

wwPDB X-ray Structure Validation Summary Report (i)

Oct 15, 2023 – 07:27 PM EDT

PDB ID : 7RYT

Title: Crystal structure of Mycobacterium tuberculosis acetylated Homoserine

transacetylase with Coenzyme A

Authors: Jayasinghe, Y.P.; Ronning, D.R.

Deposited on : 2021-08-26

Resolution : 2.67 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 (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: 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.36

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

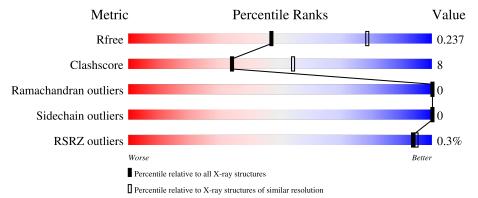
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.67 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
R_{free}	130704	3863 (2.70-2.66)
Clashscore	141614	4210 (2.70-2.66)
Ramachandran outliers	138981	4141 (2.70-2.66)
Sidechain outliers	138945	4141 (2.70-2.66)
RSRZ outliers	127900	3780 (2.70-2.66)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	368	81%	18%	•
1	В	368	86%	14%	
1	С	368	81%	18%	
1	D	368	84%	15%	•
1	Е	368	82%	18%	•

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Mol	Chain	Length	Quality of chain				
1	F	368	84%	15%	<u> </u>		



2 Entry composition (i)

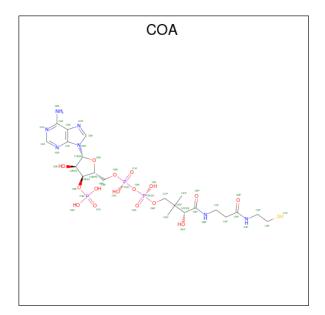
There are 5 unique types of molecules in this entry. The entry contains 16891 atoms, of which 2 are hydrogens and 0 are deuteriums.

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 Homoserine O-acetyltransferase.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	A	364	Total C N O S 2682 1672 489 515 6	0	0	0
1	В	368	Total C N O S 2719 1692 499 522 6	0	0	0
1	С	366	Total C N O S 2704 1684 497 517 6	0	0	0
1	D	366	Total C N O S 2708 1686 497 519 6	0	0	0
1	Е	365	Total C H N O S 2696 1679 1 493 517 6	0	0	0
1	F	366	Total C H N O S 2701 1681 1 496 517 6	0	0	0

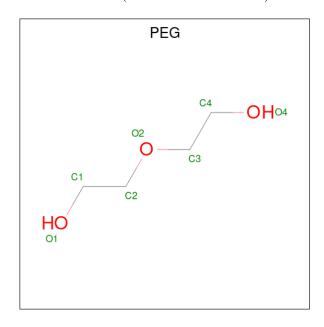
• Molecule 2 is COENZYME A (three-letter code: COA) (formula: $C_{21}H_{36}N_7O_{16}P_3S$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues		A	ton	ıs			ZeroOcc	AltConf
2	A	1	Total	С	N	О	Р	S	0	0
	A	1	48	21	7	16	3	1	0	0
2	В	1	Total	С	N	О	Р	S	0	0
2	Ъ	1	48	21	7	16	3	1	0	0
2	С	C 1	Total C N O P	Р	S	0	0			
2			48	21	7	16	3	1	0	
2	D	1	Total	С	N	О	Р	S	0	0
2	ט	1	48	21	7	16	3	1	0	0
2	Е	1	Total	С	N	О	Р	S	0	0
2	12	1	48	21	7	16	3	1	0	0
2	F	1	Total	С	N	О	Р	S	0	0
	I'	1	48	21	7	16	3	1		

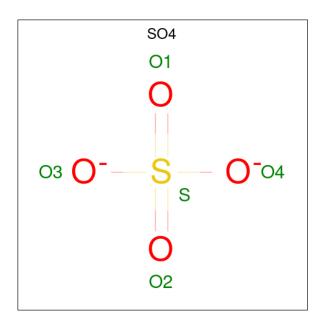
• Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 7 4 3	0	0
3	В	1	Total C O 7 4 3	0	0

 \bullet Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: $\mathrm{O_4S}).$





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	Е	1	Total O S 5 4 1	0	0

$\bullet\,$ Molecule 5 is water.

