



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 06:52 PM GMT

PDB ID : 3DST
Title : Crystal structure of RabGGTase(DELTA LRR; DELTA IG)in complex with geranylgeranyl pyrophosphate
Authors : Guo, Z.; Yu, S.; Goody, R.S.; Alexandrov, K.; Blankenfeldt, W.
Deposited on : 2008-07-14
Resolution : 1.90 Å(reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

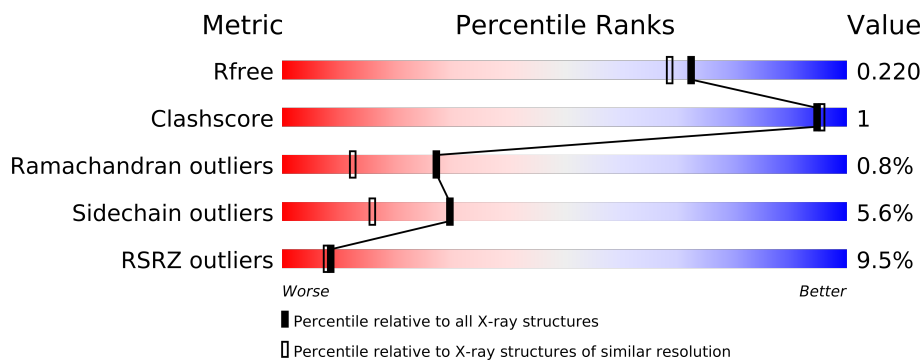
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.90 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}	66092	3684 (1.90-1.90)
Clashscore	79885	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (1.90-1.90)
RSRZ outliers	66119	3686 (1.90-1.90)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	331	
2	B	331	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5402 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Geranylgeranyl transferase type-2 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	311	Total	C	N	O	S	0	4	0
			2517	1608	431	466	12			

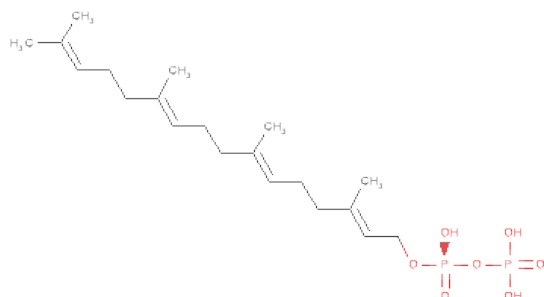
There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	HIS	-	EXPRESSION TAG	UNP Q08602
A	238	ALA	-	LINKER	UNP Q08602
A	239	GLY	-	LINKER	UNP Q08602
A	240	SER	-	LINKER	UNP Q08602
A	241	GLY	-	LINKER	UNP Q08602

- Molecule 2 is a protein called Geranylgeranyl transferase type-2 subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	325	Total	C	N	O	S	0	3	0
			2538	1624	422	472	20			

- Molecule 3 is GERANYLGERANYL DIPHOSPHATE (three-letter code: GRG) (formula: $C_{20}H_{36}O_7P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	O	P	0	0
			29	20	7	2		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 6 is water.

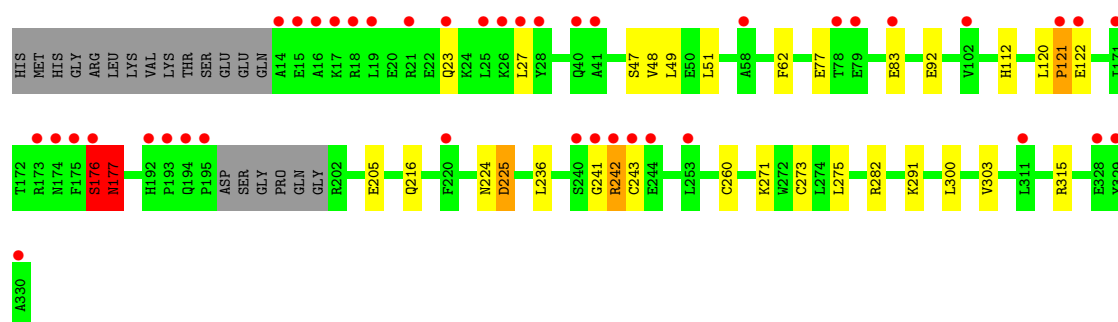
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	131	Total	O	0	0
			131	131		
6	B	185	Total	O	0	0
			185	185		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

