



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2020 – 10:50 AM BST

PDB ID : 3PZ2  
Title : Crystal structure of RabGGTase(DELTA LRR; DELTA IG) in Complex with BMS3 and lipid substrate GGPP  
Authors : Guo, Z.; Bon, R.S.; Stigter, E.A.; Waldmann, H.; Alexandrov, K.; Blankenfeldt, W.; Goody, R.S.  
Deposited on : 2010-12-14  
Resolution : 2.35 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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 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) : 2.13.1

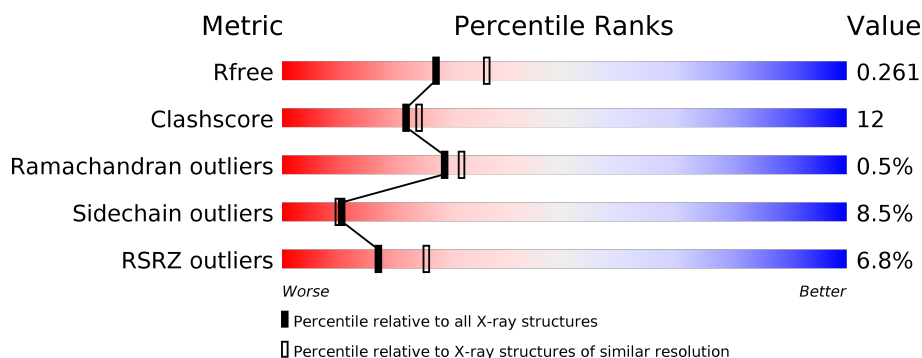
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.35 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))
$R_{free}$	130704	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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  $\geq 3$ , 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	332	<div> <div>10%</div> <div> <div></div> <div>65%</div> <div>22%</div> <div>• •</div> <div>10%</div> </div> </div>
2	B	330	<div> <div>2%</div> <div> <div></div> <div>75%</div> <div>20%</div> <div>• •</div> </div> </div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5187 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 Geranylgeranyl transferase type-2 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	298	Total	C	N	O	S	0	3	0
			2426	1550	414	450	12			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP Q08602
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	322	Total	C	N	O	S	0	2	0
			2509	1604	415	469	21			

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

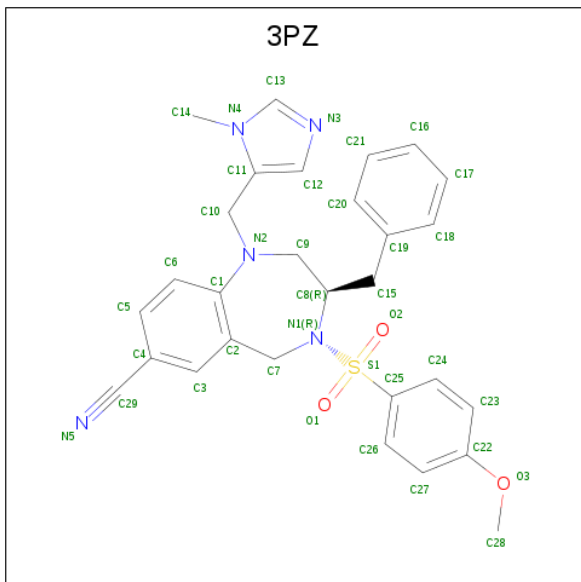
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

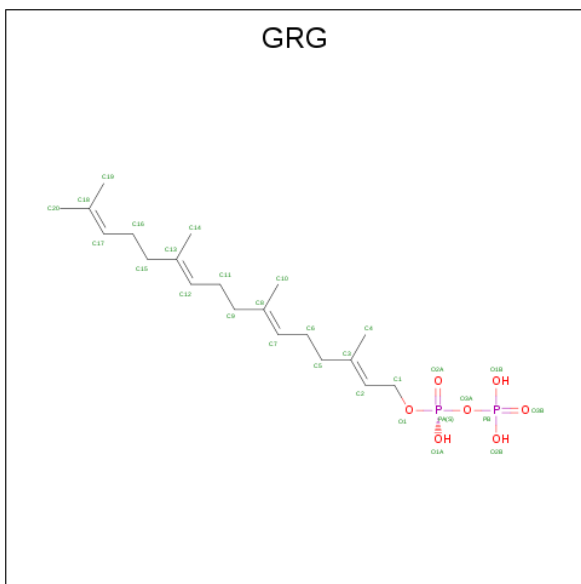
- Molecule 5 is (3R)-3-benzyl-4-[(4-methoxyphenyl)sulfonyl]-1-[(1-methyl-1H-imidazol-5-yl