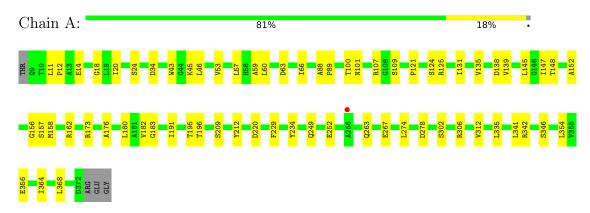
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	68	Total O 68 68	0	0
5	В	66	Total O 66 66	0	0
5	С	60	Total O 60 60	0	0
5	D	62	Total O 62 62	0	0
5	E	58	Total O 58 58	0	0
5	F	55	Total O 55 55	0	0



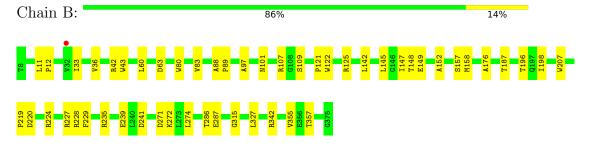
3 Residue-property plots (i)

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

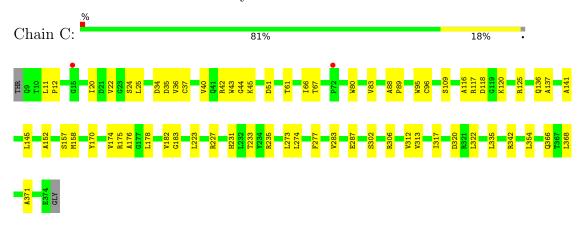
• Molecule 1: Homoserine O-acetyltransferase



• Molecule 1: Homoserine O-acetyltransferase

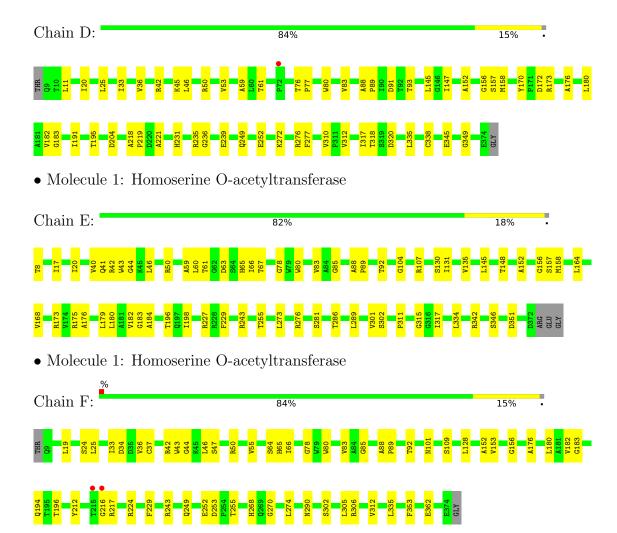


• Molecule 1: Homoserine O-acetyltransferase



• Molecule 1: Homoserine O-acetyltransferase







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	93.02Å 160.99Å 161.98Å	Domositon
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.06 - 2.67	Depositor
Resolution (A)	48.66 - 2.57	EDS
% Data completeness	98.5 (39.06-2.67)	Depositor
(in resolution range)	94.3 (48.66-2.57)	EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.98 (at 2.58Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
D D	0.179 , 0.238	Depositor
R, R_{free}	0.180 , 0.237	DCC
R_{free} test set	2001 reflections (2.67%)	wwPDB-VP
Wilson B-factor (Å ²)	25.7	Xtriage
Anisotropy	0.354	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.34 , 35.8	EDS
L-test for twinning ²	$< L >=0.46, < L^2>=0.29$	Xtriage
Estimated twinning fraction	0.026 for -h,l,k	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	16891	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.55% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities 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: COA, PEG, OAS, SO4

