



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 06:46 PM UTC

PDB ID : 4LNB / pdb_00004lnb
Title : Aspergillus fumigatus protein farnesyltransferase ternary complex with farnesyl diphosphate and ethylenediamine scaffold inhibitor 5
Authors : Mabanglo, M.F.; Hast, M.A.; Beese, L.S.
Deposited on : 2013-07-11
Resolution : 1.75 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

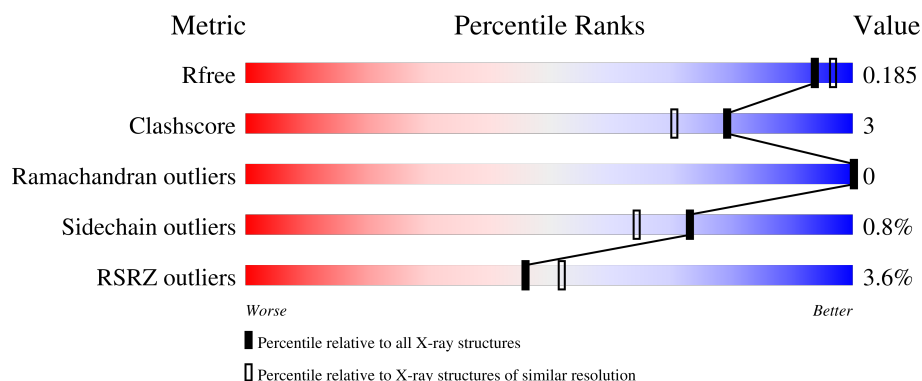
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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}	180053	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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 $\leq 5\%$. 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	367	5% 87% 6% 8%
2	B	519	2% 80% 6% 14%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6933 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 CaaX farnesyltransferase alpha subunit Ram2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	339	Total	C	N	O	S	0	4	0
			2794	1777	490	518	9			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	initiating methionine	UNP Q4WP27
A	-12	GLY	-	expression tag	UNP Q4WP27
A	-11	SER	-	expression tag	UNP Q4WP27
A	-10	SER	-	expression tag	UNP Q4WP27
A	-9	HIS	-	expression tag	UNP Q4WP27
A	-8	HIS	-	expression tag	UNP Q4WP27
A	-7	HIS	-	expression tag	UNP Q4WP27
A	-6	HIS	-	expression tag	UNP Q4WP27
A	-5	HIS	-	expression tag	UNP Q4WP27
A	-4	HIS	-	expression tag	UNP Q4WP27
A	-3	SER	-	expression tag	UNP Q4WP27
A	-2	GLN	-	expression tag	UNP Q4WP27
A	-1	ASP	-	expression tag	UNP Q4WP27
A	0	PRO	-	expression tag	UNP Q4WP27
A	146	SER	ASN	engineered mutation	UNP Q4WP27

- Molecule 2 is a protein called CaaX farnesyltransferase beta subunit Ram1.

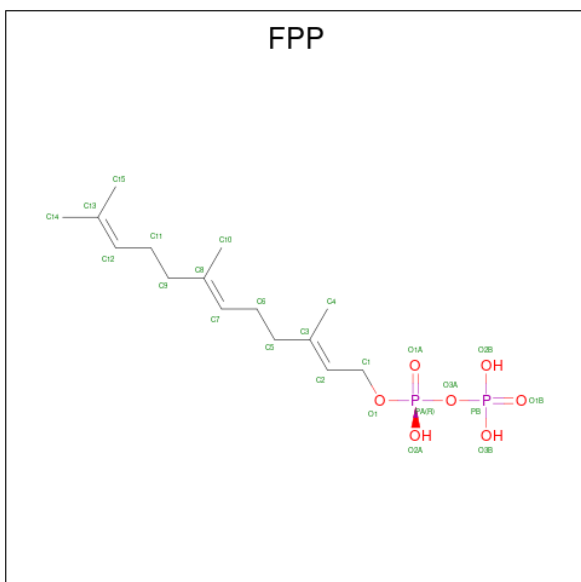
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	447	Total	C	N	O	S	0	11	0
			3518	2243	595	656	24			

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is FARNESYL DIPHOSPHATE (CCD ID: FPP) (formula: $C_{15}H_{28}O_7P_2$).