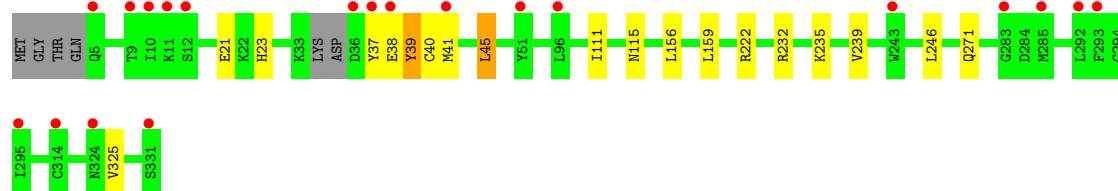
- Molecule 1: Geranylgeranyl transferase type-2 subunit alpha

Chain A: 



- Molecule 2: Geranylgeranyl transferase type-2 subunit beta

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.26Å 90.62Å 114.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.21 – 1.90 29.21 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.5 (29.21-1.90) 99.5 (29.21-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.44 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.180 , 0.220 0.185 , 0.220	Depositor DCC
R_{free} test set	2789 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	39.6	Xtriage
Anisotropy	0.262	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 39.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 55563 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5402	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GRG, ZN, CA

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	0.46	0/2589	0.70	4/3519 (0.1%)
2	B	0.51	0/2606	0.69	6/3535 (0.2%)
All	All	0.49	0/5195	0.70	10/7054 (0.1%)

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	6
2	B	0	2
All	All	0	8

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	225	ASP	N-CA-C	-8.78	87.28	111.00
2	B	41	MET	N-CA-C	-6.24	94.15	111.00
1	A	315	ARG	NE-CZ-NH2	-6.16	117.22	120.30
2	B	232	ARG	NE-CZ-NH2	-6.01	117.30	120.30
1	A	282	ARG	NE-CZ-NH2	-5.84	117.38	120.30
2	B	222	ARG	NE-CZ-NH2	-5.53	117.54	120.30
2	B	232	ARG	NE-CZ-NH1	5.49	123.05	120.30
1	A	176	SER	C-N-CA	5.31	134.97	121.70
2	B	45	LEU	CA-CB-CG	5.31	127.50	115.30
2	B	45	LEU	CB-CG-CD2	5.06	119.60	111.00

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	121	PRO	Peptide
1	A	176	SER	Peptide
1	A	224	ASN	Peptide
1	A	241	GLY	Peptide
1	A	243	CYS	Peptide
1	A	47	SER	Peptide
2	B	38	GLU	Peptide
2	B	40	CYS	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2517	0	0	4	0
2	B	2538	0	0	3	0
3	B	29	0	0	1	0
4	B	1	0	0	0	0
5	B	1	0	0	0	0
6	A	131	0	0	1	0
6	B	185	0	0	1	0
All	All	5402	0	0	7	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 1.

All (7) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:177:ASN:N	6:A:438:HOH:O	2.34	0.59
2:B:235:LYS:NZ	3:B:334:GRG:O2B	2.41	0.53
2:B:37:TYR:N	6:B:469:HOH:O	2.43	0.52
1:A:260:CYS:O	1:A:273[B]:CYS:SG	2.70	0.50
1:A:205:GLU:OE1	1:A:242:ARG:NH1	2.46	0.48
1:A:92:GLU:OE2	1:A:112:HIS:CE1	2.69	0.46
2:B:23:HIS:NE2	2:B:271:GLN:NE2	2.64	0.45

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	311/331 (94%)	300 (96%)	7 (2%)	4 (1%)	18	5
2	B	324/331 (98%)	321 (99%)	2 (1%)	1 (0%)	50	37
All	All	635/662 (96%)	621 (98%)	9 (1%)	5 (1%)	27	12

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	48	VAL
1	A	177	ASN
2	B	39	TYR
1	A	121	PRO
1	A	176	SER

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	267/293 (91%)	247 (92%)	20 (8%)	19	8
2	B	277/284 (98%)	267 (96%)	10 (4%)	47	33
All	All	544/577 (94%)	514 (94%)	30 (6%)	30	16