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		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.25	0/2726	0.42	0/3718	
1	В	0.25	0/2763	0.42	0/3766	
1	С	0.24	0/2748	0.41	0/3746	
1	D	0.24	0/2752	0.42	0/3751	
1	Е	0.25	0/2739	0.42	0/3735	
1	F	0.25	0/2744	0.43	0/3742	
All	All	0.25	0/16472	0.42	0/22458	

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	2682	0	2632	40	0
1	В	2719	0	2672	36	0
1	С	2704	0	2658	50	0
1	D	2708	0	2662	42	0
1	Е	2695	1	2650	50	0
1	F	2700	1	2647	43	0
2	A	48	0	32	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	В	48	0	32	3	0
2	С	48	0	32	5	0
2	D	48	0	32	10	0
2	Е	48	0	32	6	0
2	F	48	0	32	3	0
3	A	7	0	10	1	0
3	В	7	0	10	0	0
4	A	5	0	0	0	0
4	Ε	5	0	0	0	0
5	A	68	0	0	1	0
5	В	66	0	0	1	0
5	С	60	0	0	0	0
5	D	62	0	0	1	0
5	Ε	58	0	0	3	0
5	F	55	0	0	1	0
All	All	16889	2	16133	274	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 8.

The worst 5 of 274 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:A:312:VAL:HG21	1:A:335:LEU:HD13	1.54	0.88
1:C:118:ASP:OD2	1:C:120:LYS:HE3	1.78	0.84
1:F:46:LEU:HD11	1:F:50:ARG:HA	1.62	0.82
1:F:224:ARG:HG3	1:F:274:LEU:CD1	2.10	0.82
1:D:80:TRP:HB3	1:D:83:VAL:HB	1.64	0.80

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	Perce	ntiles
1	A	361/368 (98%)	348 (96%)	13 (4%)	0	100	100
1	В	365/368~(99%)	353 (97%)	12 (3%)	0	100	100
1	С	363/368 (99%)	344 (95%)	19 (5%)	0	100	100
1	D	363/368 (99%)	346 (95%)	17 (5%)	0	100	100
1	E	362/368~(98%)	349 (96%)	13 (4%)	0	100	100
1	F	363/368 (99%)	345 (95%)	18 (5%)	0	100	100
All	All	2177/2208 (99%)	2085 (96%)	92 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	Perce	ntiles
1	A	269/273~(98%)	269 (100%)	0	100	100
1	В	273/273 (100%)	273 (100%)	0	100	100
1	С	271/273 (99%)	271 (100%)	0	100	100
1	D	272/273 (100%)	272 (100%)	0	100	100
1	E	271/273 (99%)	271 (100%)	0	100	100
1	F	270/273 (99%)	270 (100%)	0	100	100
All	All	1626/1638 (99%)	1626 (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. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.



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

6 non-standard protein/DNA/RNA residues 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	Mol Type Chain Res L		Link	В	ond leng	gths	Bond angles				
MIOI	Type	Chain		LIIIK	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
1	OAS	В	157	1	7,8,9	0.99	0	5,9,11	1.05	0	
1	OAS	F	157	1	7,8,9	1.01	0	5,9,11	1.05	0	
1	OAS	A	157	1	7,8,9	1.01	0	5,9,11	1.06	0	
1	OAS	С	157	1	7,8,9	1.00	0	5,9,11	1.08	0	
1	OAS	D	157	1	7,8,9	1.00	0	5,9,11	1.05	0	
1	OAS	Е	157	1	7,8,9	1.00	0	5,9,11	1.08	0	