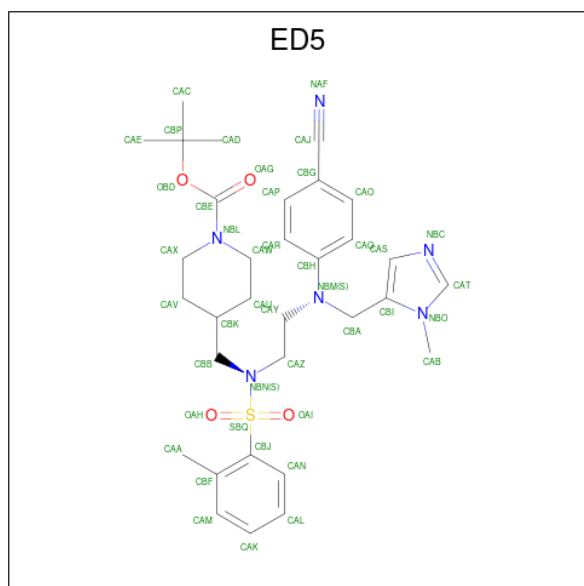


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	O	P	0	0
			24	15	7	2		

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Zn 1 1	0	0

- Molecule 6 is tert-butyl 4-({(2-{{(4-cyanophenyl)[(1-methyl-1H-imidazol-5-yl)methyl]amino}ethyl)[(2-methylphenyl)sulfonyl]amino}methyl)piperidine-1-carboxylate (CCD ID: ED5) (formula: C₃₂H₄₂N₆O₄S).



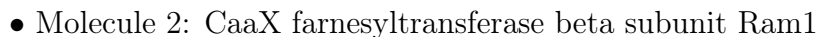
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total	C	N	O	S	0	0
			43	32	6	4	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	227	Total O 227 227	0	0
7	B	306	Total O 306 306	0	0

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- Molecule 1: CaaX farnesyltransferase alpha subunit Ram2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	63.32Å 91.25Å 83.05Å 90.00° 110.93° 90.00°	Depositor
Resolution (Å)	37.07 – 1.75 37.07 – 1.75	Depositor EDS
% Data completeness (in resolution range)	94.0 (37.07-1.75) 88.7 (37.07-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 1.75Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.159 , 0.184 0.162 , 0.185	Depositor DCC
R_{free} test set	4139 reflections (2.65%)	wwPDB-VP
Wilson B-factor (Å ²)	19.2	Xtriage
Anisotropy	0.347	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 36.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6933	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.98% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FPP, ZN, EDO, ED5

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.31	0/2884	0.64	0/3914
2	B	0.34	0/3642	0.68	0/4949
All	All	0.33	0/6526	0.66	0/8863

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

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	2794	0	2696	14	0
2	B	3518	0	3407	18	0
3	A	12	0	18	2	0
3	B	8	0	12	1	0
4	B	24	0	25	2	0
5	B	1	0	0	0	0
6	B	43	0	42	1	0
7	A	227	0	0	0	0
7	B	306	0	0	2	0
All	All	6933	0	6200	34	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 3.

