



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2025 – 05:44 PM EDT

PDB ID : 7HS4 / pdb\_00007hs4  
Title : PanDDA analysis group deposition – Crystal Structure of FatA in complex with Z1216861874  
Authors : Kot, E.; Ni, X.; Tomlinson, C.W.E.; Fearon, D.; Aschenbrenner, J.C.; Fairhead, M.; Koekemoer, L.; Marx, M.L.; Wright, N.D.; Mulholland, N.P.; Montgomery, M.G.; von Delft, F.  
Deposited on : 2024-12-23  
Resolution : 1.95 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](mailto: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>.

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

MolProbity	:	4-5-2 with Phenix2.0rc1
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.45.1

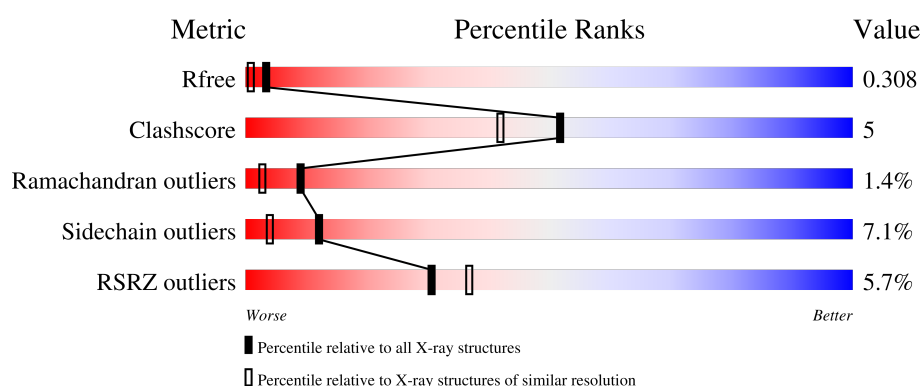
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.95 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))
$R_{free}$	164625	3187 (1.96-1.96)
Clashscore	180529	3412 (1.96-1.96)
Ramachandran outliers	177936	3390 (1.96-1.96)
Sidechain outliers	177891	3390 (1.96-1.96)
RSRZ outliers	164620	3186 (1.96-1.96)

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  $\geq 3$ , 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	295	<div> <div>2%</div> <div>73%</div> <div>16%</div> <div>10%</div> </div>
1	B	295	<div> <div>8%</div> <div>72%</div> <div>16%</div> <div>10%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4640 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.

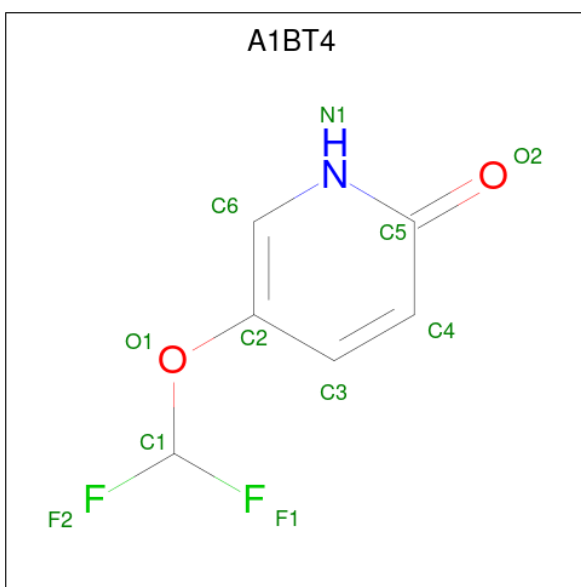
- Molecule 1 is a protein called Oleoyl-acyl carrier protein thioesterase 1, chloroplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	S	0	5	0
			2204	1369	390	429	16			
1	B	265	Total	C	N	O	S	0	3	0
			2195	1369	391	425	10			

There are 14 discrepancies between the modelled and reference sequences:

