



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 08:10 pm GMT

PDB ID : 5E8H  
Title : Crystal structure of geranylarnesyl pyrophosphate synthases 2 from Arabidopsis thaliana  
Authors : Wang, C.; Chen, Q.; Wang, G.; Zhang, P.  
Deposited on : 2015-10-14  
Resolution : 2.30 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

<http://wwpdb.org/validation/2016/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  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

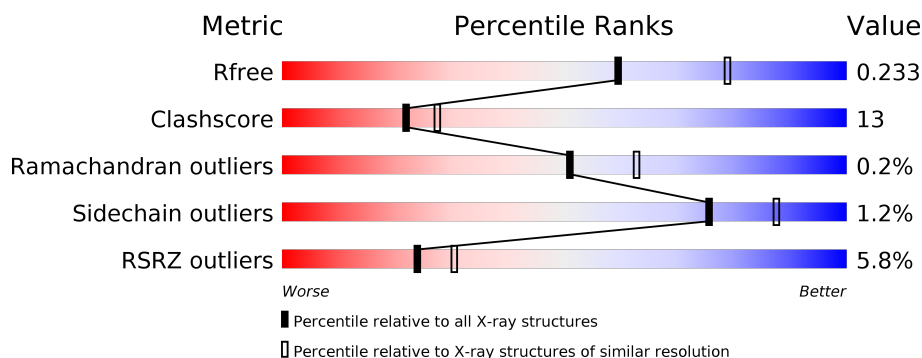
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	100719	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

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. 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	330	<div> <div>5%</div> <div> <div></div> <div>71%</div> <div>12%</div> <div>•</div> <div>16%</div> </div> </div>
1	B	330	<div> <div>4%</div> <div> <div></div> <div>63%</div> <div>18%</div> <div>18%</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4386 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 pyrophosphate synthase 3, chloroplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	278	Total	C	N	O	S	0	0	0
			2091	1319	363	394	15			
1	B	270	Total	C	N	O	S	0	0	0
			2036	1288	354	379	15			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	MET	-	expression tag	UNP Q9LUD9
A	308	LEU	-	expression tag	UNP Q9LUD9
A	309	GLU	-	expression tag	UNP Q9LUD9
A	310	HIS	-	expression tag	UNP Q9LUD9
A	311	HIS	-	expression tag	UNP Q9LUD9
A	312	HIS	-	expression tag	UNP Q9LUD9
A	313	HIS	-	expression tag	UNP Q9LUD9
A	314	HIS	-	expression tag	UNP Q9LUD9
A	315	HIS	-	expression tag	UNP Q9LUD9
B	-14	MET	-	expression tag	UNP Q9LUD9
B	308	LEU	-	expression tag	UNP Q9LUD9
B	309	GLU	-	expression tag	UNP Q9LUD9
B	310	HIS	-	expression tag	UNP Q9LUD9
B	311	HIS	-	expression tag	UNP Q9LUD9
B	312	HIS	-	expression tag	UNP Q9LUD9
B	313	HIS	-	expression tag	UNP Q9LUD9
B	314	HIS	-	expression tag	UNP Q9LUD9
B	315	HIS	-	expression tag	UNP Q9LUD9

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	126	Total	O	0	0
			126	126		

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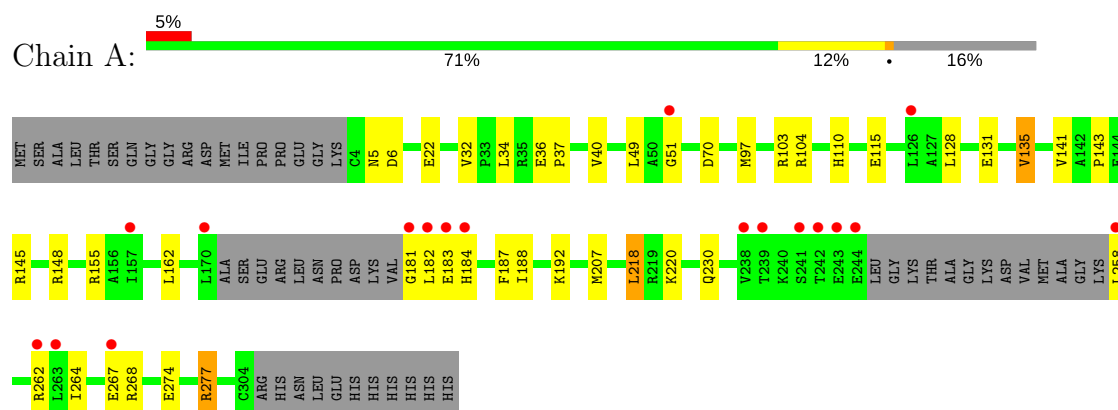
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	133	Total 133	O 133	0	0

