



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 11:46 AM GMT

PDB ID : 3PZ4
Title : Crystal structure of FTase(ALPHA-subunit; BETA-subunit DELTA C10) in complex with BMS3 and lipid substrate FPP
Authors : Guo, Z.; Bon, R.S.; Stigter, E.A.; Waldmann, H.; Alexandrov, K.; Blankenfeldt, W.; Goody, R.S.
Deposited on : 2010-12-14
Resolution : 2.10 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

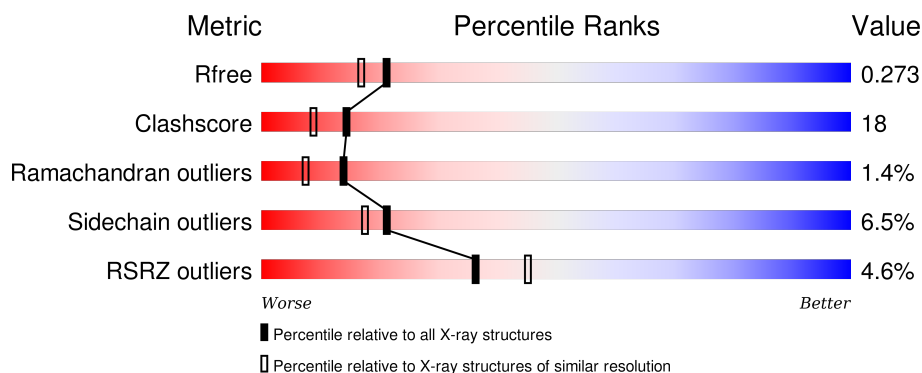
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	379	<div> <div>5%</div> <div>50%</div> <div>28%</div> <div>• •</div> <div>17%</div> </div>
2	B	426	<div> <div>3%</div> <div>65%</div> <div>26%</div> <div>• •</div> <div>5%</div> </div>

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	FPP	B	428	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6208 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 Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	315	Total	C	N	O	S	0	0	0
			2670	1703	470	492	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP Q04631
A	0	HIS	-	EXPRESSION TAG	UNP Q04631

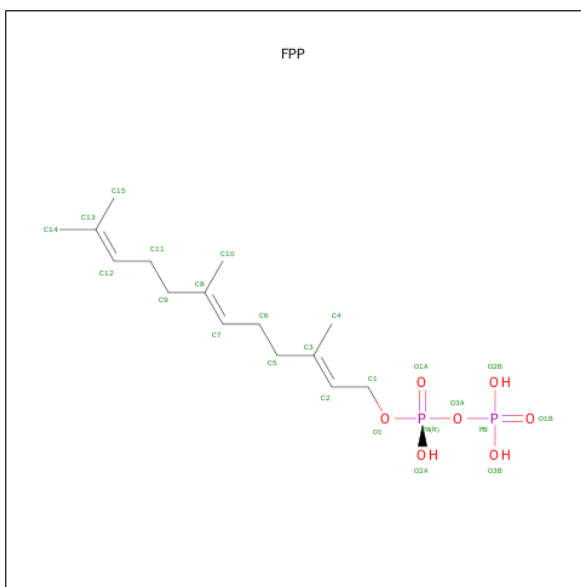
- Molecule 2 is a protein called Protein farnesyltransferase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	403	Total	C	N	O	S	0	0	0
			3169	2026	545	575	23			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

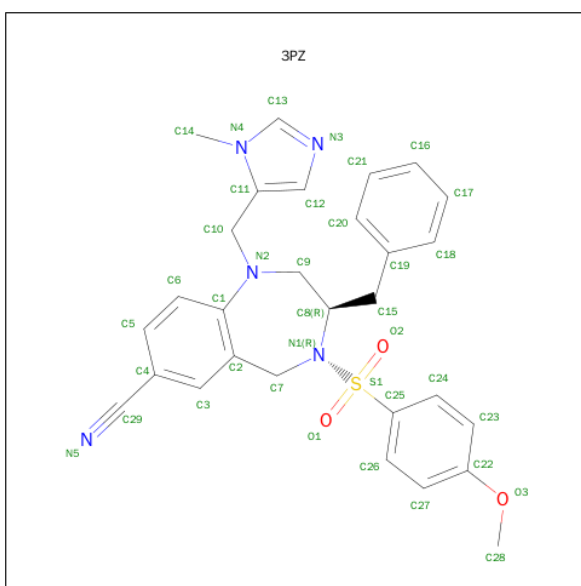
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		

- Molecule 4 is FARNESYL DIPHOSPHATE (three-letter code: FPP) (formula: C₁₅H₂₈O₇P₂).