All (34) 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)
2:B:90:VAL:HG12	2:B:90:VAL:O	2.00	0.59
1:A:300:TYR:O	1:A:309:SER:OG	2.26	0.53
2:B:176[A]:MET:HE1	3:B:604:EDO:H21	1.91	0.52
2:B:409:GLN:NE2	7:B:965:HOH:O	2.43	0.51
2:B:196:GLU:HG2	7:B:841:HOH:O	2.12	0.50
2:B:94:ILE:O	2:B:99:ARG:NH1	2.43	0.49
2:B:247:LYS:NZ	2:B:541:LEU:O	2.40	0.49
2:B:232:ILE:HD13	2:B:244:ILE:HD11	1.94	0.49
2:B:533:TRP:O	2:B:537:GLN:HG2	2.13	0.48
1:A:148:HIS:HE1	3:A:401:EDO:H22	1.80	0.47
1:A:154[A]:HIS:CD2	1:A:191:MET:HG3	2.50	0.47
1:A:154[A]:HIS:HE1	1:A:203:ASP:OD2	1.98	0.46
1:A:273:VAL:HG12	1:A:287:VAL:HG22	1.98	0.46
1:A:73:HIS:O	1:A:76:VAL:HG12	2.15	0.46
1:A:73:HIS:CE1	1:A:75:THR:HB	2.51	0.46
2:B:477:VAL:HG22	2:B:487:PHE:HB3	1.97	0.45
2:B:387:ASP:HB3	2:B:390:TYR:CD2	2.52	0.44
2:B:335:ALA:HB1	4:B:601:FPP:H92	1.98	0.44
2:B:443:LEU:HB2	2:B:456:THR:HA	1.99	0.44
2:B:135:LYS:NZ	2:B:150:ASP:OD2	2.38	0.44
1:A:148:HIS:CE1	3:A:401:EDO:H22	2.53	0.43
1:A:154[A]:HIS:CD2	1:A:191:MET:HE2	2.53	0.43
2:B:196:GLU:CD	2:B:196:GLU:H	2.26	0.43
1:A:54:GLU:O	1:A:79:TYR:OH	2.26	0.43
2:B:463:LEU:O	2:B:466:VAL:HG22	2.18	0.43
1:A:321:LYS:HB2	1:A:329:ARG:HG3	2.01	0.42
1:A:98:LEU:HD11	1:A:111:ILE:HG23	2.01	0.42
2:B:517:HIS:HA	2:B:518:PRO:HD3	1.91	0.42
4:B:601:FPP:H103	4:B:601:FPP:H61	1.98	0.41
6:B:603:ED5:HAQ	6:B:603:ED5:HBAA	1.87	0.41
1:A:79:TYR:CE2	1:A:83:ILE:HD11	2.56	0.41
2:B:293:PRO:HA	2:B:294:PRO:HD3	1.94	0.40
2:B:335:ALA:HA	2:B:393:TRP:HB3	2.03	0.40
1:A:116:GLN:O	1:A:120[A]:SER:OG	2.24	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	339/367 (92%)	330 (97%)	9 (3%)	0	100	100
2	B	452/519 (87%)	448 (99%)	4 (1%)	0	100	100
All	All	791/886 (89%)	778 (98%)	13 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	295/315 (94%)	294 (100%)	1 (0%)	86	83
2	B	379/428 (89%)	375 (99%)	4 (1%)	65	52
All	All	674/743 (91%)	669 (99%)	5 (1%)	73	67

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	307	GLU
2	B	196	GLU
2	B	224	SER
2	B	521	VAL
2	B	540	ASP

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

Mol	Chain	Res	Type
1	A	20	ASN
1	A	142	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 1 is monoatomic - leaving 7 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	FPP	B	601	-	22,23,23	3.20	7 (31%)	27,31,31	2.36	11 (40%)
3	EDO	B	605	-	3,3,3	0.59	0	2,2,2	0.64	0
3	EDO	A	401	-	3,3,3	0.60	0	2,2,2	0.67	0
3	EDO	A	403	-	3,3,3	0.61	0	2,2,2	0.60	0
3	EDO	B	604	-	3,3,3	0.58	0	2,2,2	0.64	0
3	EDO	A	402	-	3,3,3	0.58	0	2,2,2	0.66	0
6	ED5	B	603	5	46,46,46	2.36	14 (30%)	60,66,66	2.19	14 (23%)

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	FPP	B	601	-	-	7/25/25/25	-
3	EDO	B	605	-	-	0/1/1/1	-
3	EDO	A	401	-	-	1/1/1/1	-
3	EDO	A	403	-	-	0/1/1/1	-
3	EDO	B	604	-	-	0/1/1/1	-
3	EDO	A	402	-	-	0/1/1/1	-
6	ED5	B	603	5	-	9/40/50/50	0/4/4/4

