

Full wwPDB X-ray Structure Validation Report (i)

Oct 9, 2023 – 10:29 PM EDT

PDB ID : 7RN5

Title : Discovery of an Anion-Dependent Farnesyltransferase Inhibitor from a Pheno-

typic Screen

Authors: Hruza, A.; Strickland, C.L.

Deposited on : 2021-07-29

Resolution : 2.28 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 : 4.02b-467

Mogul : ?.? (???), CSD ??CSD?? (????)

Xtriage (Phenix) : 1.13

EDS : 2.35.1

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)

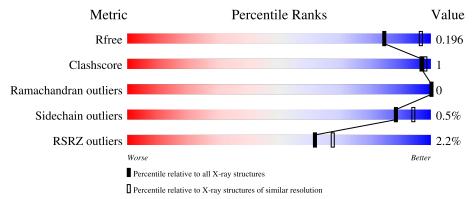
Validation Pipeline (wwPDB-VP) : 2.35.1

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 2.28 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	6980 (2.30-2.26)
Clashscore	141614	7711 (2.30-2.26)
Ramachandran outliers	138981	7597 (2.30-2.26)
Sidechain outliers	138945	7598 (2.30-2.26)
RSRZ outliers	127900	6849 (2.30-2.26)

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	377	81%	•	17%
2	В	437	89%		• 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
7	PPV	В	504	_	-	_	X



2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 12005 atoms, of which 5782 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 Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha.

Mol	Chain	Residues		\mathbf{Atoms}			ZeroOcc	AltConf	Trace		
1	А	313	Total	С	Н	N	О	S	2602	2	0
1	11	010	5278	1701	2602	472	498	5	2002	_	O

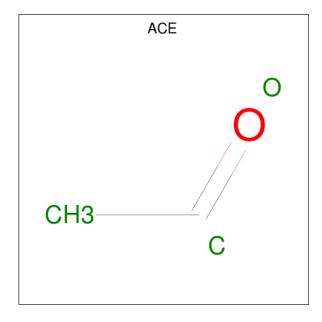
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Α	156	THR	ILE	conflict	UNP Q04631

• Molecule 2 is a protein called Protein farnesyltransferase subunit beta.

Mol	Chain	Residues			Atom	ıs			ZeroOcc	AltConf	Trace
2	В	404	Total 6282	C 2031	H 3104	N 546	O 578	S 23	3104	0	0

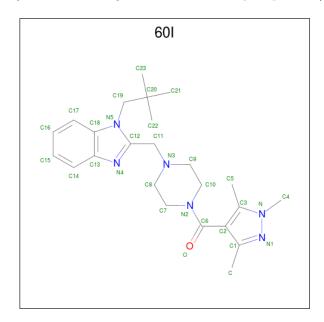
• Molecule 3 is ACETYL GROUP (three-letter code: ACE) (formula: C₂H₄O).





Mol	Chain	Residues	${f Atoms}$				ZeroOcc	AltConf
3	A	1	Total 6		H 3		3	0
3	A	1	Total 6	C 2		O 1	3	0

• Molecule 4 is $[4-[[3-(2,2-dimethylpropyl)-1 \{H\}-benzimidazol-2-yl]methyl]$ piperazin-1-y l]-(1,3,5-trimethylpyrazol-4-yl)methanone (three-letter code: 60I) (formula: $C_{24}H_{34}N_6O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
4	В	1	Total 132		H 70		O 2	70	1

• Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

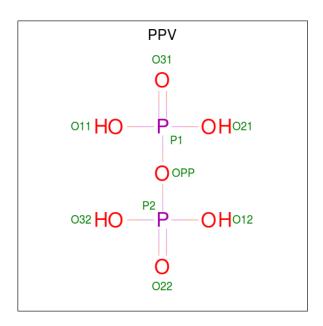
\mathbf{Mol}	Chain	Residues	Atoms	ZeroOcc	AltConf
5	В	1	Total Zn 1 1	0	0

• Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

• Molecule 7 is PYROPHOSPHATE (three-letter code: PPV) (formula: $H_4O_7P_2$).





Mol	Chain	Residues	Aton	Atoms		AltConf
7	В	1	Total (O P 7 2	0	0

• Molecule 8 is water.