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

- Molecule 5 is (3R)-3-BENZYL-4-[(4-METHOXYPHENYL)SULFONYL]-1-[(1-METHYL-1H-IMIDAZOL-5-YL)METHYL]-2,3,4,5-TETRAHYDRO-1H-1,4-BENZODIAZEPINE-7-CARBONITRILE (three-letter code: 3PZ) (formula: $C_{29}H_{29}N_5O_3S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	S	0	0
			38	29	5	3	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	137	Total 137	O 137	0	0
6	B	169	Total 169	O 169	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	170.75Å 170.75Å 69.08Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.91 – 2.10 29.57 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.91-2.10) 99.8 (29.57-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.90 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.225 , 0.267 0.233 , 0.273	Depositor DCC
R_{free} test set	3365 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	26.4	Xtriage
Anisotropy	0.385	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 30.9	EDS
Estimated twinning fraction	0.094 for h,-h-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Outliers	0 of 67102 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6208	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.94% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

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: 3PZ, ZN, FPP

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	0.81	0/2736	0.86	9/3716 (0.2%)
2	B	0.80	1/3255 (0.0%)	0.83	7/4421 (0.2%)
All	All	0.80	1/5991 (0.0%)	0.84	16/8137 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	1	1
All	All	1	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	299	CYS	CB-SG	-6.47	1.71	1.82

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	138	ARG	NE-CZ-NH2	-8.74	115.93	120.30
1	A	173	ARG	NE-CZ-NH1	7.87	124.23	120.30
1	A	142	ARG	NE-CZ-NH2	7.66	124.13	120.30
1	A	138	ARG	NE-CZ-NH1	6.03	123.31	120.30
2	B	21	GLU	N-CA-C	5.96	127.10	111.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	21	GLU	CA

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	251	SER	Peptide
2	B	21	GLU	Peptide

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	2670	0	2587	111	0
2	B	3169	0	3098	111	1
3	B	1	0	0	0	0
4	B	24	0	25	2	0
5	B	38	0	29	0	0
6	A	137	0	0	32	5
6	B	169	0	0	20	6
All	All	6208	0	5739	210	7

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 18.

The worst 5 of 210 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:355:TYR:HA	6:A:509:HOH:O	1.48	1.09
2:B:33:GLU:OE1	6:B:581:HOH:O	1.79	1.01
6:A:509:HOH:O	2:B:329:MET:SD	2.19	0.98
1:A:296:LEU:HD22	1:A:322:MET:CE	1.97	0.94
2:B:266:ARG:HA	6:B:582:HOH:O	1.68	0.92

The worst 5 of 7 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)
6:A:418:HOH:O	6:B:454:HOH:O[3_654]	1.63	0.57
6:B:500:HOH:O	6:B:515:HOH:O[3_655]	1.84	0.36
6:B:470:HOH:O	6:B:536:HOH:O[2_544]	2.08	0.12
6:A:428:HOH:O	6:B:519:HOH:O[3_655]	2.12	0.08
6:A:416:HOH:O	6:B:529:HOH:O[3_655]	2.13	0.07

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	313/379 (83%)	282 (90%)	25 (8%)	6 (2%)	10	4
2	B	401/426 (94%)	374 (93%)	23 (6%)	4 (1%)	19	13
All	All	714/805 (89%)	656 (92%)	48 (7%)	10 (1%)	14	7

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	252	ASP
1	A	256	LEU
1	A	329	ASN
2	B	266	ARG
1	A	71	GLU

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	289/339 (85%)	267 (92%)	22 (8%)	16	12
2	B	340/362 (94%)	321 (94%)	19 (6%)	26	22
All	All	629/701 (90%)	588 (94%)	41 (6%)	21	17

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	352	ARG
2	B	21	GLU
2	B	352	ASP
1	A	354	GLU
1	A	358	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	285	GLN
1	A	325	ASN
2	B	293	ASN
1	A	246	ASN
2	B	344	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	428	-	21,23,23	2.00	8 (38%)	27,31,31	1.71	8 (29%)
5	3PZ	B	429	3	38,42,42	3.47	8 (21%)	47,60,60	2.23	13 (27%)

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	428	-	-	0/25/25/25	0/0/0/0
5	3PZ	B	429	3	-	0/24/40/40	0/4/5/5

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	429	3PZ	C1-N2	-4.68	1.34	1.43
4	B	428	FPP	C6-C7	-3.56	1.40	1.50
4	B	428	FPP	C11-C12	-2.84	1.42	1.50
4	B	428	FPP	C1-C2	-2.66	1.40	1.49
5	B	429	3PZ	C11-N4	-2.40	1.33	1.38

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	429	3PZ	O2-S1-O1	-6.87	107.62	119.47
5	B	429	3PZ	C7-C2-C3	-6.63	110.44	119.28
5	B	429	3PZ	N3-C13-N4	-4.28	106.49	112.28
5	B	429	3PZ	C28-O3-C22	-3.73	108.78	117.51
4	B	428	FPP	O3A-PA-O1	-3.17	94.52	102.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	428	FPP	2	0

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, 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	315/379 (83%)	0.52	20 (6%) 23 31	20, 45, 89, 123	0
2	B	403/426 (94%)	0.33	13 (3%) 51 60	19, 37, 73, 97	0
All	All	718/805 (89%)	0.41	33 (4%) 36 45	19, 40, 84, 123	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	422	GLY	5.9
2	B	423	PHE	5.0
2	B	64	PHE	4.7
1	A	55	PHE	4.4
1	A	305	SER	4.3

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
4	FPP	B	428	24/24	0.96	0.15	3.31	27,35,46,53	0
5	3PZ	B	429	38/38	0.91	0.13	1.17	20,31,67,71	0
3	ZN	B	1	1/1	1.00	0.12	0.02	24,24,24,24	0

6.5 Other polymers ⓘ

There are no such residues in this entry.