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
1	OAS	В	157	1	-	2/5/7/9	-
1	OAS	F	157	1	-	2/5/7/9	-
1	OAS	A	157	1	-	2/5/7/9	-
1	OAS	С	157	1	-	2/5/7/9	-
1	OAS	D	157	1	-	2/5/7/9	-
1	OAS	Е	157	1	-	2/5/7/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	${ m E}$	157	OAS	C2A-C1A-OG-CB
1	В	157	OAS	C2A-C1A-OG-CB
1	Ε	157	OAS	OAC-C1A-OG-CB

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Mol	Chain	Res	Type	Atoms
1	В	157	OAS	OAC-C1A-OG-CB
1	A	157	OAS	C2A-C1A-OG-CB

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	В	157	OAS	2	0
1	A	157	OAS	3	0
1	С	157	OAS	1	0
1	D	157	OAS	2	0
1	E	157	OAS	3	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

10 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	Dog	Link	Во	ond leng	ths	Bond angles		
MIOI	Type	Chain	Res	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PEG	A	402	-	6,6,6	0.90	0	5,5,5	0.66	0
2	COA	В	402	-	41,50,50	0.66	0	52,75,75	0.57	0
2	COA	D	401	-	41,50,50	0.67	0	52,75,75	0.60	0
4	SO4	A	403	-	4,4,4	0.79	0	6,6,6	0.71	0
2	COA	Е	401	-	41,50,50	0.65	0	52,75,75	0.61	0
2	COA	A	401	-	41,50,50	0.65	0	52,75,75	0.64	0
2	COA	С	401	-	41,50,50	0.67	0	52,75,75	0.62	0
4	SO4	Е	402	-	4,4,4	0.78	0	6,6,6	0.73	0
3	PEG	В	401	-	6,6,6	0.91	0	5,5,5	0.66	0
2	COA	F	401	-	41,50,50	0.65	0	52,75,75	0.58	0



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	PEG	A	402	-	-	3/4/4/4	-
2	COA	В	402	-	-	21/44/64/64	0/3/3/3
2	COA	D	401	-	-	18/44/64/64	0/3/3/3
2	COA	Е	401	-	-	11/44/64/64	0/3/3/3
2	COA	A	401	-	-	15/44/64/64	0/3/3/3
2	COA	С	401	-	-	27/44/64/64	0/3/3/3
3	PEG	В	401	-	-	0/4/4/4	-
2	COA	F	401	_	-	19/44/64/64	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 114 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	COA	C3B-C4B-C5B-O5B
2	A	401	COA	O4B-C4B-C5B-O5B
2	A	401	COA	CCP-O6A-P2A-O4A
2	A	401	COA	CCP-O6A-P2A-O5A
2	A	401	COA	CEP-CBP-CCP-O6A

There are no ring outliers.

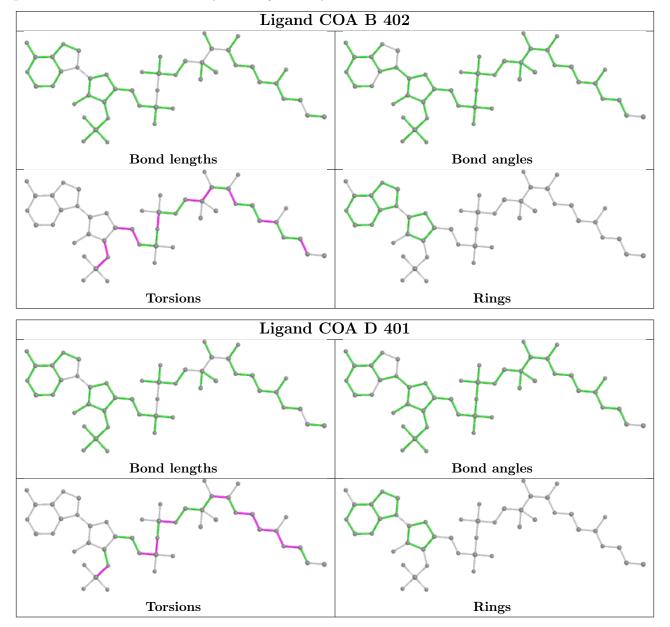
7 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	PEG	1	0
2	В	402	COA	3	0
2	D	401	COA	10	0
2	Е	401	COA	6	0
2	A	401	COA	6	0
2	С	401	COA	5	0
2	F	401	COA	3	0

