (99%)	0.07	11 (3%) 39 45	20, 27, 36, 54	1 (0%)
1	F	282/283 (99%)	0.05	11 (3%) 39 45	21, 27, 37, 54	1 (0%)
1	G	282/283 (99%)	0.08	10 (3%) 44 50	20, 25, 35, 54	0
1	H	282/283 (99%)	-0.06	8 (2%) 53 59	19, 25, 36, 54	1 (0%)
1	I	282/283 (99%)	-0.08	6 (2%) 63 68	19, 26, 36, 54	1 (0%)
1	J	282/283 (99%)	0.15	17 (6%) 21 27	19, 25, 35, 54	0
1	K	282/283 (99%)	-0.19	4 (1%) 75 78	19, 25, 37, 54	0
1	L	282/283 (99%)	-0.09	7 (2%) 57 62	18, 25, 35, 54	1 (0%)
All	All	3384/3396 (99%)	-0.00	104 (3%) 49 55	18, 26, 37, 54	7 (0%)

The worst 5 of 104 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	171	ASP	10.1
1	L	171	ASP	6.4
1	K	171	ASP	5.9
1	K	172	GLU	5.2
1	E	172	GLU	4.8

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 [i](#)

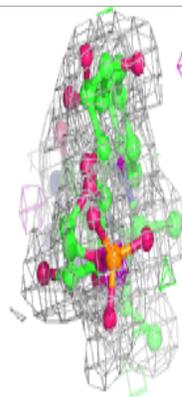
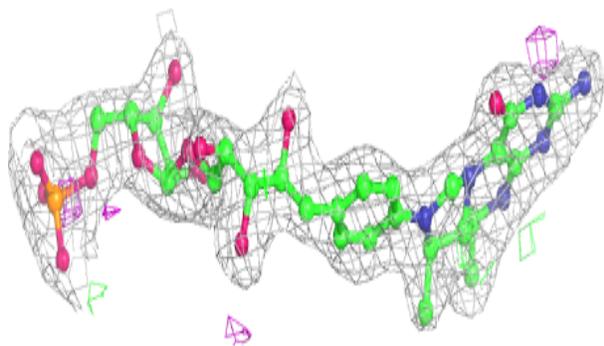
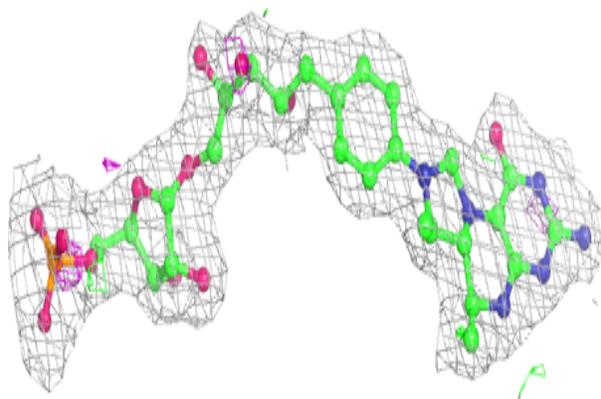
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NA	F	285	1/1	0.66	0.13	53,53,53,53	0
3	CA	B	285	1/1	0.73	0.09	98,98,98,98	0
2	E4M	G	284	45/54	0.89	0.12	28,35,54,59	0
2	E4M	A	284	45/54	0.89	0.12	39,45,70,73	0
2	E4M	J	284	45/54	0.90	0.15	37,43,64,68	0
2	E4M	F	284	45/54	0.91	0.10	27,33,58,63	0
2	E4M	D	284	45/54	0.91	0.13	29,39,57,61	0
2	E4M	C	284	45/54	0.91	0.12	29,39,58,62	0
2	E4M	L	284	45/54	0.92	0.10	24,31,49,57	0
2	E4M	K	284	45/54	0.93	0.13	25,33,59,65	0
2	E4M	B	284	45/54	0.93	0.12	26,33,55,62	0
2	E4M	E	284	45/54	0.93	0.10	27,32,54,61	0
2	E4M	I	284	45/54	0.94	0.09	24,30,56,57	0
2	E4M	H	284	45/54	0.94	0.09	25,32,50,62	0
3	CA	J	285	1/1	0.98	0.24	63,63,63,63	0
3	CA	L	285	1/1	0.98	0.20	55,55,55,55	0
3	CA	K	286	1/1	0.98	0.26	52,52,52,52	0
3	CA	I	285	1/1	0.99	0.26	52,52,52,52	0
3	CA	E	285	1/1	0.99	0.04	28,28,28,28	0
3	CA	K	285	1/1	1.00	0.06	30,30,30,30	0

