

# Full wwPDB X-ray Structure Validation Report (i)

#### Nov 19, 2023 – 06:17 PM JST

PDB ID	:	6LZB
Title	:	crystal structure of Human Methionine aminopeptidase (HsMetAP1b) in com-
		plex with AN-P2-5H-06
Authors	:	sandeep, C.B.; Addlagatta, A.
Deposited on	:	2020-02-18
Resolution	:	1.29 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

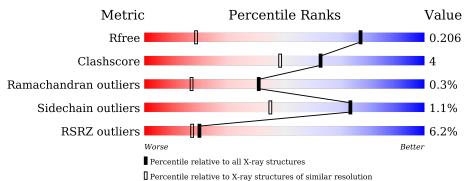
MolProbity Mogul Xtriage (Phenix) EDS	:	4.02b-467 1.8.5 (274361), CSD as541be (2020) 1.13 2.36
buster-report Percentile statistics Refmac	: : :	1.1.7 (2018) 20191225.v01 (using entries in the PDB archive December 25th 2019) 5.8.0158 7.0.044 (Gargrove)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)		Parkinson et al. (1996) 2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 1.29 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	1058 (1.30-1.30)
Clashscore	141614	1101 (1.30-1.30)
Ramachandran outliers	138981	1058 (1.30-1.30)
Sidechain outliers	138945	1058 (1.30-1.30)
RSRZ outliers	127900	1029 (1.30-1.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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		
			6%		
1	А	329	84%	8%	• 8%

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
4	GOL	А	406	-	-	Х	-



# 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 2694 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 Methionine aminopeptidase 1.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	304	Total 2455	C 1546	N 442	0 447	S 20	0	7	0

Chain	Residue	Modelled	Actual	Comment	Reference
А	65	MET	-	initiating methionine	UNP P53582
А	66	GLY	-	expression tag	UNP P53582
А	67	SER	-	expression tag	UNP P53582
А	68	SER	-	expression tag	UNP P53582
А	69	HIS	-	expression tag	UNP P53582
А	70	HIS	-	expression tag	UNP P53582
А	71	HIS	-	expression tag	UNP P53582
А	72	HIS	-	expression tag	UNP P53582
А	73	HIS	-	expression tag	UNP P53582
А	74	HIS	-	expression tag	UNP P53582
А	75	SER	-	expression tag	UNP P53582
А	76	SER	-	expression tag	UNP P53582
А	77	GLY	-	expression tag	UNP P53582
А	78	LEU	-	expression tag	UNP P53582
А	79	VAL	-	expression tag	UNP P53582
А	80	PRO	-	expression tag	UNP P53582
А	81	ARG	-	expression tag	UNP P53582
А	82	GLY	-	expression tag	UNP P53582
А	83	SER	-	expression tag	UNP P53582
А	84	HIS	-	expression tag	UNP P53582
А	85	MET	-	expression tag	UNP P53582
А	86	LEU	-	expression tag	UNP P53582
А	87	GLU	-	expression tag	UNP P53582
А	88	ASP	-	expression tag	UNP P53582
А	89	PRO	-	expression tag	UNP P53582

There are 25 discrepancies between the modelled and reference sequences:

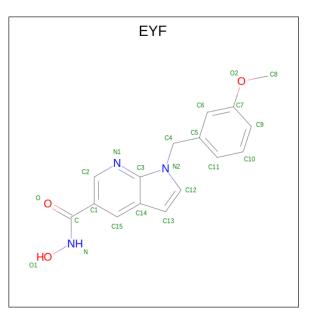
• Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co) (labeled as "Ligand



of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	2	Total Co 2 2	0	0

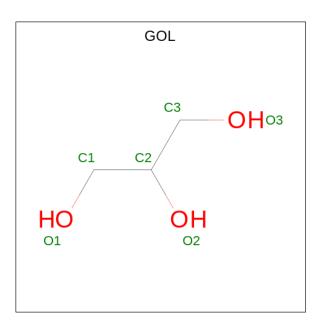
• Molecule 3 is 1-[(3-methoxyphenyl)methyl]-  $\{N\}$ -oxidanyl-pyrrolo[2,3-b]pyridine-5-carbox amide (three-letter code: EYF) (formula:  $C_{16}H_{15}N_3O_3$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	A	Aton	ns		ZeroOcc	AltConf
3	А	1	Total 22	C 16	N 3	O 3	0	0

• Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 6  3  3 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 6  3  3 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 6  3  3 \end{array}$	0	0

• Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Na 1 1	0	0

• Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	1	Total Mg 1 1	0	0

• Molecule 7 is water.