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



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

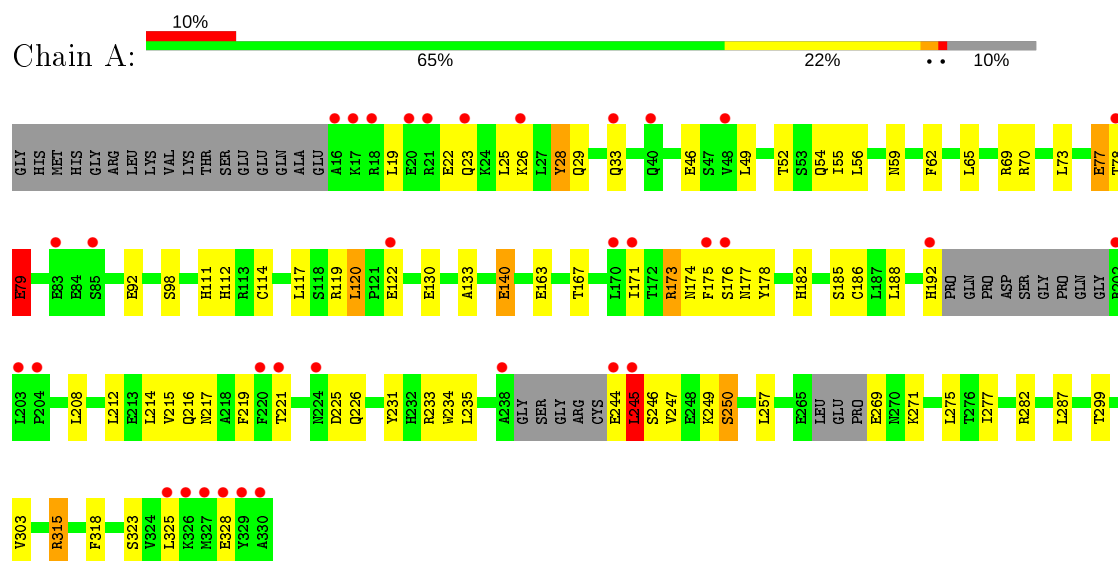
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	64	Total 64	O 64	0	0
7	B	119	Total 119	O 119	0	0

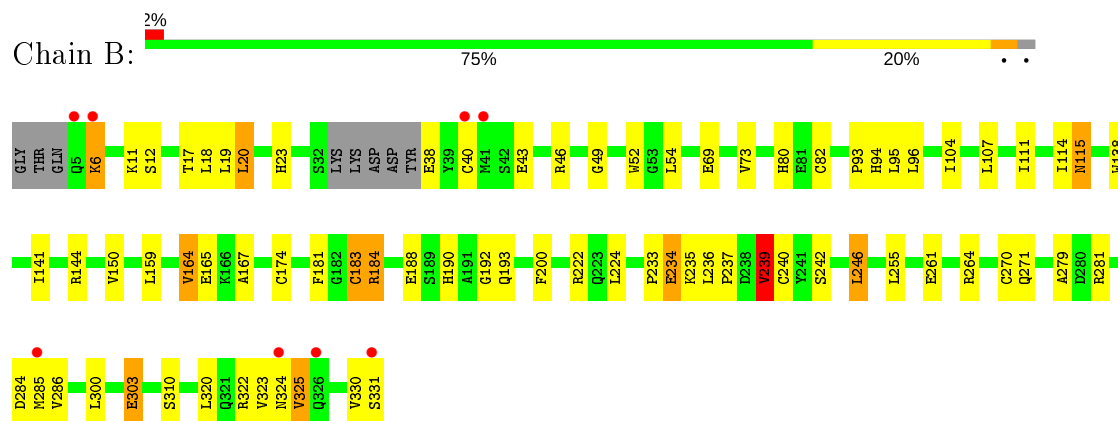
### 3 Residue-property plots [i](#)

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: Geranylgeranyl transferase type-2 subunit alpha



- Molecule 2: Geranylgeranyl transferase type-2 subunit beta



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.45Å 84.58Å 117.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.35 29.91 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.5 (30.00-2.35) 99.5 (29.91-2.35)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.39 (at 2.36Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.188 , 0.256 0.193 , 0.261	Depositor DCC
$R_{free}$ test set	1403 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.3	Xtriage
Anisotropy	0.260	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 40.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5187	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.83% 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: GRG, ZN, CA, 3PZ