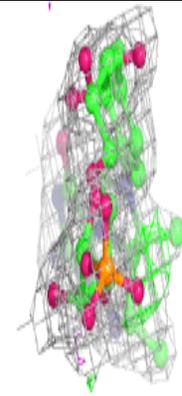
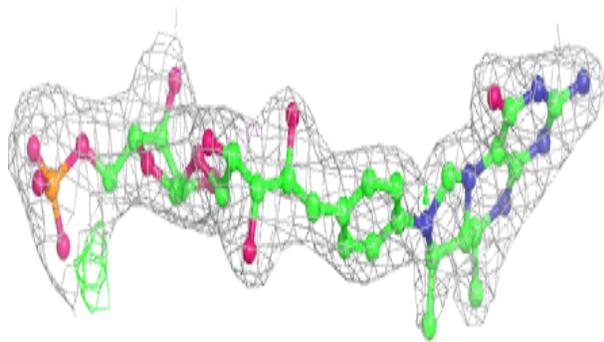
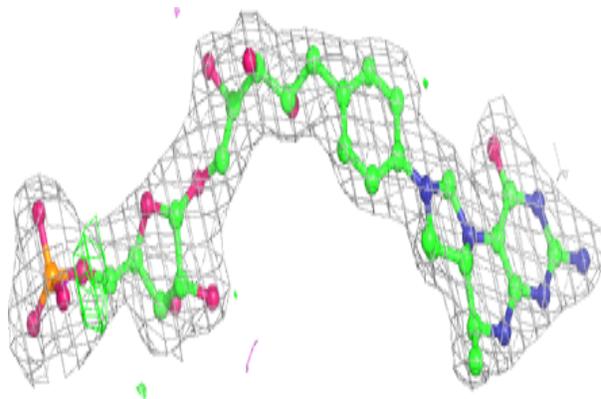
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around E4M G 284:

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

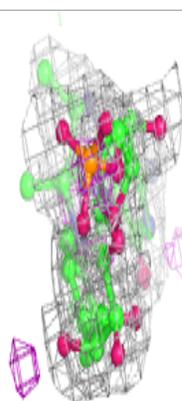
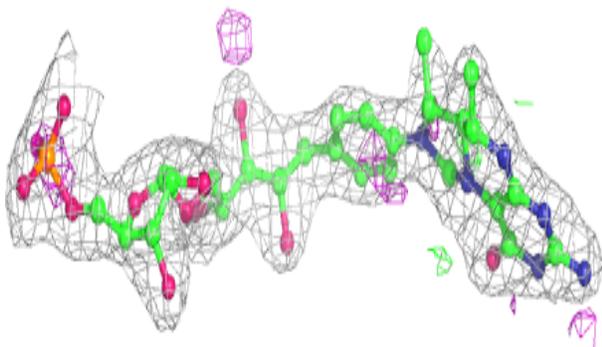
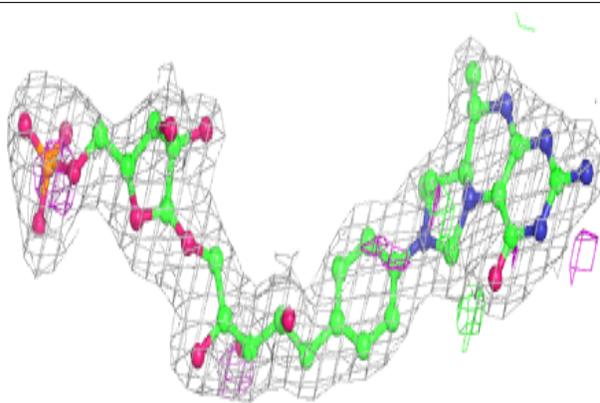
**Electron density around E4M A 284:**