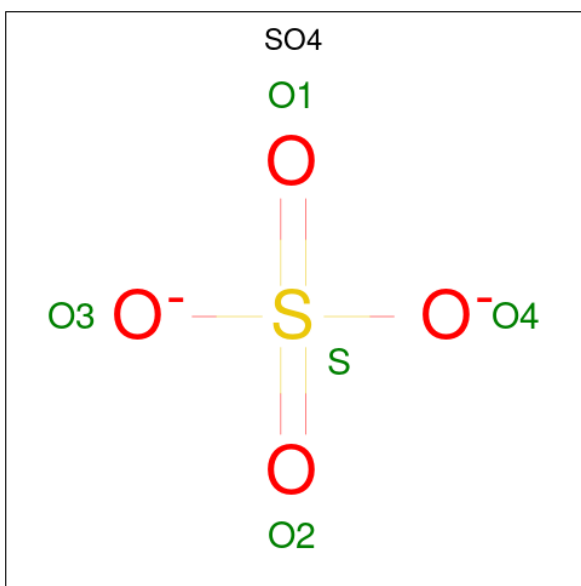
Chain	Residue	Modelled	Actual	Comment	Reference
A	74	MET	-	initiating methionine	UNP Q42561
A	363	HIS	-	expression tag	UNP Q42561
A	364	HIS	-	expression tag	UNP Q42561
A	365	HIS	-	expression tag	UNP Q42561
A	366	HIS	-	expression tag	UNP Q42561
A	367	HIS	-	expression tag	UNP Q42561
A	368	HIS	-	expression tag	UNP Q42561
B	74	MET	-	initiating methionine	UNP Q42561
B	363	HIS	-	expression tag	UNP Q42561
B	364	HIS	-	expression tag	UNP Q42561
B	365	HIS	-	expression tag	UNP Q42561
B	366	HIS	-	expression tag	UNP Q42561
B	367	HIS	-	expression tag	UNP Q42561
B	368	HIS	-	expression tag	UNP Q42561

- Molecule 2 is 5-(difluoromethoxy)pyridin-2(1H)-one (CCD ID: A1BT4) (formula: C<sub>6</sub>H<sub>5</sub>F<sub>2</sub>NO<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0
			11	6	2	1	2	
2	B	1	Total	C	F	N	O	0
			11	6	2	1	2	

- Molecule 3 is SULFATE ION (CCD ID: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



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

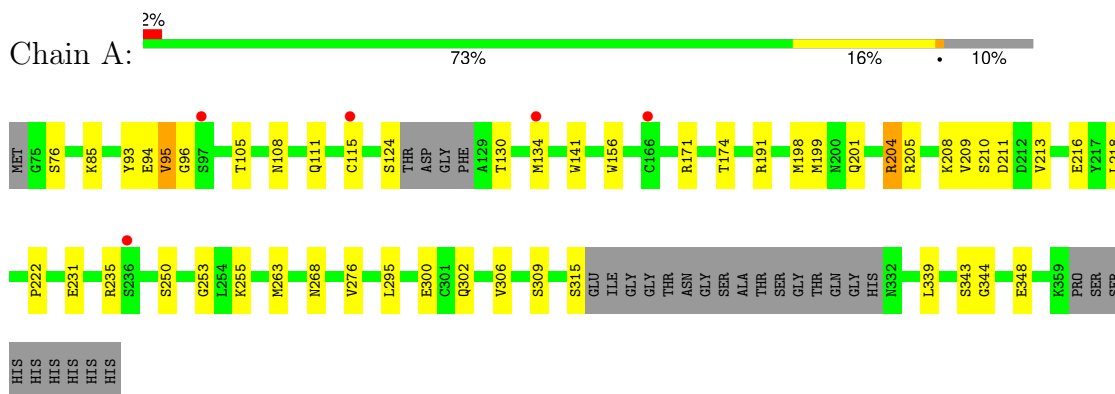
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	114	Total 114	O 114	0	0
4	B	95	Total 95	O 95	0	0