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	0.78	1/2489 (0.0%)	0.80	5/3375 (0.1%)
2	B	0.97	3/2572 (0.1%)	0.85	4/3487 (0.1%)
All	All	0.88	4/5061 (0.1%)	0.83	9/6862 (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	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	183	CYS	CB-SG	-15.55	1.55	1.82
2	B	240	CYS	CB-SG	-6.60	1.71	1.82
1	A	186	CYS	CB-SG	-6.33	1.71	1.82
2	B	150	VAL	CB-CG2	5.94	1.65	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	315	ARG	NE-CZ-NH2	-8.29	116.16	120.30
2	B	183	CYS	CB-CA-C	-6.31	97.79	110.40
1	A	245	LEU	N-CA-C	-6.24	94.16	111.00
2	B	184	ARG	NE-CZ-NH1	5.93	123.27	120.30
1	A	245	LEU	CA-CB-CG	-5.64	102.33	115.30
1	A	315	ARG	NE-CZ-NH1	5.45	123.03	120.30
2	B	239	VAL	CB-CA-C	-5.36	101.22	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	144	ARG	NE-CZ-NH1	5.31	122.95	120.30
1	A	246	SER	N-CA-C	-5.21	96.93	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	219	PHE	Peptide
1	A	244	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	2426	0	2365	59	0
2	B	2509	0	2462	57	0
3	B	1	0	0	0	0
4	B	1	0	0	0	0
5	B	38	0	29	3	0
6	B	29	0	33	2	0
7	A	64	0	0	17	0
7	B	119	0	0	22	0
All	All	5187	0	4889	117	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 12.