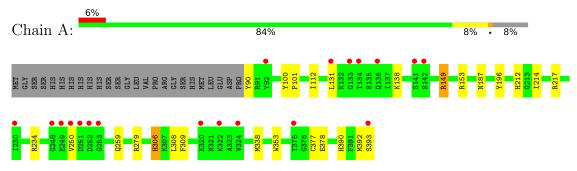
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	188	Total O 195 195	0	7



# 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: Methionine aminopeptidase 1





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	47.57Å 77.25Å 48.62Å	Denesiter
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $91.54^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	40.53 - 1.29	Depositor
Resolution (A)	40.50 - 1.29	EDS
% Data completeness	99.0 (40.53-1.29)	Depositor
(in resolution range)	99.0 (40.50-1.29)	EDS
R <sub>merge</sub>	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.67 (at 1.29 Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
D D	0.163 , $0.200$	Depositor
$R, R_{free}$	0.170 , $0.206$	DCC
$R_{free}$ test set	4192 reflections $(4.81\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	14.6	Xtriage
Anisotropy	0.535	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.34 , $45.1$	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.50, < L^2 > = 0.33$	Xtriage
	0.002 for l,k,-h	
Estimated twinning fraction	0.029 for h,-k,-l	Xtriage
	0.019 for l,-k,h	
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	2694	wwPDB-VP
Average B, all atoms $(Å^2)$	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.62% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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, EYF, CO, MG, GOL

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

Mol	Chain	Bond lengths		Bond angles	
Moi Chai	Unain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.92	0/2529	1.07	8/3429~(0.2%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	149	ARG	NE-CZ-NH2	-7.80	116.40	120.30
1	А	234	ARG	NE-CZ-NH1	6.50	123.55	120.30
1	А	234	ARG	CG-CD-NE	-6.35	98.46	111.80
1	А	279[A]	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	А	279[B]	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	А	196	TYR	CB-CA-C	5.33	121.05	110.40
1	А	279[A]	ARG	NE-CZ-NH2	-5.01	117.79	120.30
1	А	279[B]	ARG	NE-CZ-NH2	-5.01	117.79	120.30

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	А	2455	0	2417	19	0
2	А	2	0	0	0	0
3	А	22	0	0	2	0

Continued on next page...



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	А	18	0	24	4	0
5	А	1	0	0	0	0
6	А	1	0	0	0	0
7	А	195	0	0	10	2
All	All	2694	0	2441	21	2

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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 4.

All (21) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338[B]:MET:CE	7:A:555[B]:HOH:O	1.80	1.24
3:A:403:EYF:N1	4:A:406:GOL:H12	1.65	1.10
1:A:392[B]:MET:SD	7:A:657:HOH:O	2.07	1.10
1:A:90:TYR:N	7:A:504:HOH:O	2.06	0.86
1:A:338[B]:MET:HE1	7:A:555[B]:HOH:O	1.61	0.70
1:A:212:HIS:HE1	4:A:406:GOL:H2	1.64	0.63
1:A:338[B]:MET:HE3	7:A:555[B]:HOH:O	1.63	0.60
1:A:112:ILE:CD1	1:A:187:ASN:HA	2.32	0.59
1:A:212:HIS:CE1	4:A:406:GOL:H2	2.39	0.58
1:A:131:LEU:HD12	1:A:308:LEU:HD11	1.86	0.56
1:A:153[A]:ARG:CG	7:A:522:HOH:O	2.56	0.53
1:A:149:ARG:NH1	1:A:378:GLU:OE2	2.39	0.53
1:A:250:VAL:HA	7:A:623[B]:HOH:O	2.09	0.51
1:A:259:GLN:HE22	1:A:392[B]:MET:HE2	1.77	0.50
3:A:403:EYF:N1	4:A:406:GOL:C1	2.57	0.45
1:A:390:HIS:O	7:A:505:HOH:O	2.21	0.44
1:A:153[A]:ARG:HG3	7:A:522:HOH:O	2.16	0.44
1:A:138:LYS:HD3	1:A:306:HIS:CE1	2.53	0.43
1:A:214:ILE:HD11	1:A:353[A]:TRP:CE3	2.54	0.42
1:A:100:TYR:HB3	1:A:101:PRO:HA	2.01	0.42
1:A:217:ARG:NE	7:A:515:HOH:O	2.47	0.40