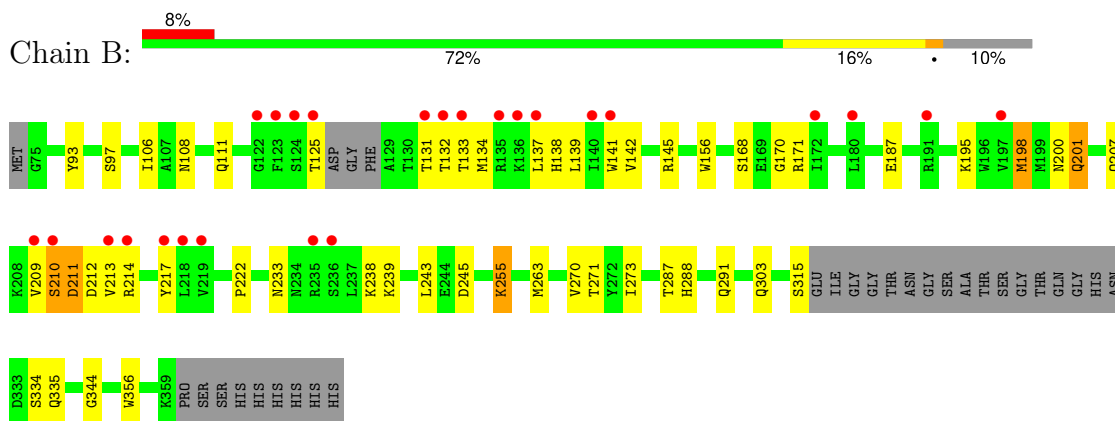
### 3 Residue-property plots

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: Oleoyl-acyl carrier protein thioesterase 1, chloroplastic



- Molecule 1: Oleoyl-acyl carrier protein thioesterase 1, chloroplastic



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	98.91Å 98.94Å 128.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	78.30 – 1.95 78.30 – 1.95	Depositor EDS
% Data completeness (in resolution range)	97.6 (78.30-1.95) 97.6 (78.30-1.95)	Depositor EDS
$R_{merge}$	0.29	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.02 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.8.0267, REFMAC5	Depositor
R, $R_{free}$	0.252 , 0.309 0.266 , 0.308	Depositor DCC
$R_{free}$ test set	2247 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.9	Xtriage
Anisotropy	0.101	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 41.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.479 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	4640	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.36% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<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.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: A1BT4, 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	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	1.12	1/2242 (0.0%)	1.45	5/3033 (0.2%)
1	B	1.10	1/2233 (0.0%)	1.41	3/3022 (0.1%)
All	All	1.11	2/4475 (0.0%)	1.43	8/6055 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	96	GLY	C-O	5.94	1.29	1.23
1	B	271	THR	C-O	5.07	1.30	1.24

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	95	VAL	CA-C-N	5.63	128.74	122.55
1	A	95	VAL	C-N-CA	5.63	128.74	122.55
1	A	300	GLU	CB-CA-C	5.56	118.98	109.80
1	B	245	ASP	CB-CA-C	5.54	118.19	109.27
1	A	95	VAL	CA-C-O	-5.48	115.50	121.92
1	B	255	LYS	CB-CA-C	-5.39	102.99	110.16
1	A	222	PRO	N-CA-CB	5.04	107.55	103.32
1	B	106	ILE	CA-C-O	-5.01	115.86	121.17

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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	2204	0	2161	26	0
1	B	2195	0	2166	25	0
2	A	11	0	0	0	0
2	B	11	0	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	114	0	0	5	1
4	B	95	0	0	3	1
All	All	4640	0	4327	44	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.