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	GLN

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Mol	Chain	Res	Type
1	A	27	LEU
1	A	49	LEU
1	A	51	LEU
1	A	62	PHE
1	A	77	GLU
1	A	83	GLU
1	A	120	LEU
1	A	122	GLU
1	A	176	SER
1	A	177	ASN
1	A	216	GLN
1	A	225	ASP
1	A	236	LEU
1	A	242	ARG
1	A	271	LYS
1	A	275	LEU
1	A	291	LYS
1	A	300	LEU
1	A	303	VAL
2	B	21	GLU
2	B	39	TYR
2	B	45	LEU
2	B	111	ILE
2	B	115	ASN
2	B	156	LEU
2	B	159	LEU
2	B	239	VAL
2	B	246	LEU
2	B	325	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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, 2 are monoatomic - leaving 1 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	$\# Z > 2$
3	GRG	B	334	-	28,28,28	2.01	9 (32%)	37,37,37	1.20	3 (8%)

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	GRG	B	334	-	-	0/31/31/31	0/0/0/0

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	334	GRG	C2-C3	3.78	1.40	1.32
3	B	334	GRG	C6-C7	-3.68	1.39	1.50
3	B	334	GRG	C11-C12	-3.56	1.40	1.50
3	B	334	GRG	C7-C8	3.45	1.39	1.32
3	B	334	GRG	C16-C17	-3.34	1.40	1.50
3	B	334	GRG	C12-C13	3.05	1.39	1.32
3	B	334	GRG	C17-C18	2.69	1.41	1.32
3	B	334	GRG	C1-C2	-2.68	1.40	1.49
3	B	334	GRG	PB-O1B	2.15	1.62	1.54

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	334	GRG	PA-O3A-PB	-3.96	120.08	131.68
3	B	334	GRG	C14-C13-C15	2.67	119.44	115.39
3	B	334	GRG	C4-C3-C5	2.12	118.62	115.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	311/331 (93%)	0.85	41 (13%) 4 3	27, 42, 72, 98	0
2	B	325/331 (98%)	0.47	20 (6%) 20 20	25, 33, 54, 68	0
All	All	636/662 (96%)	0.65	61 (9%) 8 8	25, 38, 64, 98	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	176	SER	10.6
1	A	240	SER	7.8
1	A	241	GLY	7.5
1	A	14	ALA	7.0
1	A	16	ALA	6.9
1	A	330	ALA	5.6
1	A	19	LEU	5.5
2	B	37	TYR	5.1
2	B	10	ILE	4.9
1	A	15	GLU	4.8
1	A	175	PHE	4.4
1	A	195	PRO	4.4
1	A	21	ARG	4.3
1	A	23	GLN	4.2
1	A	26	LYS	4.1
2	B	331	SER	4.0
1	A	220	PHE	3.9
1	A	40	GLN	3.8
2	B	283	GLY	3.7
1	A	243	CYS	3.7
1	A	242	ARG	3.7
1	A	17	LYS	3.5
1	A	193	PRO	3.4
1	A	28[A]	TYR	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	194	GLN	3.2
2	B	9	THR	3.2
1	A	58	ALA	3.1
1	A	122	GLU	3.1
1	A	18	ARG	3.1
2	B	12	SER	3.0
1	A	25	LEU	2.9
2	B	314	CYS	2.9
2	B	11	LYS	2.9
2	B	293	PHE	2.9
1	A	253	LEU	2.9
1	A	102	VAL	2.8
1	A	79	GLU	2.8
2	B	285	MET	2.8
2	B	51	TYR	2.7
1	A	244	GLU	2.7
1	A	329	TYR	2.6
1	A	121	PRO	2.6
1	A	171	ILE	2.6
1	A	174	ASN	2.5
2	B	295	ILE	2.5
1	A	41	ALA	2.5
1	A	311	LEU	2.4
2	B	324	ASN	2.3
2	B	36	ASP	2.3
1	A	173	ARG	2.3
2	B	243	TRP	2.2
1	A	78	THR	2.2
2	B	96	LEU	2.2
1	A	192	HIS	2.2
1	A	83	GLU	2.1
2	B	5	GLN	2.1
1	A	328	GLU	2.1
2	B	41	MET	2.1
2	B	38	GLU	2.1
2	B	292	LEU	2.1
1	A	27	LEU	2.1

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	CA	B	333	1/1	0.16	0.36	129,129,129,129	0
3	GRG	B	334	29/29	0.16	-0.04	26,38,67,69	0
4	ZN	B	332	1/1	0.12	-0.82	51,51,51,51	0

6.5 Other polymers

There are no such residues in this entry.