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

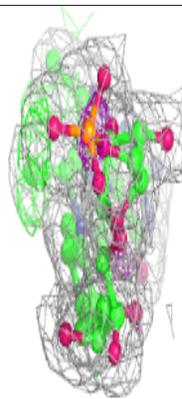
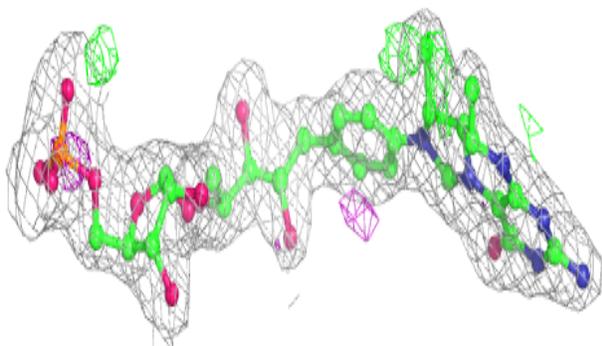
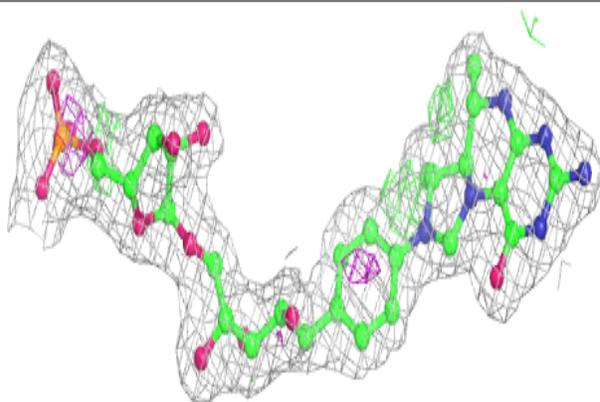


Electron density around E4M J 284:

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

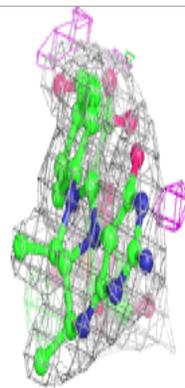
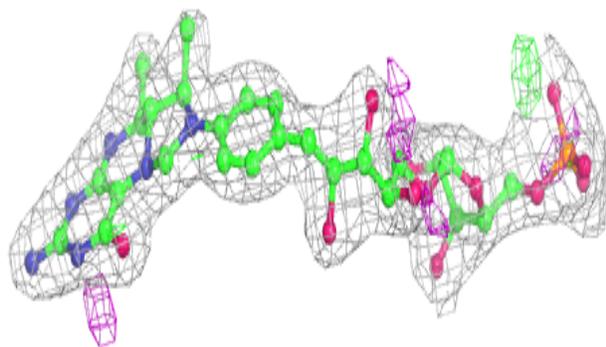
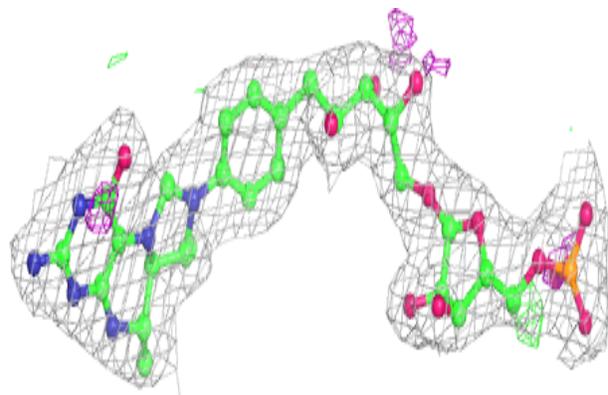
**Electron density around E4M F 284:**