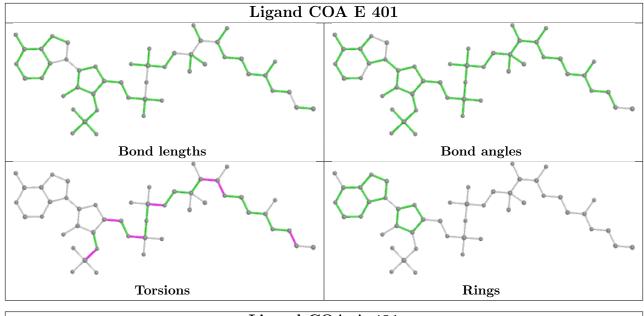
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

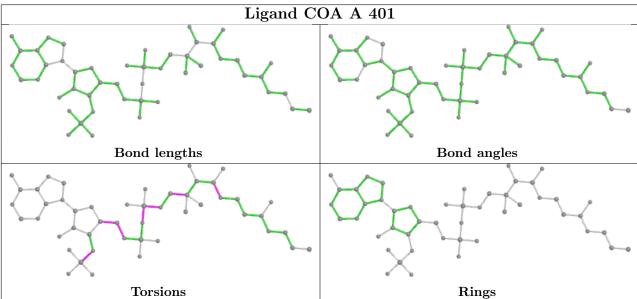


also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted 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.

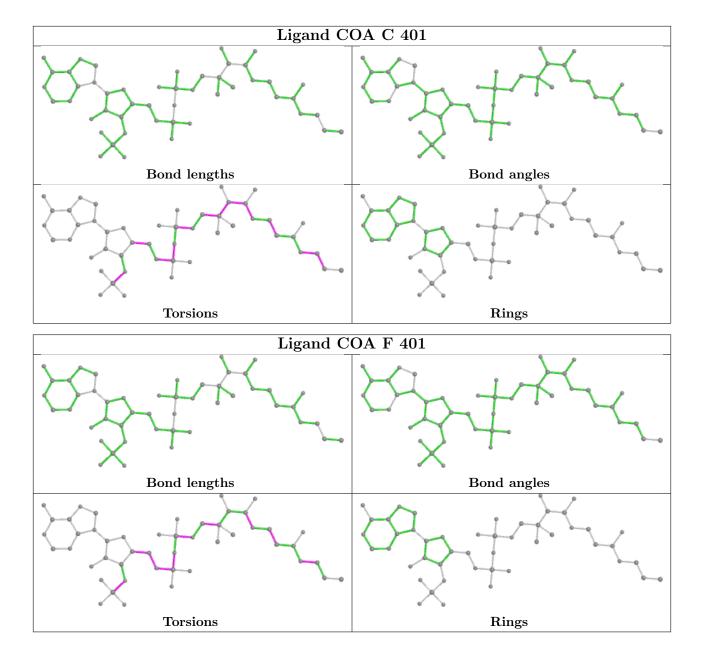












5.7 Other polymers (i)

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>	# RSRZ > 2	$OWAB(A^2)$	Q < 0.9
1	A	363/368 (98%)	-0.41	1 (0%) 94 95	10, 23, 44, 56	0
1	В	367/368~(99%)	-0.46	1 (0%) 94 95	10, 20, 38, 55	0
1	С	365/368~(99%)	-0.41	2 (0%) 91 92	11, 23, 48, 61	0
1	D	365/368~(99%)	-0.44	1 (0%) 94 95	11, 21, 42, 69	0
1	E	364/368 (98%)	-0.41	0 100 100	13, 26, 42, 49	0
1	F	365/368~(99%)	-0.42	2 (0%) 91 92	10, 23, 45, 60	0
All	All	2189/2208 (99%)	-0.43	7 (0%) 94 95	10, 23, 44, 69	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	216	GLY	4.9
1	D	72	PRO	3.4
1	С	15	GLY	2.8
1	A	256	ALA	2.2
1	С	72	PRO	2.2