All (117) 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:17:THR:HB	7:B:444:HOH:O	1.46	1.15
2:B:331:SER:HB3	7:B:443:HOH:O	1.53	1.08
2:B:261:GLU:HG2	7:B:407:HOH:O	1.58	1.02
1:A:176:SER:O	7:A:391:HOH:O	1.77	1.02
1:A:282:ARG:HD2	7:A:361:HOH:O	1.66	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:40:CYS:HB3	7:B:406:HOH:O	1.67	0.94
2:B:323:VAL:HG23	2:B:325:VAL:HG13	1.49	0.94
2:B:82[B]:CYS:SG	7:B:383:HOH:O	2.25	0.93
2:B:43:GLU:OE1	7:B:366:HOH:O	1.87	0.91
2:B:17:THR:HG22	7:B:417:HOH:O	1.77	0.84
2:B:324:ASN:HB2	7:B:435:HOH:O	1.81	0.81
1:A:26:LYS:HG3	7:A:377:HOH:O	1.82	0.80
2:B:322:ARG:HD3	7:B:411:HOH:O	1.82	0.80
1:A:287:LEU:HD11	1:A:325:LEU:HB3	1.63	0.80
2:B:235:LYS:HE2	7:B:360:HOH:O	1.84	0.77
1:A:225:ASP:HB3	7:A:368:HOH:O	1.84	0.77
1:A:173:ARG:HD3	7:A:388:HOH:O	1.88	0.72
2:B:18:LEU:HG	2:B:20:LEU:HD13	1.70	0.72
2:B:285:MET:HE1	7:B:420:HOH:O	1.89	0.71
2:B:94:HIS:HD2	2:B:96:LEU:H	1.40	0.70
1:A:140:GLU:HB3	1:A:176:SER:HB3	1.73	0.70
1:A:163:GLU:O	1:A:167:THR:HG23	1.93	0.69
1:A:173:ARG:NE	1:A:174:ASN:ND2	2.41	0.68
2:B:190:HIS:HD2	2:B:192:GLY:H	1.42	0.67
2:B:242:SER:O	2:B:246:LEU:HB2	1.95	0.67
2:B:322:ARG:CD	7:B:411:HOH:O	2.42	0.67
1:A:19:LEU:CB	7:A:389:HOH:O	2.44	0.65
2:B:94:HIS:HE1	7:B:339:HOH:O	1.82	0.62
1:A:182:HIS:O	1:A:185:SER:HB3	1.98	0.61
2:B:284:ASP:HB3	7:B:437:HOH:O	1.99	0.61
2:B:188:GLU:OE1	7:B:377:HOH:O	2.15	0.61
2:B:323:VAL:HG23	2:B:325:VAL:CG1	2.27	0.61
1:A:173:ARG:CZ	1:A:174:ASN:HD21	2.14	0.60
1:A:70:ARG:HH11	1:A:112:HIS:HD2	1.50	0.60
2:B:264:ARG:NH1	2:B:303:GLU:OE1	2.34	0.60
1:A:25:LEU:O	1:A:29:GLN:HB2	2.03	0.59
2:B:239:VAL:CG2	2:B:279:ALA:O	2.51	0.59
2:B:323:VAL:CG2	2:B:325:VAL:HG13	2.29	0.59
1:A:173:ARG:NE	1:A:174:ASN:HD21	2.01	0.58
1:A:245:LEU:HD22	1:A:250:SER:N	2.18	0.58
1:A:173:ARG:HE	1:A:174:ASN:ND2	2.02	0.58
1:A:175:PHE:HA	1:A:177:ASN:ND2	2.19	0.57
2:B:19:LEU:H	2:B:271:GLN:HE22	1.52	0.57
2:B:54:LEU:HD12	2:B:104:ILE:HG23	1.88	0.56
2:B:239:VAL:HG22	2:B:270:CYS:SG	2.45	0.56
1:A:26:LYS:NZ	7:A:380:HOH:O	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:GLU:HB3	1:A:176:SER:CB	2.36	0.54
2:B:80:HIS:HB3	7:B:400:HOH:O	2.07	0.54
2:B:183:CYS:HA	2:B:193:GLN:HG2	1.88	0.54
2:B:330:VAL:HG12	2:B:331:SER:OG	2.08	0.54
5:B:333:3PZ:C21	6:B:334:GRG:H111	2.38	0.54
7:A:369:HOH:O	2:B:193:GLN:NE2	2.40	0.53
1:A:92:GLU:OE2	1:A:112:HIS:HE1	1.92	0.53
1:A:192:HIS:CE1	7:A:390:HOH:O	2.61	0.53
1:A:299:THR:O	1:A:303:VAL:HG23	2.09	0.52
5:B:333:3PZ:H13	7:B:375:HOH:O	2.09	0.52
2:B:239:VAL:HG21	2:B:279:ALA:O	2.09	0.52
2:B:235:LYS:NZ	6:B:334:GRG:O3B	2.32	0.52
1:A:140:GLU:OE2	1:A:176:SER:HB2	2.09	0.51
1:A:117:LEU:HA	1:A:120:LEU:HD22	1.90	0.51
1:A:59:ASN:OD1	7:A:393:HOH:O	2.19	0.51
1:A:26:LYS:CG	7:A:377:HOH:O	2.50	0.51
2:B:286:VAL:HG22	7:B:420:HOH:O	2.09	0.51
1:A:130:GLU:O	1:A:133:ALA:HB3	2.11	0.50
2:B:141:ILE:O	2:B:184:ARG:HD3	2.12	0.50
2:B:115:ASN:C	2:B:115:ASN:HD22	2.14	0.50
2:B:18:LEU:CG	2:B:20:LEU:HD13	2.41	0.50
2:B:49:GLY:HA2	2:B:52:TRP:CE3	2.47	0.49
1:A:140:GLU:CB	1:A:176:SER:HB3	2.42	0.49
1:A:111:HIS:HE1	2:B:138:TRP:O	1.95	0.49
1:A:233:ARG:HH12	1:A:275:LEU:HD21	1.76	0.49
1:A:171:ILE:O	1:A:174:ASN:O	2.31	0.49
1:A:208:LEU:HD11	1:A:235:LEU:O	2.12	0.48
1:A:56:LEU:HD12	1:A:69:ARG:HD2	1.94	0.48
1:A:269:GLU:HB2	7:A:358:HOH:O	2.14	0.48
1:A:328:GLU:CG	7:A:370:HOH:O	2.62	0.47
1:A:315:ARG:HD3	7:A:365:HOH:O	2.13	0.47
2:B:23:HIS:NE2	2:B:271:GLN:NE2	2.50	0.47
2:B:190:HIS:CD2	2:B:192:GLY:H	2.27	0.47
1:A:282:ARG:NH2	1:A:318:PHE:HB3	2.31	0.46
1:A:52:THR:HG22	1:A:65:LEU:HD22	1.97	0.46
1:A:178:TYR:CE2	2:B:233:PRO:HG2	2.51	0.46
2:B:104:ILE:O	2:B:107:LEU:HB2	2.16	0.46
1:A:328:GLU:HG2	7:A:370:HOH:O	2.16	0.46
1:A:73:LEU:O	1:A:77:GLU:HB3	2.15	0.46
2:B:46:ARG:HG2	7:B:366:HOH:O	2.15	0.45
1:A:245:LEU:CD2	1:A:249:LYS:HB3	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:246:LEU:HG	2:B:255:LEU:HD11	1.97	0.45
1:A:173:ARG:NH2	1:A:174:ASN:HD21	2.15	0.44
1:A:78:THR:OG1	1:A:79:GLU:N	2.51	0.44
2:B:80:HIS:ND1	2:B:93:PRO:HD3	2.33	0.44
2:B:224:LEU:HD12	2:B:237:PRO:HD3	2.00	0.44
1:A:245:LEU:HD23	1:A:245:LEU:HA	1.55	0.44
1:A:28:TYR:CE1	1:A:55:ILE:HG23	2.53	0.43
2:B:111:ILE:HA	2:B:111:ILE:HD13	1.85	0.43
1:A:140:GLU:HG2	1:A:176:SER:HB3	1.99	0.43
2:B:310:SER:HB2	2:B:320:LEU:CD1	2.49	0.43
1:A:140:GLU:CB	1:A:176:SER:CB	2.97	0.43
1:A:26:LYS:N	7:A:377:HOH:O	2.50	0.43
1:A:245:LEU:HD13	1:A:250:SER:HB2	2.00	0.43
2:B:164:VAL:O	2:B:167:ALA:HB3	2.19	0.43
1:A:231:TYR:O	1:A:234:TRP:HB3	2.18	0.43
1:A:245:LEU:HD23	1:A:249:LYS:HB3	1.99	0.42
1:A:315:ARG:HD2	7:A:331:HOH:O	2.19	0.42
2:B:324:ASN:CB	7:B:435:HOH:O	2.54	0.41
2:B:6:LYS:HD2	2:B:234:GLU:O	2.20	0.41
2:B:114:ILE:HG21	2:B:114:ILE:HD13	1.87	0.41
2:B:174:CYS:O	2:B:181:PHE:HA	2.20	0.41
1:A:257:LEU:CD1	1:A:277:ILE:HG23	2.50	0.41
1:A:73:LEU:O	1:A:77:GLU:CB	2.69	0.41
1:A:22:GLU:O	1:A:26:LYS:HG3	2.21	0.41
2:B:285:MET:CE	7:B:420:HOH:O	2.61	0.41
5:B:333:3PZ:H14	7:B:392:HOH:O	2.20	0.41
1:A:28:TYR:CD1	1:A:55:ILE:HG23	2.56	0.41
2:B:200:PHE:C	2:B:200:PHE:CD1	2.94	0.40
1:A:212:LEU:O	1:A:216:GLN:HB2	2.22	0.40
2:B:300:LEU:HA	2:B:300:LEU:HD23	1.97	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	293/332 (88%)	278 (95%)	13 (4%)	2 (1%)	22	23
2	B	320/330 (97%)	313 (98%)	6 (2%)	1 (0%)	41	47
All	All	613/662 (93%)	591 (96%)	19 (3%)	3 (0%)	29	32