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

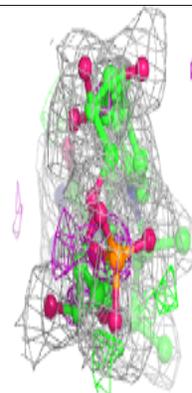
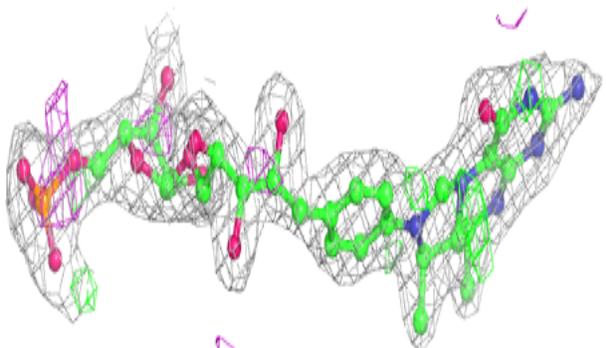
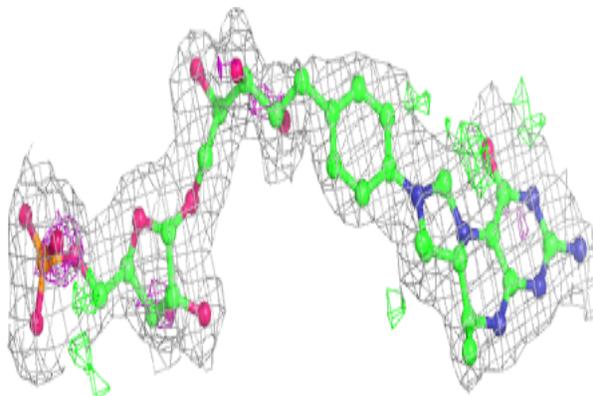


Electron density around E4M D 284:

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

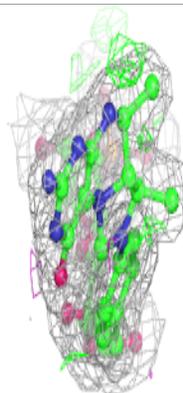
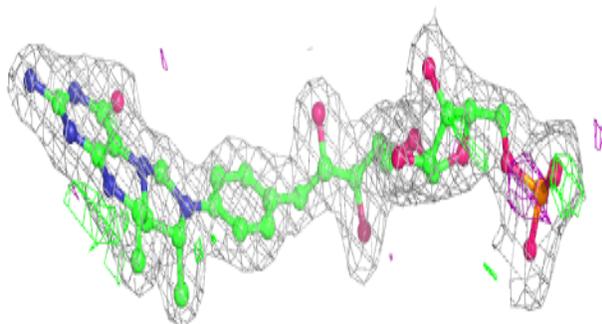
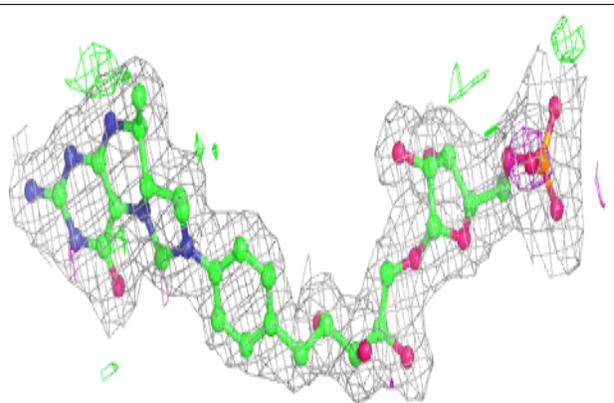
**Electron density around E4M C 284:**