6.2 Non-standard residues in protein, DNA, RNA chains (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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
1	OAS	F	157	9/10	0.87	0.22	15,18,26,27	9
1	OAS	Е	157	9/10	0.88	0.19	16,19,30,35	0
1	OAS	В	157	9/10	0.89	0.22	13,16,24,30	9
1	OAS	D	157	9/10	0.90	0.23	15,17,27,28	9

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	OAS	С	157	9/10	0.91	0.19	17,21,30,31	9
1	OAS	A	157	9/10	0.93	0.19	12,15,21,33	9

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

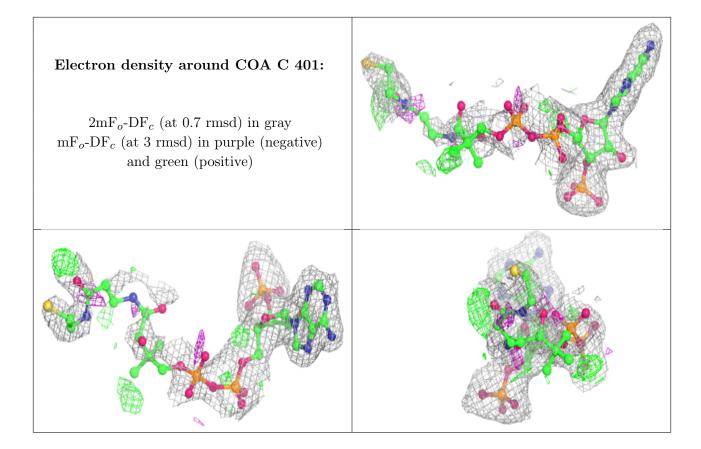
6.4 Ligands (i)

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.

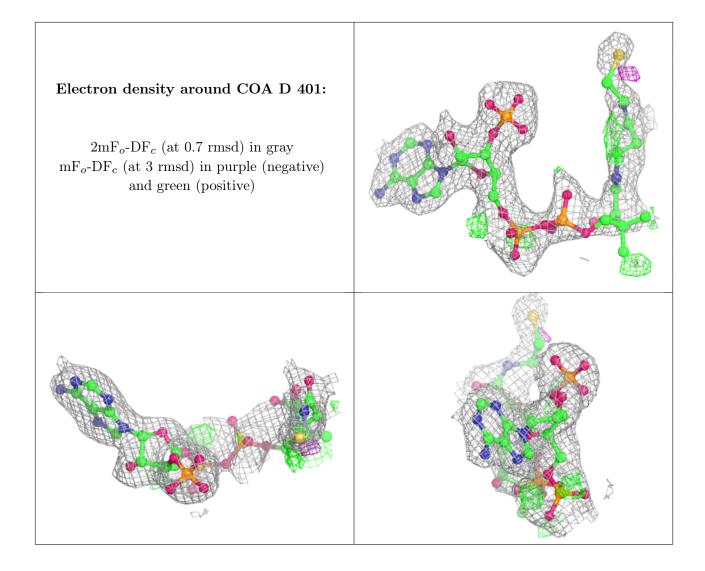
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\operatorname{B-factors}(\mathring{\mathrm{A}}^2)$	Q<0.9
3	PEG	A	402	7/7	0.77	0.23	44,49,54,55	0
4	SO4	Е	402	5/5	0.80	0.40	68,78,107,109	0
4	SO4	A	403	5/5	0.86	0.21	33,51,59,73	0
3	PEG	В	401	7/7	0.90	0.30	35,39,48,51	0
2	COA	С	401	48/48	0.91	0.21	13,43,94,117	0
2	COA	D	401	48/48	0.92	0.19	13,42,74,88	0
2	COA	Е	401	48/48	0.92	0.17	17,36,47,55	48
2	COA	В	402	48/48	0.93	0.18	12,30,54,62	48
2	COA	F	401	48/48	0.93	0.19	14,40,57,60	0
2	COA	A	401	48/48	0.95	0.16	17,32,42,48	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.