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	601	FPP	C7-C8	8.22	1.52	1.33
6	B	603	ED5	CAJ-NAF	8.13	1.32	1.14
4	B	601	FPP	C2-C3	8.12	1.51	1.33
6	B	603	ED5	CBE-NBL	7.40	1.48	1.35
4	B	601	FPP	C12-C13	6.55	1.52	1.32
6	B	603	ED5	OBD-CBE	4.72	1.42	1.33
6	B	603	ED5	CBH-NBM	4.26	1.50	1.38
4	B	601	FPP	C11-C12	-3.55	1.39	1.50
6	B	603	ED5	SBQ-NBN	3.52	1.68	1.63
4	B	601	FPP	C1-C2	-3.43	1.39	1.49
6	B	603	ED5	CAZ-NBN	3.39	1.53	1.48
4	B	601	FPP	C6-C7	-3.20	1.40	1.50
6	B	603	ED5	CBI-NBO	-2.89	1.33	1.38
6	B	603	ED5	CBB-NBN	2.78	1.52	1.47
4	B	601	FPP	O1-C1	-2.73	1.39	1.44
6	B	603	ED5	OBD-CBP	-2.45	1.44	1.48
6	B	603	ED5	CAS-CBI	2.35	1.39	1.36
6	B	603	ED5	CAL-CAN	2.27	1.42	1.38
6	B	603	ED5	CBA-CBI	2.24	1.53	1.50
6	B	603	ED5	CBG-CAJ	2.09	1.49	1.44
6	B	603	ED5	CAS-NBC	-2.08	1.34	1.37

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	603	ED5	OAH-SBQ-OAI	-7.01	108.65	119.59
6	B	603	ED5	NBO-CAT-NBC	-6.54	109.05	112.94
6	B	603	ED5	OBD-CBE-NBL	5.81	119.60	110.78
4	B	601	FPP	C4-C3-C2	-5.11	110.50	123.63
6	B	603	ED5	OAI-SBQ-NBN	5.06	111.45	106.69
4	B	601	FPP	C9-C8-C7	-4.50	111.06	121.17
6	B	603	ED5	OBD-CBE-OAG	-4.47	119.23	126.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	601	FPP	C10-C8-C7	-4.42	112.27	123.63
4	B	601	FPP	C5-C3-C2	-4.38	111.34	121.17
6	B	603	ED5	CAY-CAZ-NBN	4.29	119.73	112.43
6	B	603	ED5	CAM-CBF-CBJ	3.34	119.80	116.27
4	B	601	FPP	C10-C8-C9	-3.30	109.50	115.23
6	B	603	ED5	OAG-CBE-NBL	-3.13	118.51	124.30
6	B	603	ED5	OAH-SBQ-NBN	3.13	109.63	106.69
4	B	601	FPP	C6-C7-C8	-2.95	120.87	127.62
4	B	601	FPP	C15-C13-C12	-2.91	113.93	122.66
4	B	601	FPP	C14-C13-C12	-2.81	114.21	122.66
6	B	603	ED5	CBB-NBN-SBQ	-2.73	111.36	117.32
6	B	603	ED5	CAA-CBF-CBJ	-2.72	121.60	124.17
6	B	603	ED5	CAZ-NBN-CBB	-2.41	112.88	116.80
6	B	603	ED5	CBP-OBDB-CBE	2.39	123.56	120.92
6	B	603	ED5	CAS-NBC-CAT	2.35	108.31	105.24
4	B	601	FPP	C11-C12-C13	-2.31	119.95	127.64
4	B	601	FPP	C1-C2-C3	-2.23	122.54	126.20
4	B	601	FPP	C4-C3-C5	-2.20	111.40	115.23

There are no chirality outliers.