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

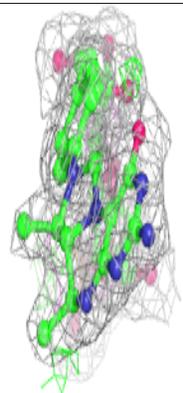
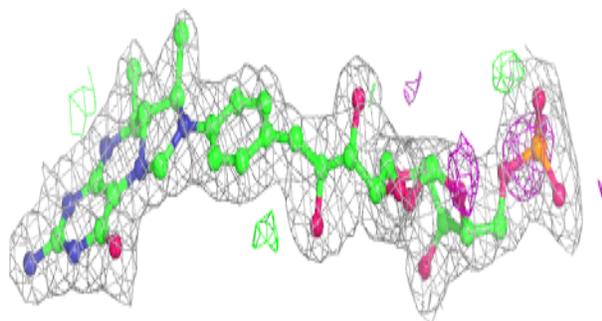
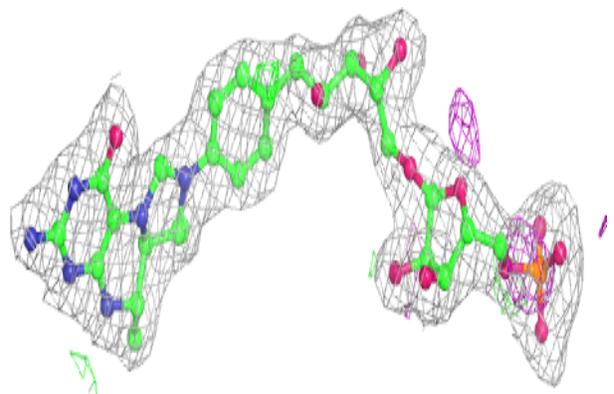


Electron density around E4M L 284:

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

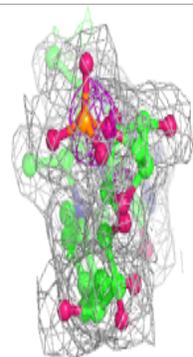
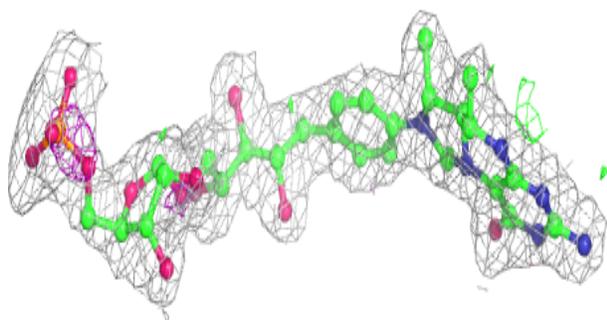
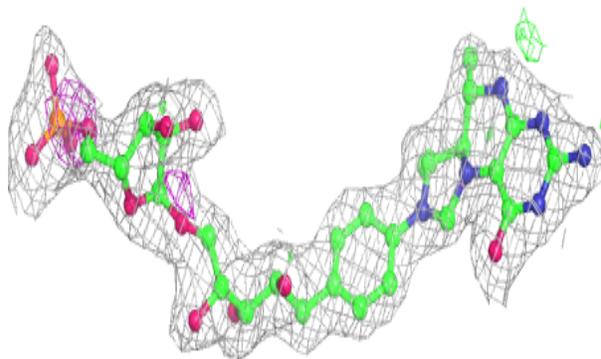
**Electron density around E4M K 284:**

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

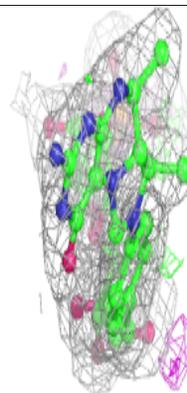
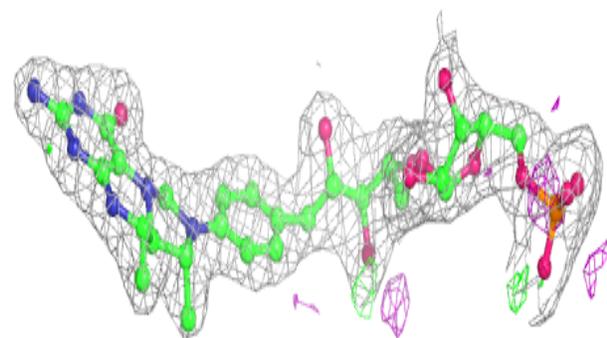
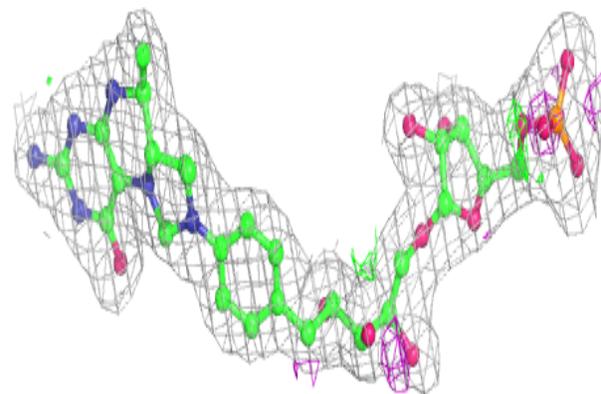