All (2) 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)
7:A:582:HOH:O	7:A:665:HOH:O[1_455]	1.85	0.35
7:A:524:HOH:O	7:A:665:HOH:O[1_455]	2.06	0.14



### 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	А	309/329~(94%)	303~(98%)	5 (2%)	1 (0%)	41 17

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	306	HIS

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	А	268/283~(95%)	265~(99%)	3 (1%)	73 45

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	309	PHE
1	А	377	CYS
1	А	393	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	259	GLN
1	А	365	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 monosaccharides in this entry.

#### 5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	Turne	e Chain	Res	Res Link	Bo	Bond lengths			Bond angles		
NIOI	Type				Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2	
4	GOL	А	404	-	$5,\!5,\!5$	2.12	3 (60%)	$5,\!5,\!5$	1.14	1 (20%)	
4	GOL	А	406	-	$5,\!5,\!5$	0.20	0	$5,\!5,\!5$	0.35	0	
4	GOL	А	405	-	$5,\!5,\!5$	0.15	0	$5,\!5,\!5$	0.27	0	
3	EYF	А	403	1,2	23,24,24	1.95	6 (26%)	28,33,33	2.71	10 (35%)	

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
4	GOL	А	404	-	-	1/4/4/4	-
4	GOL	А	406	-	-	4/4/4/4	-
4	GOL	А	405	-	-	2/4/4/4	-
3	EYF	А	403	1,2	-	4/12/12/12	0/3/3/3



Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
3	А	403	EYF	C-N	-5.99	1.25	1.32
3	А	403	EYF	C4-N2	-3.65	1.43	1.49
4	А	404	GOL	O1-C1	2.79	1.54	1.42
3	А	403	EYF	C2-N1	2.72	1.36	1.31
4	А	404	GOL	O2-C2	2.59	1.51	1.43
3	А	403	EYF	C13-C14	-2.55	1.26	1.45
3	А	403	EYF	C2-C1	2.52	1.43	1.39
4	А	404	GOL	C1-C2	-2.41	1.41	1.51
3	А	403	EYF	C15-C1	2.30	1.41	1.37

All (9) bond length outliers are listed below:

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
3	А	403	EYF	C1-C-N	7.86	128.76	116.16
3	А	403	EYF	O-C-N	-6.29	111.21	122.94
3	А	403	EYF	C4-C5-C6	-4.37	113.47	120.25
3	А	403	EYF	C5-C4-N2	4.08	119.38	112.71
3	А	403	EYF	C1-C15-C14	-3.47	115.89	121.24
3	А	403	EYF	C11-C5-C6	2.98	122.71	118.54
3	А	403	EYF	O1-N-C	-2.82	112.66	119.64
3	А	403	EYF	C13-C14-C15	-2.45	127.76	136.62
3	А	403	EYF	C15-C1-C	2.38	128.58	121.03
3	А	403	EYF	C2-C1-C	-2.23	113.41	120.51
4	А	404	GOL	O2-C2-C1	2.06	118.18	109.12

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	А	405	GOL	C1-C2-C3-O3
4	А	406	GOL	C1-C2-C3-O3
3	А	403	EYF	C6-C7-O2-C8
3	А	403	EYF	C9-C7-O2-C8
4	А	405	GOL	O2-C2-C3-O3
4	А	406	GOL	O1-C1-C2-C3
4	А	406	GOL	O1-C1-C2-O2
4	А	406	GOL	O2-C2-C3-O3
4	А	404	GOL	O1-C1-C2-C3
3	А	403	EYF	N2-C4-C5-C11
3	А	403	EYF	N2-C4-C5-C6