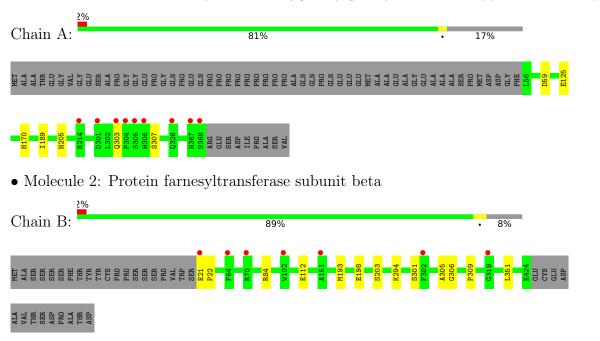
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	144	Total O 144 144	0	0
8	В	146	Total O 146 146	0	0



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: Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61	Depositor
Cell constants	171.12Å 171.12Å 69.18Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.00 - 2.28	Depositor
resolution (A)	34.00 - 2.28	EDS
% Data completeness	100.0 (34.00-2.28)	Depositor
(in resolution range)	100.0 (34.00-2.28)	EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) > 1$	2.11 (at 2.29Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.169 , 0.195	Depositor
it, it free	0.168 , 0.196	DCC
R_{free} test set	2676 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	44.2	Xtriage
Anisotropy	0.269	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	$0.35 \; , 46.4$	EDS
L-test for twinning ²	$< L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	0.028 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	12005	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.64% 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: 60I, ZN, ACE, PPV, MG

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		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.41	0/2748	0.51	0/3731	
2	В	0.44	0/3264	0.55	0/4433	
All	All	0.43	0/6012	0.54	0/8164	

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	2676	2602	2592	5	0
2	В	3178	3104	3104	6	0
3	A	6	6	6	0	0
4	В	62	70	0	0	0
5	В	1	0	0	0	0
6	В	1	0	0	0	0
7	В	9	0	0	1	0
8	A	144	0	0	0	0
8	В	146	0	0	0	0
All	All	6223	5782	5702	10	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 1.

All (10) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}({ m \AA})$	overlap (Å)
2:B:294:LYS:NZ	7:B:504:PPV:O12	2.34	0.61
1:A:170:HIS:HD2	2:B:198:GLU:OE2	1.83	0.60
1:A:189:ILE:HD11	1:A:205:HIS:CD2	2.39	0.58
1:A:303:GLN:O	1:A:307:SER:HB2	2.04	0.58
2:B:301:SER:O	2:B:305:ALA:HB3	2.08	0.54
1:A:189:ILE:HD11	1:A:205:HIS:HD2	1.76	0.51
1:A:59:ASP:OD2	1:A:125:GLU:OE1	2.30	0.50
2:B:21:GLU:N	2:B:22:PRO:HD2	2.28	0.48
2:B:193:MET:SD	2:B:203:SER:HB3	2.57	0.44
2:B:306:GLY:O	2:B:309:PRO:HD2	2.19	0.41

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	313/377 (83%)	301 (96%)	12 (4%)	0	100 100	
2	В	402/437 (92%)	397 (99%)	5 (1%)	0	100 100	
All	All	715/814 (88%)	698 (98%)	17 (2%)	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	Percentiles		
1	A	294/338 (87%)	294 (100%)	0	100	100	
2	В	341/371 (92%)	338 (99%)	3 (1%)	78	88	
All	All	635/709 (90%)	632 (100%)	3 (0%)	88	94	

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

Mol	Chain	Res	Type
2	В	84	ARG
2	В	112	GLU
2	В	351	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	170	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

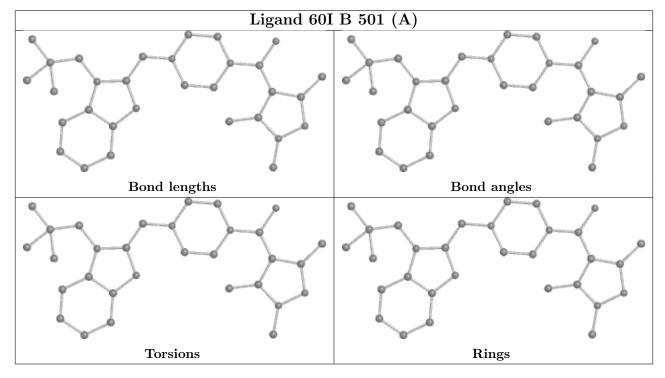


There are no torsion outliers.