All (44) 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:138:HIS:O	1:B:200:ASN:O	1.78	1.00
1:B:198:MET:HE1	1:B:213:VAL:HG11	1.49	0.94
1:A:205:ARG:NE	4:A:501:HOH:O	1.94	0.93
1:A:205:ARG:NH2	4:A:501:HOH:O	2.13	0.80
1:B:171:ARG:HA	1:B:209:VAL:HG22	1.75	0.66
1:B:210:SER:O	1:B:211:ASP:HB2	1.99	0.62
1:B:137:LEU:HB2	4:B:587:HOH:O	1.99	0.62
1:A:115[B]:CYS:SG	1:B:156:TRP:HZ2	2.25	0.59
1:B:198:MET:CE	1:B:213:VAL:HG11	2.28	0.59
1:A:156:TRP:CZ3	1:B:263:MET:HE1	2.41	0.56
1:B:134:MET:HE1	1:B:141:TRP:HE1	1.70	0.56
1:A:205:ARG:CZ	4:A:501:HOH:O	2.31	0.55
1:A:171:ARG:NH2	1:A:211:ASP:OD1	2.40	0.55
1:A:130:THR:HA	1:A:134[A]:MET:HE2	1.89	0.55
1:A:130:THR:HA	1:A:134[C]:MET:HE2	1.89	0.55
1:A:95:VAL:HG11	1:A:156:TRP:HB2	1.89	0.55
1:B:131:THR:HG23	1:B:134:MET:HE3	1.90	0.52
1:A:115[B]:CYS:HG	1:B:156:TRP:HZ2	1.56	0.52
1:B:200:ASN:O	1:B:201:GLN:CB	2.60	0.49
1:A:85:LYS:NZ	4:A:508:HOH:O	2.47	0.48
1:A:253:GLY:HA2	1:A:306:VAL:CG1	2.44	0.47
1:B:214:ARG:HA	1:B:217:TYR:CE1	2.50	0.47
1:A:94:GLU:HB3	1:A:105:THR:HG21	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:198:MET:HE1	1:A:213:VAL:HG11	1.97	0.46
1:A:199:MET:HE1	1:A:204:ARG:NH1	2.31	0.45
1:B:287:THR:OG1	1:B:288:HIS:ND1	2.47	0.45
1:B:222:PRO:HG3	4:B:545:HOH:O	2.16	0.45
1:A:263:MET:O	1:B:97:SER:HA	2.16	0.45
1:A:111:GLN:HE22	1:A:268:ASN:HD21	1.64	0.44
1:A:141:TRP:CH2	1:A:174:THR:HG23	2.52	0.44
1:B:243:LEU:C	1:B:243:LEU:HD23	2.42	0.44
1:B:108:ASN:OD1	1:B:270:VAL:HG21	2.17	0.44
1:A:108:ASN:HB3	1:B:93:TYR:CE2	2.53	0.44
1:A:115[B]:CYS:SG	1:B:156:TRP:CZ2	3.08	0.43
1:B:134:MET:HE1	1:B:141:TRP:NE1	2.32	0.43
1:A:93:TYR:CE1	1:B:108:ASN:HB3	2.54	0.42
1:A:255:LYS:HE3	4:A:607:HOH:O	2.19	0.42
1:A:250:SER:HA	1:A:309:SER:O	2.20	0.42
1:B:288:HIS:HB3	1:B:356:TRP:HB3	2.02	0.42
1:A:276:VAL:HG21	1:A:295:LEU:HD11	2.02	0.41
1:A:198:MET:HE2	1:A:209:VAL:HA	2.02	0.41
1:B:195:LYS:HD3	4:B:514:HOH:O	2.20	0.41
1:B:270:VAL:O	1:B:273:ILE:HB	2.21	0.41
1:A:339:LEU:HD11	1:A:348:GLU:HG3	2.03	0.41

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)
4:A:590:HOH:O	4:B:585:HOH:O[6_444]	2.03	0.17

## 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	269/295 (91%)	263 (98%)	5 (2%)	1 (0%)	30	21
1	B	265/295 (90%)	254 (96%)	5 (2%)	6 (2%)	5	1
All	All	534/590 (90%)	517 (97%)	10 (2%)	7 (1%)	9	3

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	201	GLN
1	B	210	SER
1	B	211	ASP
1	B	233	ASN
1	A	344	GLY
1	B	170	GLY
1	B	344	GLY

### 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	250/263 (95%)	236 (94%)	14 (6%)	17	8
1	B	246/263 (94%)	226 (92%)	20 (8%)	9	3
All	All	496/526 (94%)	462 (93%)	34 (7%)	12	4

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	76	SER
1	A	124	SER
1	A	191	ARG
1	A	201	GLN
1	A	204	ARG
1	A	208	LYS
1	A	210	SER
1	A	216	GLU
1	A	218	LEU

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Mol	Chain	Res	Type
1	A	231	GLU
1	A	235	ARG
1	A	302	GLN
1	A	315	SER
1	A	343	SER
1	B	111	GLN
1	B	125	THR
1	B	132	THR
1	B	133	THR
1	B	139	LEU
1	B	142	VAL
1	B	145	ARG
1	B	168	SER
1	B	187	GLU
1	B	198	MET
1	B	207	GLN
1	B	212	ASP
1	B	238	LYS
1	B	239	LYS
1	B	255	LYS
1	B	291	GLN
1	B	303	GLN
1	B	315	SER
1	B	334	SER
1	B	335	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	111	GLN
1	A	223	GLN
1	B	207	GLN
1	B	234	ASN
1	B	302	GLN

### 5.3.3 RNA ⓘ

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	SO4	A	402	-	4,4,4	0.32	0	6,6,6	0.09	0
3	SO4	B	402	-	4,4,4	0.34	0	6,6,6	0.15	0
2	A1BT4	B	401	-	10,11,11	0.58	0	12,14,14	0.52	0
2	A1BT4	A	401	-	10,11,11	0.59	0	12,14,14	0.41	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
2	A1BT4	B	401	-	-	0/2/4/4	0/1/1/1
2	A1BT4	A	401	-	-	0/2/4/4	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