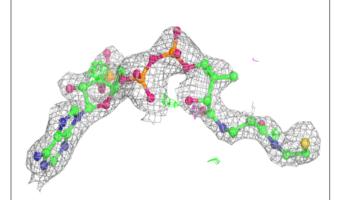


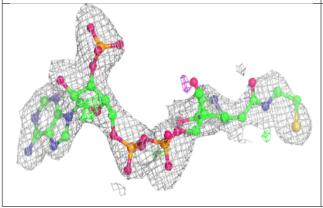


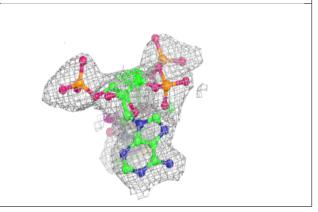


Electron density around COA E 401:

 $2 {\rm mF}_o\text{-}{\rm DF}_c$ (at 0.7 rmsd) in gray ${\rm mF}_o\text{-}{\rm DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

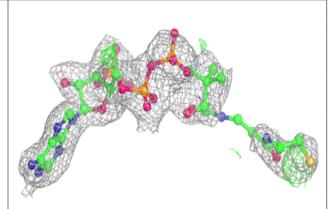


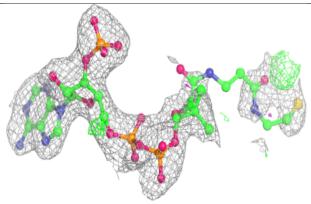


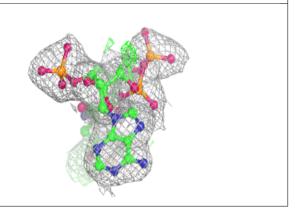


Electron density around COA B 402:

 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)



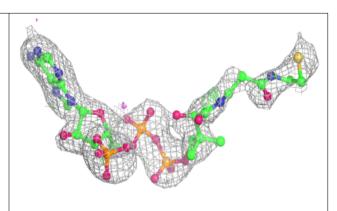


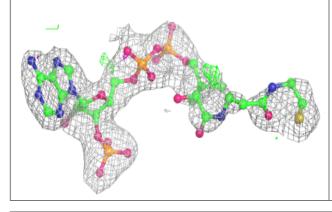


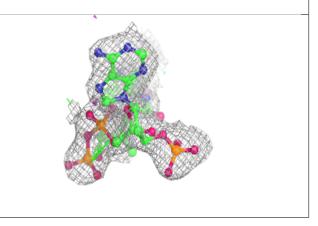


Electron density around COA F 401:

 $2 {\rm mF}_o\text{-}{\rm DF}_c$ (at 0.7 rmsd) in gray ${\rm mF}_o\text{-}{\rm DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

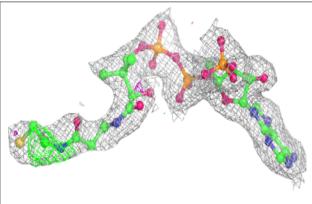


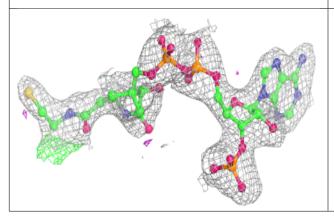


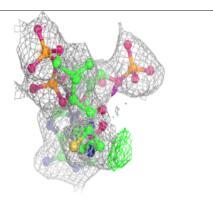


Electron density around COA A 401:

 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)









6.5 Other polymers (i)

There are no such residues in this entry.