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	79	GLU
1	A	221	THR
2	B	12	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	260/293 (89%)	232 (89%)	28 (11%)	6	6
2	B	276/283 (98%)	257 (93%)	19 (7%)	15	15
All	All	536/576 (93%)	489 (91%)	47 (9%)	10	8

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	28	TYR
1	A	33	GLN
1	A	46	GLU
1	A	49	LEU
1	A	54	GLN
1	A	62	PHE
1	A	77	GLU
1	A	79	GLU
1	A	98[A]	SER

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Mol	Chain	Res	Type
1	A	98[B]	SER
1	A	114[A]	CYS
1	A	114[B]	CYS
1	A	119	ARG
1	A	120	LEU
1	A	122	GLU
1	A	140	GLU
1	A	173	ARG
1	A	188	LEU
1	A	214	LEU
1	A	215	VAL
1	A	217	ASN
1	A	226	GLN
1	A	245	LEU
1	A	247	VAL
1	A	250	SER
1	A	271	LYS
1	A	323	SER
2	B	6	LYS
2	B	11	LYS
2	B	20	LEU
2	B	38	GLU
2	B	69	GLU
2	B	73	VAL
2	B	95	LEU
2	B	115	ASN
2	B	159	LEU
2	B	164	VAL
2	B	165	GLU
2	B	222	ARG
2	B	234	GLU
2	B	236	LEU
2	B	239	VAL
2	B	246	LEU
2	B	281	ARG
2	B	303	GLU
2	B	325	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	GLN

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Mol	Chain	Res	Type
1	A	40	GLN
1	A	75	HIS
1	A	111	HIS
1	A	112	HIS
1	A	174	ASN
1	A	177	ASN
1	A	190	GLN
1	A	192	HIS
1	A	264	GLN
2	B	5	GLN
2	B	91	HIS
2	B	94	HIS
2	B	115	ASN
2	B	190	HIS
2	B	271	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 monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 2 are 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
6	GRG	B	334	-	26,28,28	2.09	11 (42%)	33,37,37	1.65	5 (15%)
5	3PZ	B	333	3	36,42,42	2.00	6 (16%)	49,60,60	1.84	10 (20%)

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
6	GRG	B	334	-	-	1/31/31/31	-
5	3PZ	B	333	3	-	2/24/40/40	0/4/5/5