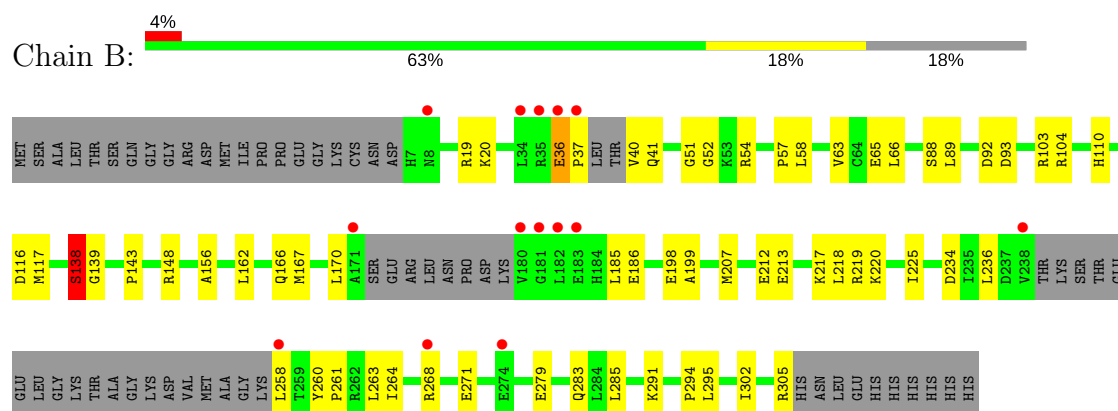
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 pyrophosphate synthase 3, chloroplastic



- Molecule 1: Geranylgeranyl pyrophosphate synthase 3, chloroplastic



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.25Å 77.09Å 114.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.52 – 2.30 36.52 – 2.29	Depositor EDS
% Data completeness (in resolution range)	89.2 (36.52-2.30) 88.7 (36.52-2.29)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	21.19 (at 2.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.207 , 0.234 0.208 , 0.233	Depositor DCC
$R_{free}$ test set	1392 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.4	Xtriage
Anisotropy	0.151	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 46.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.019 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4386	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% 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

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	0.51	0/2117	0.65	2/2863 (0.1%)
1	B	0.49	0/2060	0.69	3/2782 (0.1%)
All	All	0.50	0/4177	0.67	5/5645 (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	B	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	36	GLU	C-N-CD	-9.91	98.79	120.60
1	A	218	LEU	CA-CB-CG	-7.69	97.60	115.30
1	B	36	GLU	C-N-CA	6.79	150.53	122.00
1	A	97	MET	N-CA-C	6.47	128.47	111.00
1	B	138	SER	N-CA-C	5.13	124.85	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	138	SER	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	2091	0	2133	52	0
1	B	2036	0	2094	61	0
2	A	126	0	0	42	0
2	B	133	0	0	29	0
All	All	4386	0	4227	111	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 13.