Electron density around E4M B 284:

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

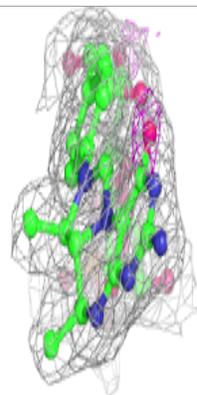
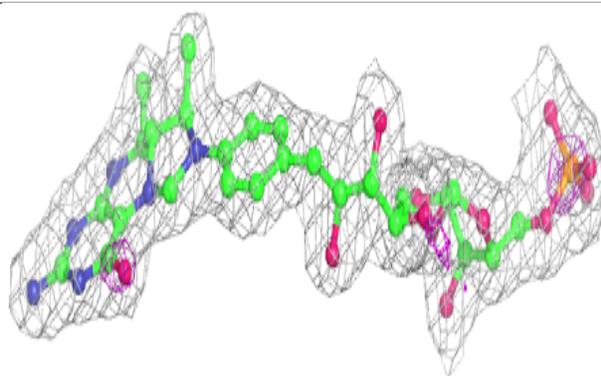
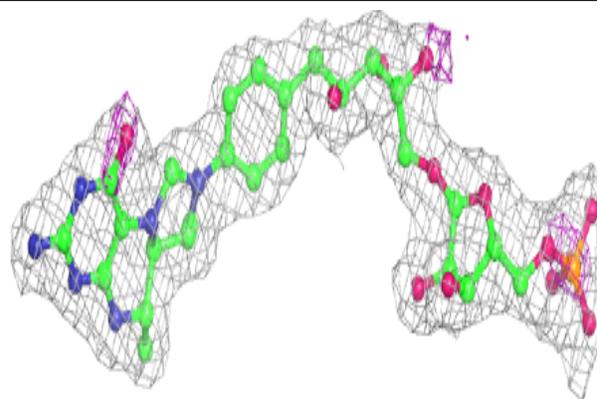
**Electron density around E4M E 284:**

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

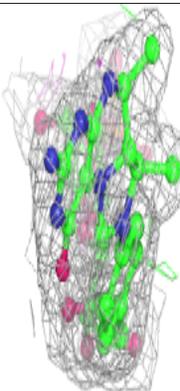
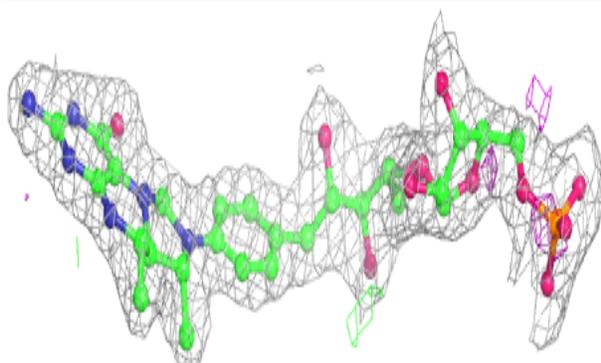
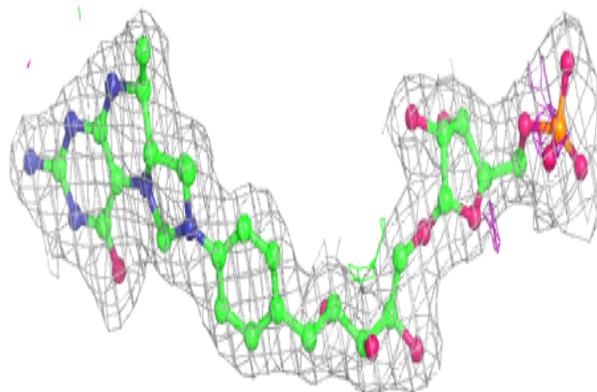


Electron density around E4M I 284:

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

**Electron density around E4M H 284:**

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



6.5 Other polymers

There are no such residues in this entry.