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	333	3PZ	C1-N2	-6.39	1.32	1.43
5	B	333	3PZ	O2-S1	6.10	1.50	1.43
5	B	333	3PZ	O1-S1	5.48	1.49	1.43
6	B	334	GRG	C11-C12	-3.59	1.38	1.50
6	B	334	GRG	O1-C1	3.53	1.48	1.43
6	B	334	GRG	C16-C17	-3.17	1.40	1.50
6	B	334	GRG	C7-C8	3.14	1.40	1.33
6	B	334	GRG	C6-C7	-2.95	1.40	1.50
6	B	334	GRG	C2-C3	2.89	1.39	1.33
6	B	334	GRG	C1-C2	-2.83	1.40	1.49
6	B	334	GRG	C17-C18	2.69	1.40	1.32
6	B	334	GRG	C15-C13	2.57	1.56	1.51
6	B	334	GRG	PB-O1B	2.49	1.64	1.54
6	B	334	GRG	PB-O2B	2.35	1.63	1.54
5	B	333	3PZ	C9-N2	2.30	1.50	1.46
5	B	333	3PZ	S1-N1	2.14	1.66	1.63
5	B	333	3PZ	C7-C2	2.02	1.54	1.51

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	333	3PZ	O2-S1-O1	-6.16	109.53	119.52
5	B	333	3PZ	C7-C2-C3	-6.15	111.27	119.17
6	B	334	GRG	C14-C13-C15	5.81	125.05	115.27
5	B	333	3PZ	C25-S1-N1	3.95	114.39	107.36
5	B	333	3PZ	C7-C2-C1	3.76	128.13	122.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	333	3PZ	N3-C13-N4	-2.80	108.10	112.26
6	B	334	GRG	O2B-PB-O3A	-2.79	95.29	104.64
5	B	333	3PZ	C15-C8-N1	-2.76	108.22	112.61
5	B	333	3PZ	C26-C25-S1	-2.66	116.95	119.76
5	B	333	3PZ	C24-C25-S1	2.63	122.52	119.76
5	B	333	3PZ	O1-S1-C25	2.45	111.14	108.05
6	B	334	GRG	PA-O3A-PB	-2.24	125.12	132.83
5	B	333	3PZ	C28-O3-C22	-2.21	112.72	117.51
6	B	334	GRG	C14-C13-C12	-2.17	118.12	123.68
6	B	334	GRG	C15-C13-C12	-2.13	116.81	121.12

There are no chirality outliers.

All (3) torsion outliers are listed below:

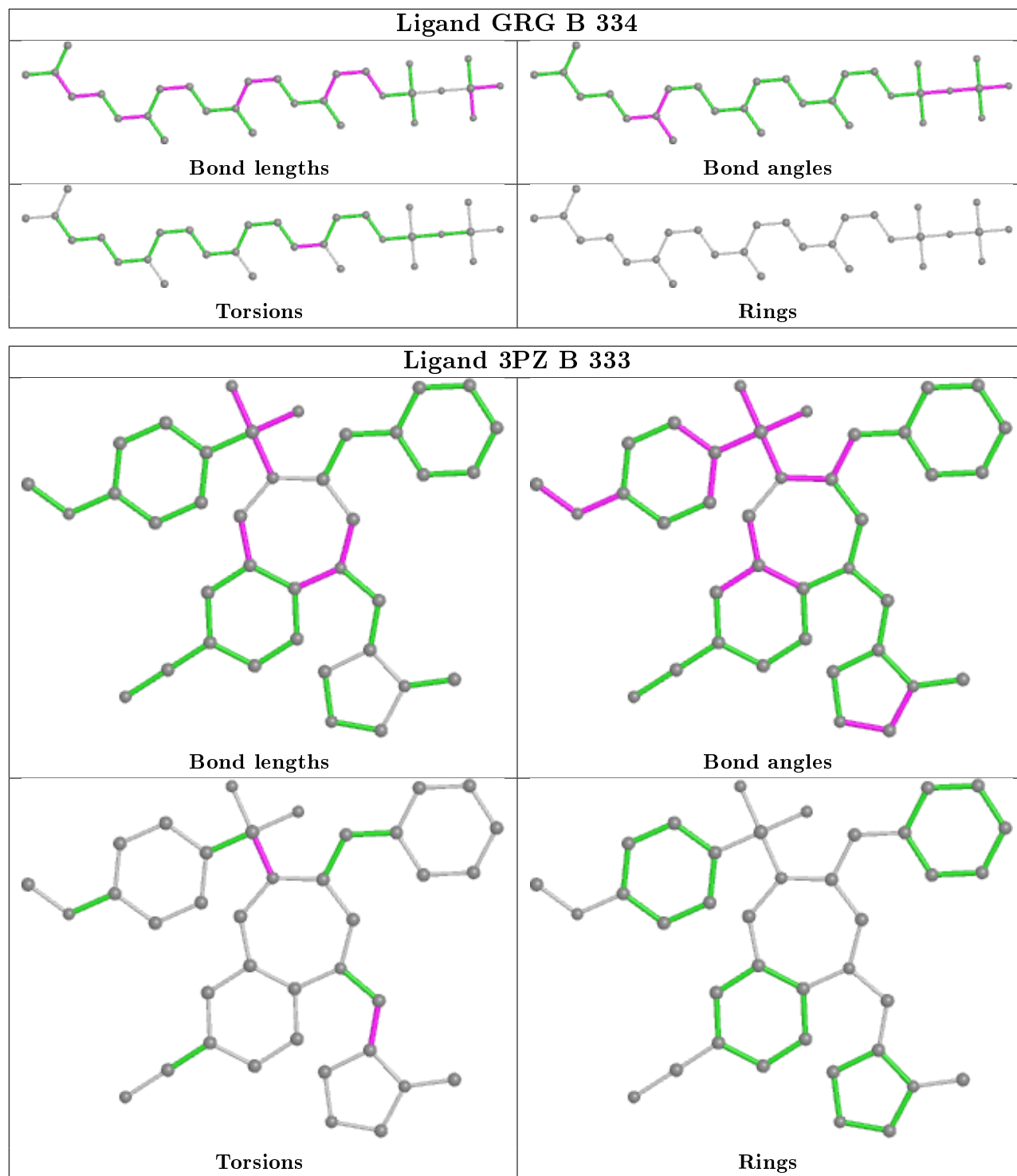
Mol	Chain	Res	Type	Atoms
5	B	333	3PZ	C7-N1-S1-O1
5	B	333	3PZ	N2-C10-C11-N4
6	B	334	GRG	C4-C3-C5-C6