All (111) 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:6:ASP:HA	2:A:404:HOH:O	1.14	1.32
1:A:104:ARG:NH2	2:A:401:HOH:O	1.80	1.11
1:A:192:LYS:HA	2:A:417:HOH:O	1.51	1.08
1:B:19:ARG:NE	2:B:401:HOH:O	1.83	1.08
1:A:183:GLU:N	2:A:402:HOH:O	1.87	1.06
1:A:258:LEU:HA	2:A:414:HOH:O	1.55	1.05
1:B:258:LEU:N	2:B:402:HOH:O	1.88	1.05
1:A:162:LEU:HA	2:A:417:HOH:O	1.56	1.05
1:B:186:GLU:HG3	2:B:403:HOH:O	1.55	1.04
1:B:170:LEU:HA	2:B:409:HOH:O	1.57	1.04
1:A:104:ARG:NH2	2:A:403:HOH:O	1.88	1.04
2:A:470:HOH:O	1:B:167:MET:SD	2.16	1.03
1:B:19:ARG:NH2	2:B:401:HOH:O	1.87	1.01
1:B:40:VAL:HB	2:B:421:HOH:O	1.60	1.01
1:B:51:GLY:C	2:B:404:HOH:O	1.99	1.00
1:A:182:LEU:C	2:A:402:HOH:O	2.01	0.98
1:B:52:GLY:N	2:B:404:HOH:O	1.97	0.97
1:A:162:LEU:HD12	2:A:417:HOH:O	1.65	0.95
1:B:186:GLU:CG	2:B:403:HOH:O	2.10	0.94
1:A:145:ARG:HG2	2:A:423:HOH:O	1.66	0.94
1:A:5:ASN:C	2:A:404:HOH:O	2.06	0.94
1:A:262:ARG:NH2	2:A:405:HOH:O	1.93	0.93
1:A:5:ASN:O	2:A:404:HOH:O	1.89	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:VAL:HG13	1:B:167:MET:HE3	1.56	0.87
1:A:104:ARG:NH1	2:A:406:HOH:O	1.98	0.87
1:A:188:ILE:HG13	2:A:413:HOH:O	1.73	0.86
1:A:104:ARG:NH2	2:A:406:HOH:O	2.09	0.85
1:A:262:ARG:NE	2:A:405:HOH:O	2.00	0.85
1:A:181:GLY:C	2:A:402:HOH:O	2.17	0.83
1:B:41:GLN:HG2	2:B:421:HOH:O	1.79	0.82
1:A:258:LEU:CA	2:A:414:HOH:O	2.20	0.80
1:B:19:ARG:CZ	2:B:401:HOH:O	2.12	0.80
1:A:181:GLY:O	2:A:402:HOH:O	2.01	0.78
1:B:291:LYS:O	2:B:405:HOH:O	2.03	0.75
1:A:258:LEU:N	2:A:414:HOH:O	2.20	0.74
1:A:162:LEU:CD1	2:A:417:HOH:O	2.28	0.73
1:A:262:ARG:NH2	2:A:415:HOH:O	2.21	0.73
1:B:66:LEU:HD23	1:B:218:LEU:HD21	1.71	0.72
1:B:213:GLU:OE2	1:B:217:LYS:HE3	1.89	0.72
1:B:148:ARG:NH1	1:B:212:GLU:OE2	2.23	0.71
1:A:141:VAL:O	2:A:409:HOH:O	2.08	0.70
1:B:198:GLU:OE2	2:B:406:HOH:O	2.09	0.70
1:B:51:GLY:CA	2:B:404:HOH:O	2.36	0.69
1:A:22:GLU:OE1	2:A:410:HOH:O	2.10	0.69
1:A:49:LEU:O	2:A:412:HOH:O	2.11	0.69
1:B:65:GLU:OE1	2:B:407:HOH:O	2.11	0.68
1:B:36:GLU:OE1	2:B:408:HOH:O	2.12	0.68
1:A:230:GLN:OE1	2:A:411:HOH:O	2.11	0.67
1:A:104:ARG:CZ	2:A:406:HOH:O	2.32	0.67
1:A:184:HIS:N	2:A:402:HOH:O	2.00	0.66
1:A:143:PRO:HB2	1:B:143:PRO:HB2	1.79	0.64
1:A:184:HIS:O	2:A:413:HOH:O	2.16	0.59
1:A:274:GLU:OE2	1:A:277:ARG:CZ	2.51	0.59
1:A:155:ARG:NH2	2:A:407:HOH:O	2.06	0.58
1:A:182:LEU:N	2:A:402:HOH:O	2.38	0.56
1:B:207:MET:HG3	2:B:454:HOH:O	2.06	0.55
1:B:93:ASP:OD2	1:B:103:ARG:NH1	2.39	0.55
1:B:110:HIS:HD2	2:B:496:HOH:O	1.90	0.55
1:B:36:GLU:HG2	1:B:37:PRO:HA	1.89	0.55
1:A:110:HIS:HE1	2:A:427:HOH:O	1.91	0.54
1:B:170:LEU:CA	2:B:409:HOH:O	2.34	0.54
1:A:187:PHE:HB3	2:A:413:HOH:O	2.09	0.53
1:B:20:LYS:HB3	1:B:58:LEU:HD22	1.91	0.53
1:B:54:ARG:O	1:B:58:LEU:HG	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:36:GLU:HG2	1:B:37:PRO:CA	2.39	0.52
1:B:225:ILE:HG23	1:B:302:ILE:HD13	1.93	0.51
1:A:115:GLU:HG3	2:A:472:HOH:O	2.13	0.49
1:B:294:PRO:HD2	2:B:405:HOH:O	2.12	0.49
1:B:185:LEU:HD13	1:B:258:LEU:HG	1.94	0.49
1:B:217:LYS:HG3	1:B:283:GLN:HE21	1.79	0.48
1:A:145:ARG:NH1	2:A:423:HOH:O	2.47	0.48
1:B:63:VAL:HG22	1:B:218:LEU:HD23	1.96	0.47
1:B:88:SER:HB3	1:B:162:LEU:HD21	1.95	0.47
1:A:262:ARG:CZ	2:A:405:HOH:O	2.25	0.47
1:A:267:GLU:HG3	1:A:268:ARG:H	1.80	0.47
1:B:54:ARG:CZ	2:B:404:HOH:O	2.63	0.47
1:B:260:TYR:OH	2:B:403:HOH:O	1.89	0.47
1:B:104:ARG:NE	2:B:426:HOH:O	2.48	0.46
1:A:182:LEU:HD21	1:A:264:ILE:HG21	1.98	0.46
1:A:220:LYS:NZ	2:A:408:HOH:O	2.08	0.46
1:B:156:ALA:HB2	1:B:199:ALA:HB2	1.98	0.45
1:B:258:LEU:HD12	1:B:263:LEU:HD11	1.98	0.45
1:B:138:SER:O	2:B:411:HOH:O	2.21	0.45
1:A:182:LEU:CA	2:A:402:HOH:O	2.55	0.45
1:A:207:MET:HG3	2:A:432:HOH:O	2.17	0.45
1:B:41:GLN:NE2	2:B:421:HOH:O	2.39	0.45
1:B:36:GLU:HG2	1:B:37:PRO:O	2.17	0.44
1:A:6:ASP:CA	2:A:404:HOH:O	1.91	0.44
1:B:236:LEU:HD11	1:B:305:ARG:HG2	2.00	0.44
1:B:92:ASP:OD1	1:B:166:GLN:NE2	2.51	0.43
1:B:217:LYS:HG3	1:B:283:GLN:NE2	2.34	0.43
1:A:32:VAL:HG22	1:A:128:LEU:HD21	2.00	0.43
1:B:234:ASP:HB3	1:B:261:PRO:HD3	2.00	0.43
1:B:264:ILE:HB	1:B:268:ARG:HD3	2.00	0.43
1:A:36:GLU:HG3	1:A:37:PRO:HA	2.00	0.43
1:A:51:GLY:O	1:A:104:ARG:NE	2.52	0.43
1:B:89:LEU:HB3	1:B:103:ARG:NH1	2.34	0.43
1:B:138:SER:N	1:B:139:GLY:HA3	2.34	0.42
1:B:285:LEU:HD23	1:B:285:LEU:HA	1.75	0.42
1:B:40:VAL:N	2:B:430:HOH:O	2.52	0.42
1:B:54:ARG:HB3	1:B:57:PRO:HG2	2.03	0.41
1:B:170:LEU:O	2:B:409:HOH:O	2.19	0.41
1:B:225:ILE:HA	1:B:225:ILE:HD13	1.71	0.41
1:A:103:ARG:HG3	1:A:104:ARG:HG2	2.01	0.41
1:A:148:ARG:HH11	1:A:148:ARG:HG2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:219:ARG:NH1	2:B:410:HOH:O	2.19	0.41
1:B:186:GLU:HG2	2:B:403:HOH:O	2.03	0.41
1:B:220:LYS:HE2	1:B:279:GLU:OE2	2.21	0.41
1:A:131:GLU:O	1:A:135:VAL:HB	2.21	0.40
1:B:116:ASP:OD1	1:B:117:MET:N	2.54	0.40
1:B:295:LEU:HA	1:B:295:LEU:HD23	1.87	0.40