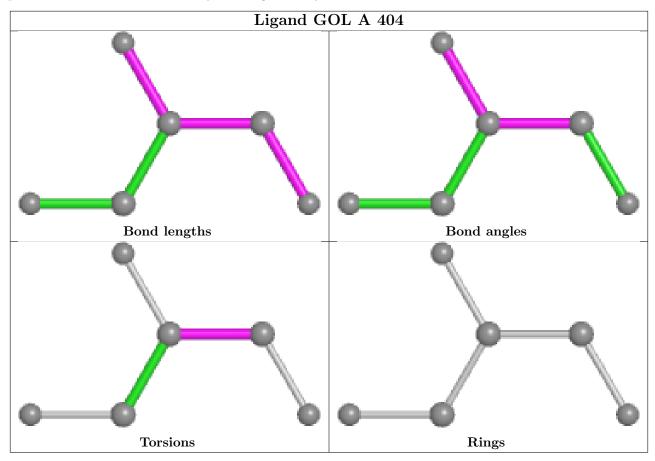


There are no ring outliers.

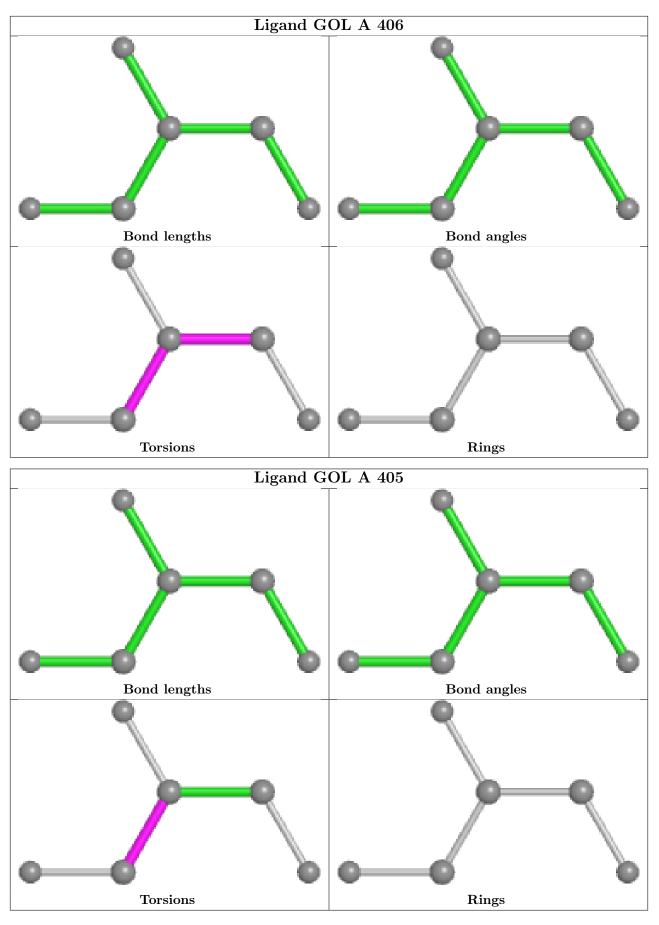
2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	А	406	GOL	4	0
3	А	403	EYF	2	0

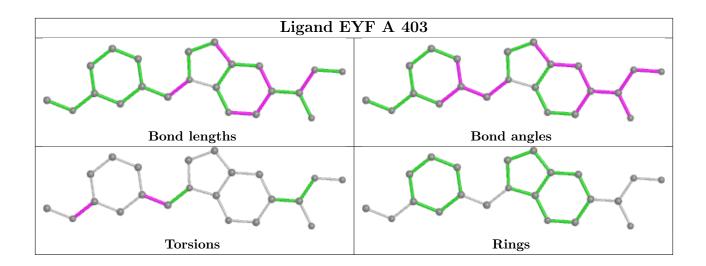
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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,  $95^{th}$  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	А	304/329~(92%)	0.22	19 (6%) 20 17	11, 25, 44, 68	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	250	VAL	4.3
1	А	134	THR	4.2
1	А	324	VAL	3.5
1	А	133	GLY	3.4
1	А	142	SER	3.1
1	А	136	GLN	3.1
1	А	322	LYS	3.0
1	А	131	LEU	2.9
1	А	252	ASP	2.8
1	А	393	SER	2.8
1	А	375	THR	2.8
1	А	251	ASP	2.5
1	А	249	GLU	2.5
1	А	253	GLY	2.3
1	А	320	LYS	2.3
1	А	92	TYR	2.1
1	А	248	GLY	2.1
1	А	141	SER	2.1
1	А	230	ILE	2.1