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	334	GRG	2	0
5	B	333	3PZ	3	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 ⓘ

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, 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	298/332 (89%)	0.60	34 (11%) 5 7	22, 56, 85, 106	0
2	B	322/330 (97%)	-0.08	8 (2%) 57 67	21, 32, 58, 76	0
All	All	620/662 (93%)	0.25	42 (6%) 17 25	21, 42, 80, 106	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	330	ALA	9.2
1	A	203	LEU	8.7
1	A	176	SER	6.3
1	A	202	ARG	6.1
1	A	171	ILE	5.9
1	A	175	PHE	5.1
1	A	238	ALA	5.0
2	B	5	GLN	5.0
1	A	16	ALA	4.6
1	A	327	MET	4.4
2	B	324	ASN	3.9
1	A	26	LYS	3.9
1	A	85	SER	3.8
2	B	331	SER	3.7
1	A	328	GLU	3.6
1	A	220	PHE	3.4
1	A	192	HIS	3.4
1	A	244	GLU	3.4
1	A	21	ARG	3.3
1	A	40	GLN	3.2
1	A	221	THR	3.2
1	A	329	TYR	3.1
1	A	20	GLU	3.1
1	A	17	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	33	GLN	2.9
1	A	204	PRO	2.9
2	B	40	CYS	2.8
2	B	6	LYS	2.6
1	A	326	LYS	2.6
2	B	326	GLN	2.6
1	A	170	LEU	2.5
2	B	285	MET	2.4
1	A	224	ASN	2.4
1	A	245	LEU	2.4
1	A	18	ARG	2.4
1	A	78	THR	2.3
2	B	41	MET	2.3
1	A	48	VAL	2.3
1	A	83	GLU	2.3
1	A	325	LEU	2.2
1	A	23	GLN	2.0
1	A	122	GLU	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](#)

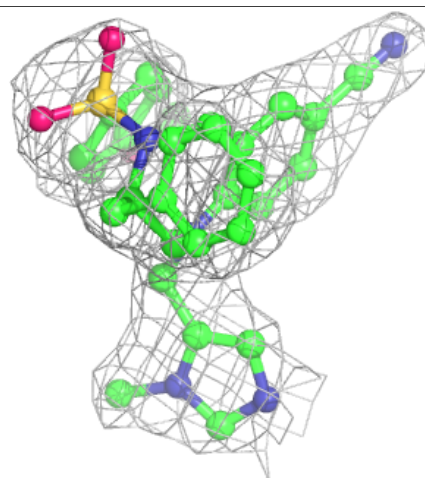
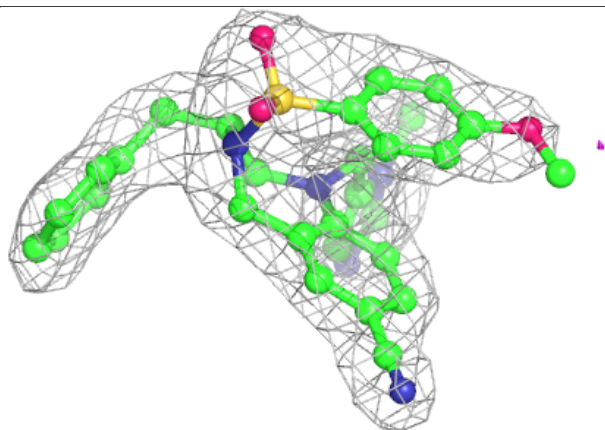
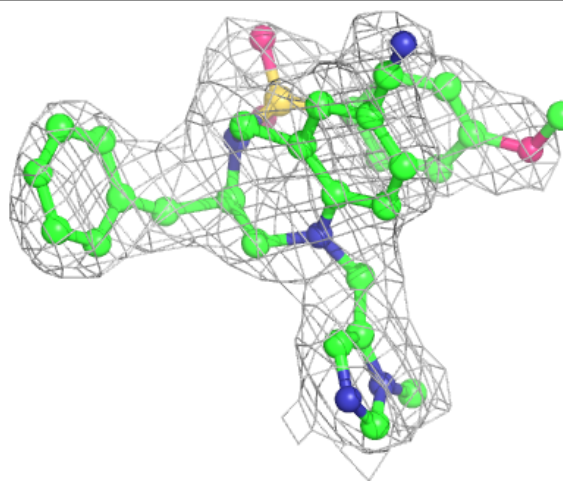
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