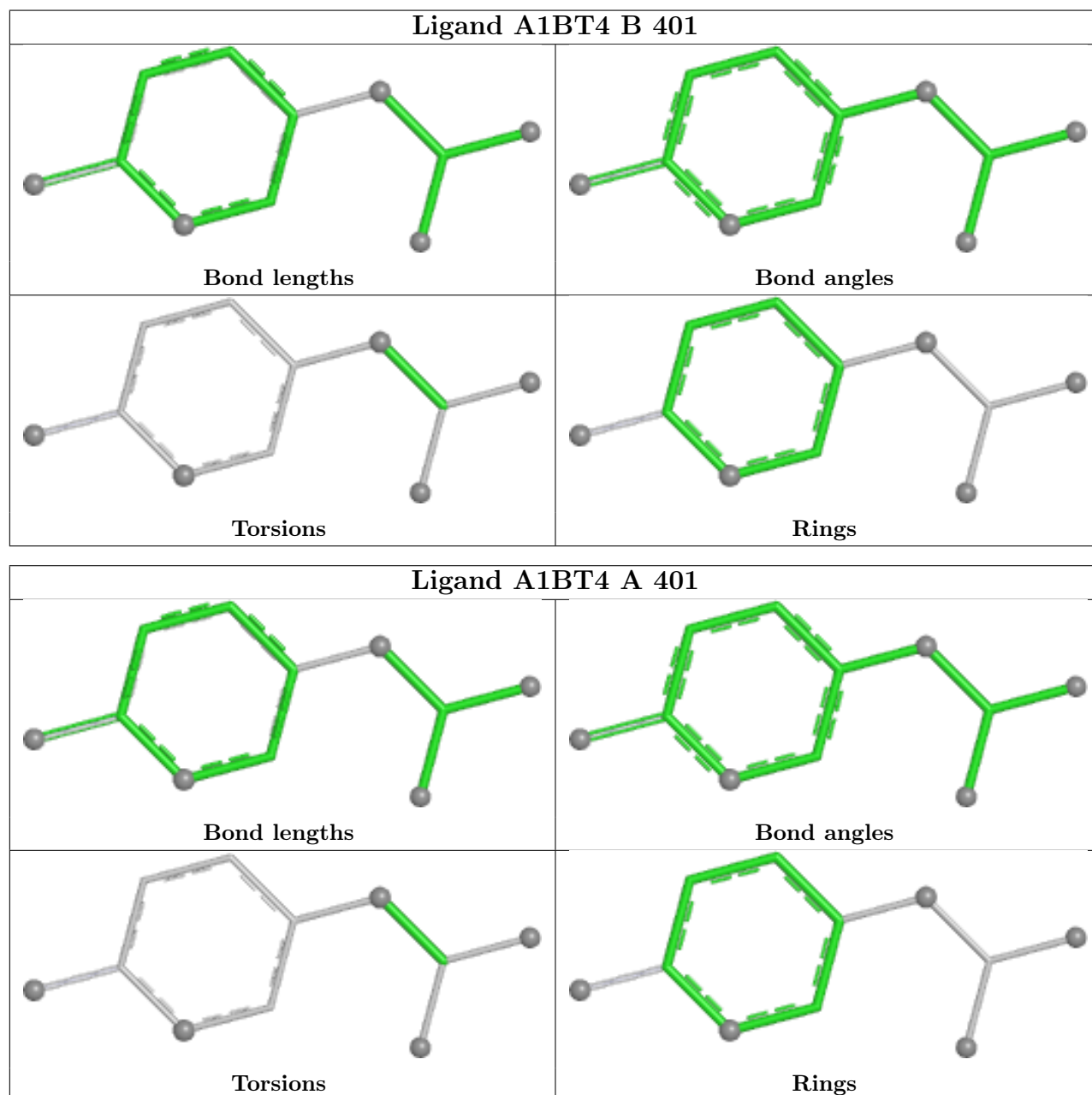
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

### 6.1 Protein, DNA and RNA chains

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	265/295 (89%)	-0.11	5 (1%) 66 72	5, 39, 72, 108	5 (1%)
1	B	265/295 (89%)	0.27	25 (9%) 15 19	5, 35, 61, 104	52 (19%)
All	All	530/590 (89%)	0.08	30 (5%) 30 37	5, 37, 68, 108	57 (10%)