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

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



#### 6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

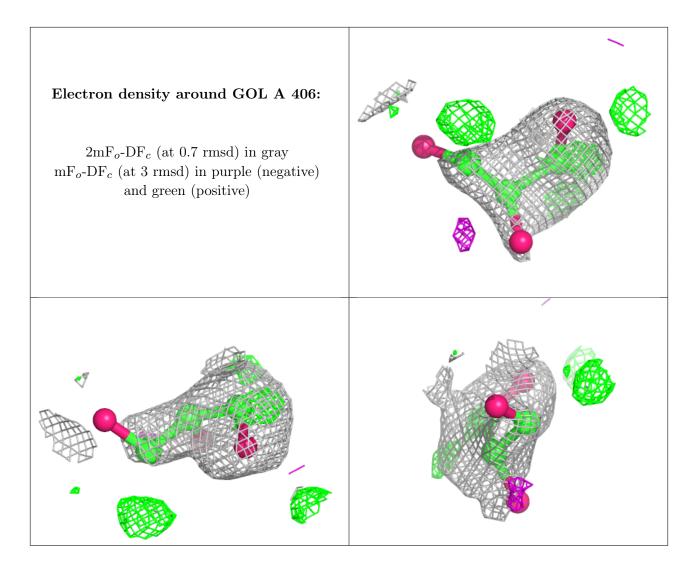
#### 6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  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.

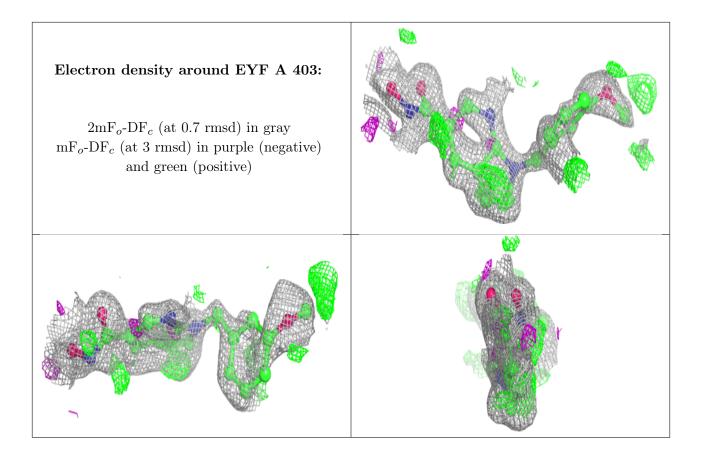
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q < 0.9
4	GOL	А	406	6/6	0.85	0.21	48,54,80,87	0
3	EYF	А	403	22/22	0.89	0.16	16,31,48,56	22
4	GOL	А	405	6/6	0.90	0.18	35,47,59,76	0
4	GOL	А	404	6/6	0.93	0.17	41,62,67,69	0
5	NA	А	407	1/1	0.99	0.05	19,19,19,19	0
6	MG	А	408	1/1	0.99	0.04	20,20,20,20	0
2	CO	А	401	1/1	1.00	0.07	16,16,16,16	0
2	CO	А	402	1/1	1.00	0.07	12,12,12,12	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.