All (17) torsion outliers are listed below:

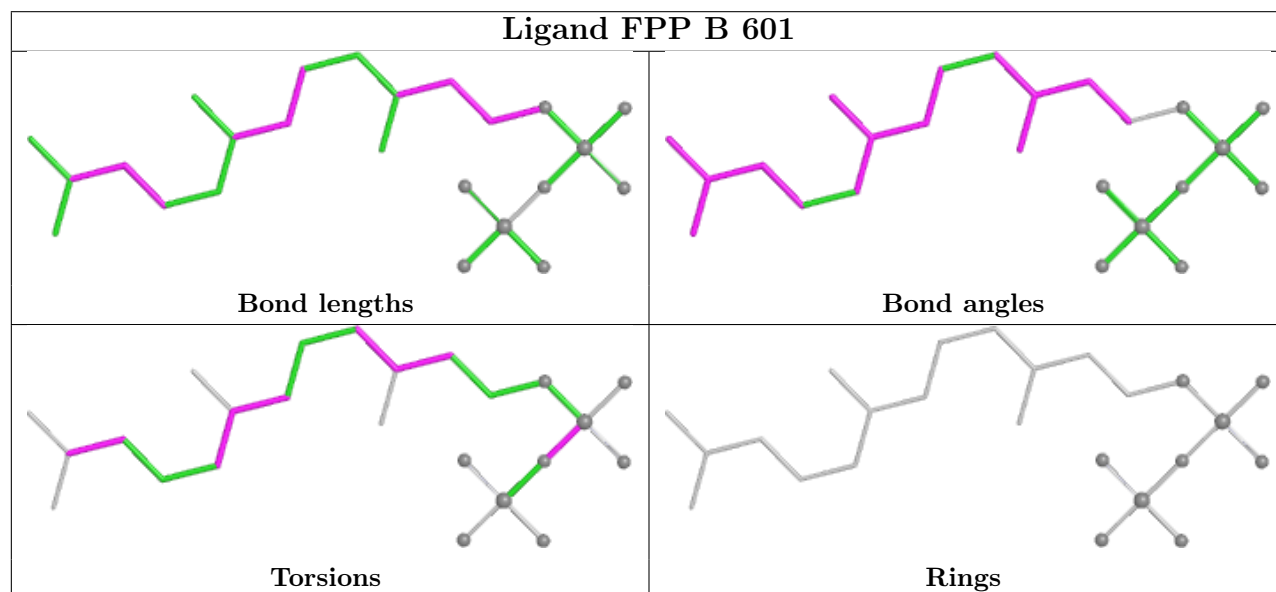
Mol	Chain	Res	Type	Atoms
6	B	603	ED5	NBL-CBE-OBDB-CBP
6	B	603	ED5	OAG-CBE-OBDB-CBP
6	B	603	ED5	CAE-CBP-OBDB-CBE
6	B	603	ED5	CAC-CBP-OBDB-CBE
6	B	603	ED5	CAD-CBP-OBDB-CBE
4	B	601	FPP	C6-C7-C8-C9
6	B	603	ED5	CAZ-NBN-SBQ-OAH
4	B	601	FPP	C11-C12-C13-C15
6	B	603	ED5	CAY-CAZ-NBN-CBB
6	B	603	ED5	CAZ-NBN-SBQ-CBJ
4	B	601	FPP	C4-C3-C5-C6
4	B	601	FPP	C7-C8-C9-C11
4	B	601	FPP	C11-C12-C13-C14
3	A	401	EDO	O1-C1-C2-O2
4	B	601	FPP	C1-C2-C3-C5
4	B	601	FPP	PB-O3A-PA-O2A
6	B	603	ED5	CBI-CBA-NBM-CBH