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	272/330 (82%)	265 (97%)	6 (2%)	1 (0%)	38	47
1	B	262/330 (79%)	258 (98%)	4 (2%)	0	100	100
All	All	534/660 (81%)	523 (98%)	10 (2%)	1 (0%)	51	63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	LEU

### 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	220/265 (83%)	216 (98%)	4 (2%)	64	79
1	B	213/265 (80%)	212 (100%)	1 (0%)	91	96
All	All	433/530 (82%)	428 (99%)	5 (1%)	75	87

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

Mol	Chain	Res	Type
1	A	70	ASP
1	A	135	VAL
1	A	218	LEU
1	A	277	ARG
1	B	271	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	230	GLN
1	B	110	HIS
1	B	230	GLN
1	B	283	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 ⓘ

There are no ligands in this entry.

## 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, 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	278/330 (84%)	0.22	18 (6%) 20 26	17, 28, 57, 86	0
1	B	270/330 (81%)	0.11	14 (5%) 28 35	16, 29, 51, 82	0
All	All	548/660 (83%)	0.16	32 (5%) 24 30	16, 29, 55, 86	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	242	THR	9.6
1	B	180	VAL	9.3
1	A	241	SER	8.2
1	A	244	GLU	7.2
1	A	182	LEU	6.2
1	B	238	VAL	5.0
1	B	35	ARG	4.9
1	B	37	PRO	4.8
1	A	183	GLU	4.6
1	A	184	HIS	4.6
1	B	34	LEU	4.3
1	A	243	GLU	3.9
1	A	263	LEU	3.8
1	A	181	GLY	3.5
1	A	170	LEU	3.4
1	A	262	ARG	3.2
1	A	51	GLY	2.9
1	A	258	LEU	2.9
1	B	36	GLU	2.9
1	A	239	THR	2.8
1	A	238	VAL	2.7
1	A	126	LEU	2.5
1	A	267	GLU	2.3
1	B	181	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	274	GLU	2.3
1	B	8	ASN	2.3
1	B	183	GLU	2.2
1	B	182	LEU	2.1
1	B	268	ARG	2.1
1	B	258	LEU	2.1
1	B	171	ALA	2.0
1	A	157	ILE	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 carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.