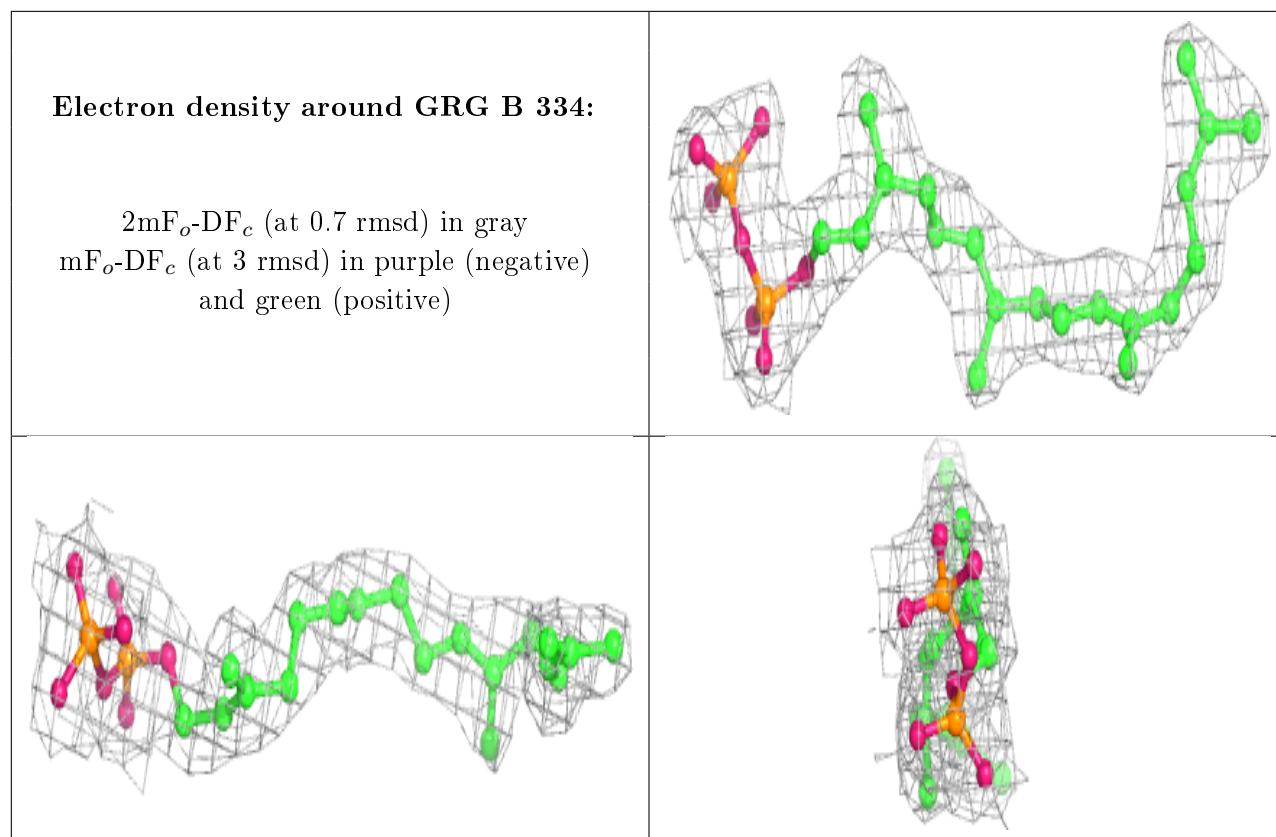
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	CA	B	332	1/1	0.80	0.14	83,83,83,83	0
5	3PZ	B	333	38/38	0.96	0.13	24,36,57,62	0
6	GRG	B	334	29/29	0.98	0.14	22,28,44,46	0
3	ZN	B	1	1/1	1.00	0.09	30,30,30,30	0

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 3PZ B 333:**

$2mF_o-DF_c$  (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.