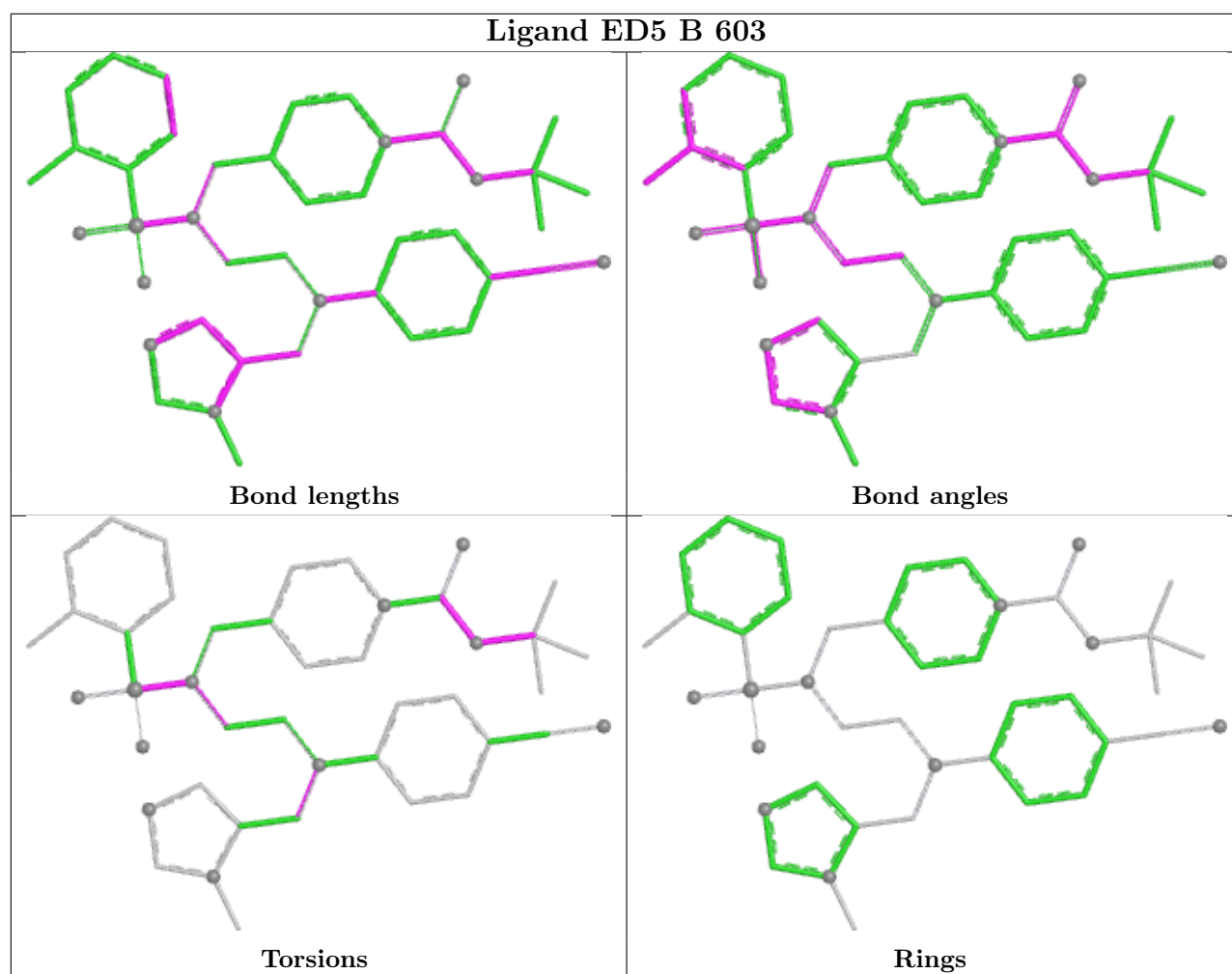
There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	601	FPP	2	0
3	A	401	EDO	2	0
3	B	604	EDO	1	0
6	B	603	ED5	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	339/367 (92%)	0.11	17 (5%)	34 39	6, 21, 56, 105	4 (1%)
2	B	447/519 (86%)	-0.24	11 (2%)	58 64	8, 16, 34, 75	11 (2%)
All	All	786/886 (88%)	-0.09	28 (3%)	46 52	6, 18, 41, 105	15 (1%)

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	25	PHE	7.6
1	A	274	VAL	6.1
1	A	349	ILE	5.6
1	A	21	ASP	5.4
1	A	273	VAL	4.5
2	B	90	VAL	4.3
2	B	540	ASP	4.0
1	A	285	VAL	3.8
2	B	411	LEU	3.7
2	B	483	PHE	3.6
2	B	412	ALA	3.5
1	A	286	ALA	3.1
2	B	480	LYS	3.0
1	A	26	GLY	2.9
1	A	303	GLU	2.8
1	A	284	ASP	2.8
2	B	469[A]	TYR	2.7
1	A	275	GLU	2.7
1	A	345	HIS	2.7
2	B	105[A]	HIS	2.7
2	B	500	GLN	2.6
1	A	22	GLY	2.5
2	B	479	SER	2.4
1	A	4	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	302	GLU	2.3
1	A	346	ALA	2.2
2	B	525	LYS	2.1
1	A	23	SER	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