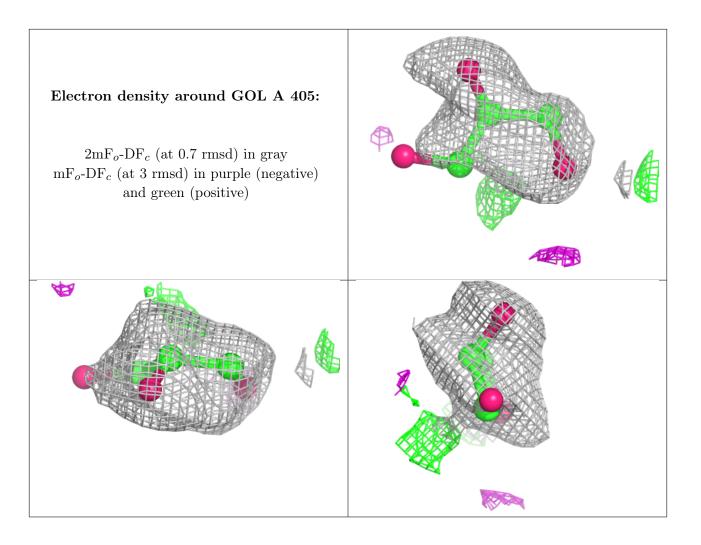




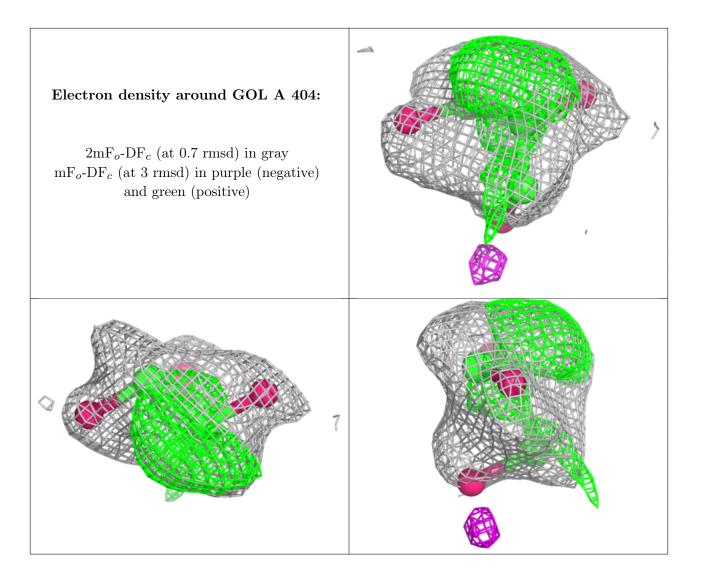




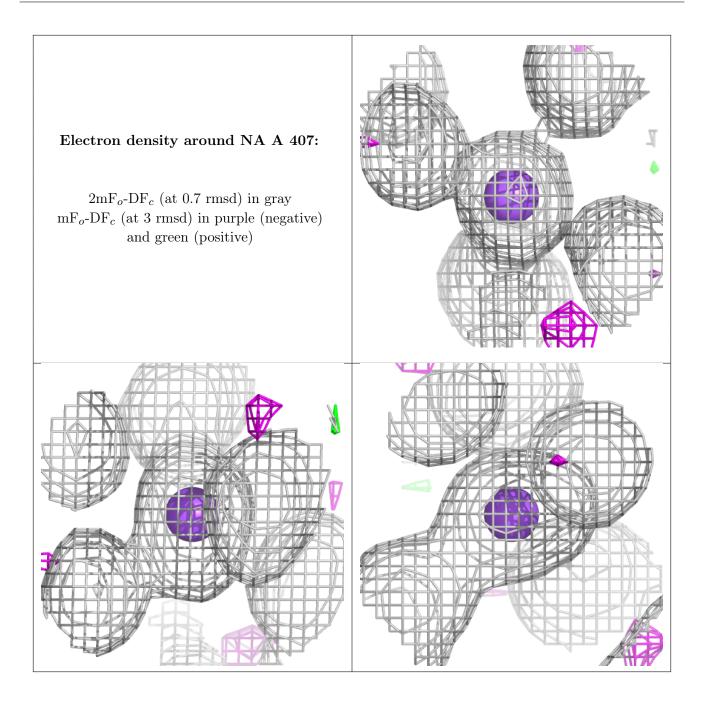




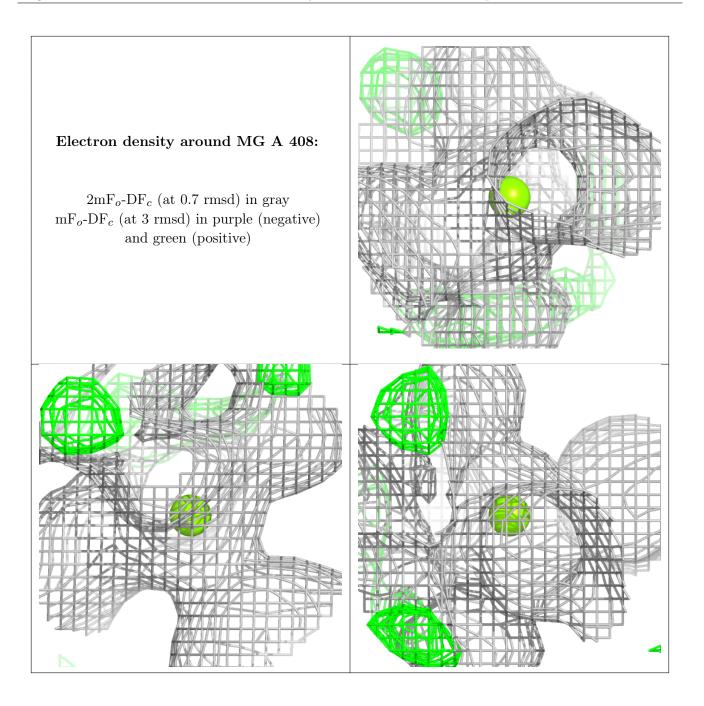