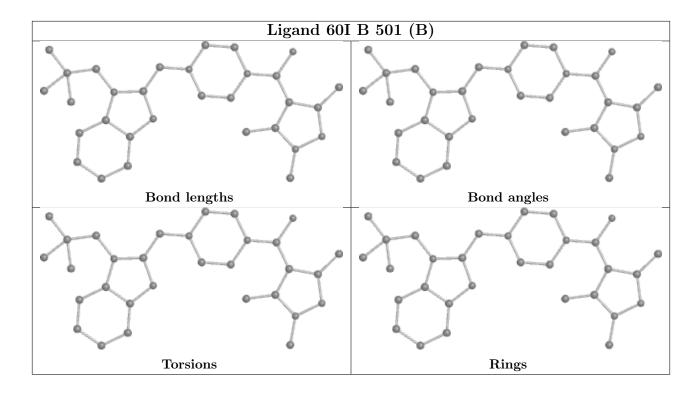
There are no ring outliers.

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 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 $>$	$\#\mathrm{RSRZ}{>}2$		$OWAB(A^2)$	Q<0.9	
1	A	313/377 (83%)	-0.27	9 (2%)	51 57		36, 54, 85, 104	0
2	В	404/437 (92%)	-0.08	7 (1%)	70 75		34, 48, 69, 89	0
All	All	717/814 (88%)	-0.16	16 (2%)	62 68	3	34, 51, 76, 104	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	64	PHE	5.8
1	A	306	HIS	4.0
1	A	305	SER	3.1
1	A	304	PRO	2.9
1	A	367	HIS	2.9
2	В	102	TRP	2.6
2	В	21	GLU	2.5
1	A	301	ASP	2.4
2	В	319	GLY	2.4
1	A	303	GLN	2.3
2	В	70	ARG	2.3
1	A	368	SER	2.3
1	A	326	GLN	2.2
2	В	151	ALA	2.1
2	В	302	PHE	2.1
1	A	214	ARG	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 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.

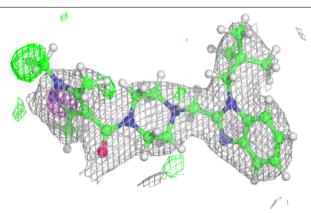
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
3	ACE	A	2002	3/3	0.66	0.18	85,86,115,116	3
7	PPV	В	504	9/9	0.78	0.55	80,80,80,80	9
3	ACE	A	2001	3/3	0.85	0.27	70,71,88,88	3
4	60I	В	501[B]	31/31	0.94	0.20	52,54,61,62	66
4	60I	В	501[A]	31/31	0.94	0.20	29,33,38,40	66
6	MG	В	503	1/1	0.96	0.27	81,81,81,81	0
5	ZN	В	502	1/1	0.99	0.03	67,67,67,67	0

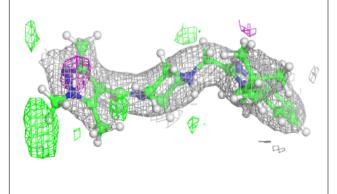
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

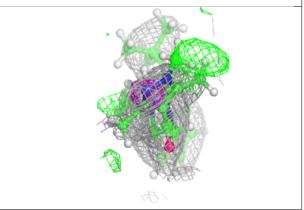


Electron density around 60I B 501 (B):

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

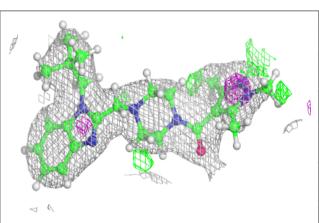


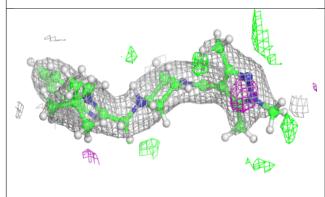


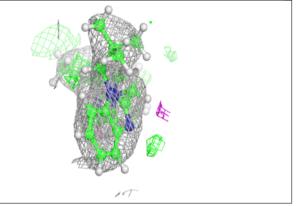


Electron density around 60I B 501 (A):

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









6.5 Other polymers (i)

There are no such residues in this entry.