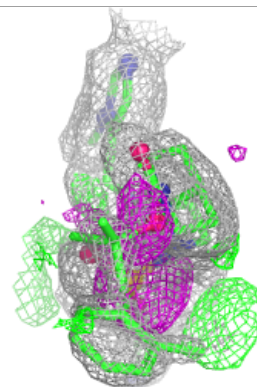
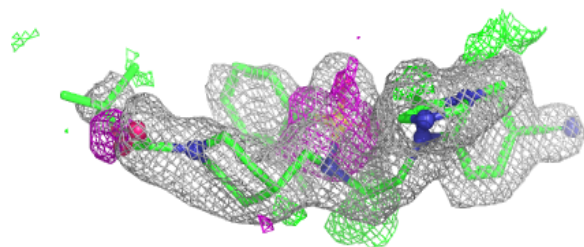
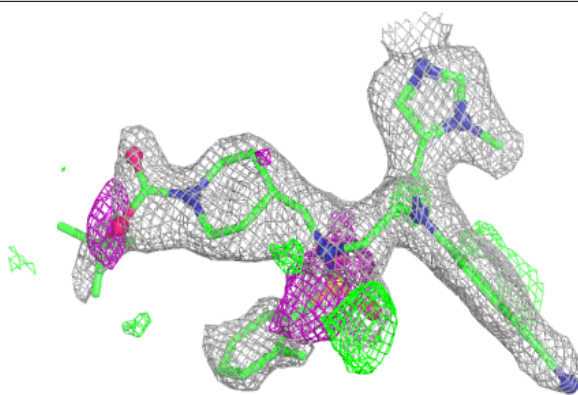
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EDO	B	605	4/4	0.76	0.17	43,43,44,44	0
3	EDO	B	604	4/4	0.90	0.10	23,26,26,27	0
6	ED5	B	603	43/43	0.90	0.14	9,38,60,62	0
3	EDO	A	403	4/4	0.91	0.11	31,32,34,36	0
3	EDO	A	401	4/4	0.95	0.15	12,24,33,38	0
3	EDO	A	402	4/4	0.95	0.07	30,33,34,34	0
4	FPP	B	601	24/24	0.98	0.07	10,19,24,28	0
5	ZN	B	602	1/1	1.00	0.01	11,11,11,11	0

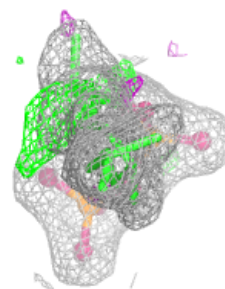
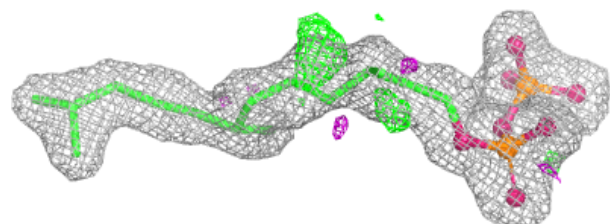
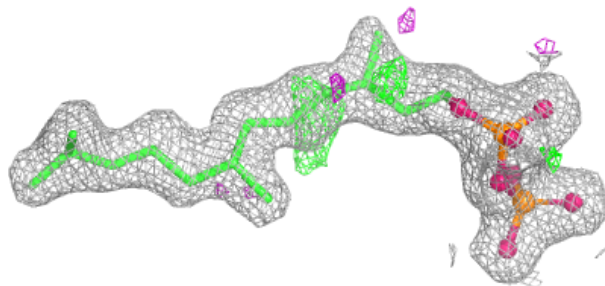
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ED5 B 603:

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

**Electron density around FPP B 601:**

$2mF_o-DF_c$ (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.