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	125	THR	4.1
1	B	213	VAL	3.6
1	B	124	SER	3.4
1	B	123	PHE	3.4
1	B	180[A]	LEU	3.3
1	B	218	LEU	3.3
1	B	137	LEU	3.1
1	B	172	ILE	3.0
1	B	217	TYR	2.9
1	A	115[A]	CYS	2.9
1	B	219	VAL	2.9
1	B	131	THR	2.7
1	A	166[A]	CYS	2.7
1	A	236	SER	2.7
1	B	197	VAL	2.6
1	B	235	ARG	2.4
1	B	133	THR	2.4
1	B	135	ARG	2.4
1	B	140	ILE	2.2
1	A	134[A]	MET	2.2
1	A	97[A]	SER	2.2
1	B	191[A]	ARG	2.2
1	B	209	VAL	2.2
1	B	236	SER	2.2

*Continued on next page...*

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Mol	Chain	Res	Type	RSRZ
1	B	132	THR	2.2
1	B	141	TRP	2.1
1	B	136	LYS	2.1
1	B	214	ARG	2.1
1	B	122	GLY	2.0
1	B	210	SER	2.0

## 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](#)

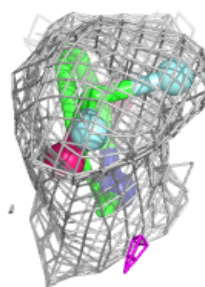
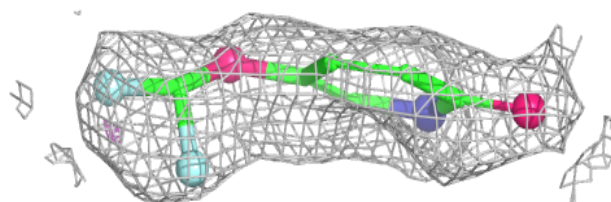
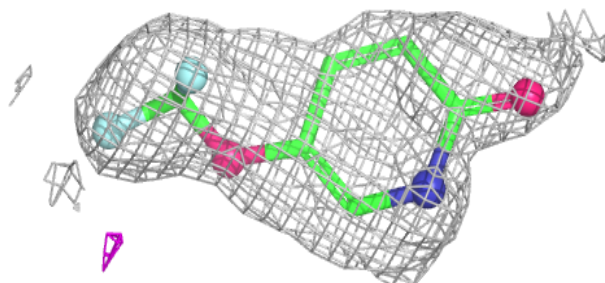
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
2	A1BT4	A	401	11/11	0.97	0.10	36,37,40,40	11
2	A1BT4	B	401	11/11	0.97	0.11	51,52,53,54	11
3	SO4	A	402	5/5	0.97	0.09	62,65,76,83	0
3	SO4	B	402	5/5	0.98	0.07	42,43,44,44	5

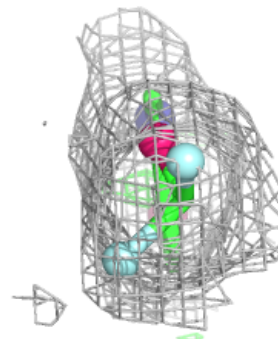
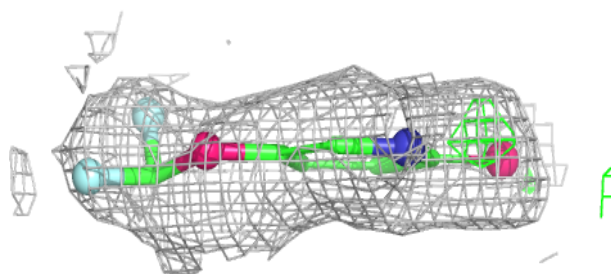
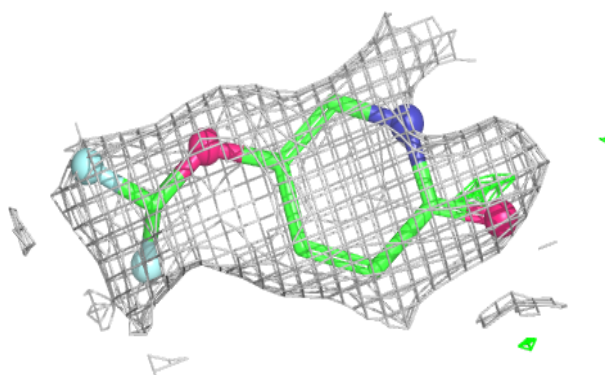
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around A1BT4 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)

**Electron density around A1BT4 B 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.