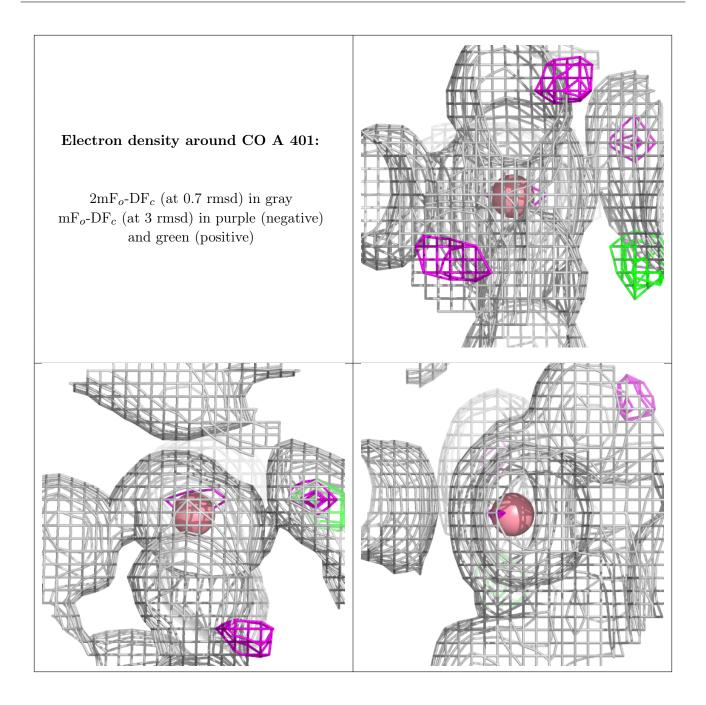




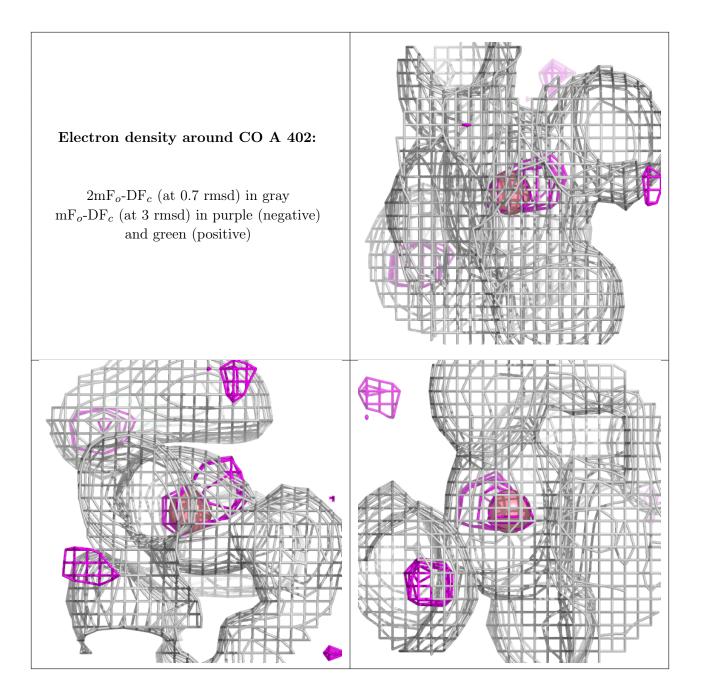












## 6.5 Other polymers (i)

There are no such residues in this entry.

