



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:56 PM GMT

PDB ID : 3VJE  
Title : Crystal structure of the Y248A mutant of C(30) carotenoid dehydrosqualene synthase from Staphylococcus aureus in complex with zaragozic acid A  
Authors : Liu, C.I.; Jeng, W.Y.; Chang, W.J.; Wang, A.H.J.  
Deposited on : 2011-10-14  
Resolution : 2.12 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  
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

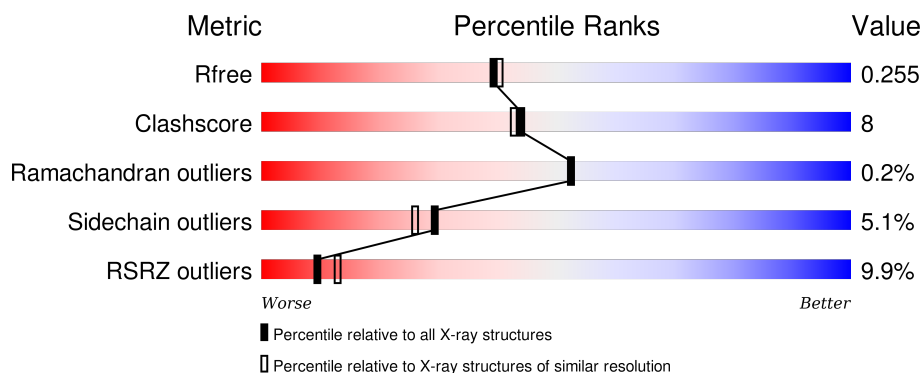
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.12 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	4587 (2.14-2.10)
Clashscore	102246	5132 (2.14-2.10)
Ramachandran outliers	100387	5080 (2.14-2.10)
Sidechain outliers	100360	5081 (2.14-2.10)
RSRZ outliers	91569	4597 (2.14-2.10)

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  $\geq 3$ , 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	293	<div> <div>9%</div> <div>82%</div> <div>14%</div> <div>• •</div> </div>
1	B	293	<div> <div>11%</div> <div>81%</div> <div>15%</div> <div>• •</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5035 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.

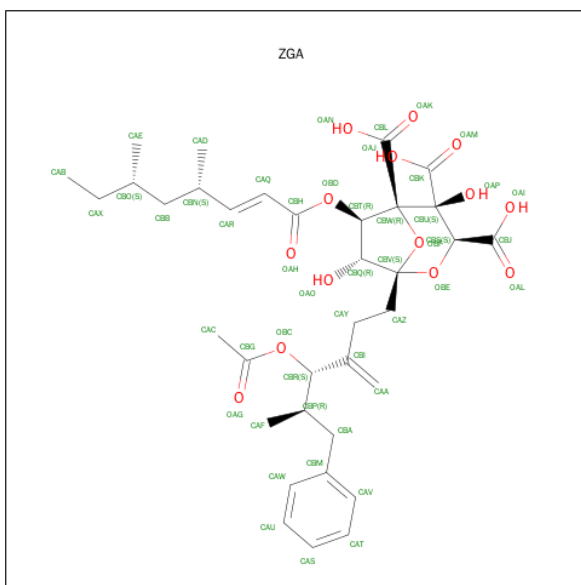
- Molecule 1 is a protein called Dehydrosqualene synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	284	Total	C	N	O	S	0	0	0
			2385	1530	400	443	12			
1	B	284	Total	C	N	O	S	0	0	0
			2385	1530	400	443	12			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	ALA	-	EXPRESSION TAG	UNP A9JQL9
A	-4	ALA	-	EXPRESSION TAG	UNP A9JQL9
A	-3	ALA	-	EXPRESSION TAG	UNP A9JQL9
A	-2	ALA	-	EXPRESSION TAG	UNP A9JQL9
A	-1	ALA	-	EXPRESSION TAG	UNP A9JQL9
A	0	ALA	-	EXPRESSION TAG	UNP A9JQL9
A	248	ALA	TYR	ENGINEERED MUTATION	UNP A9JQL9
B	-5	ALA	-	EXPRESSION TAG	UNP A9JQL9
B	-4	ALA	-	EXPRESSION TAG	UNP A9JQL9
B	-3	ALA	-	EXPRESSION TAG	UNP A9JQL9
B	-2	ALA	-	EXPRESSION TAG	UNP A9JQL9
B	-1	ALA	-	EXPRESSION TAG	UNP A9JQL9
B	0	ALA	-	EXPRESSION TAG	UNP A9JQL9
B	248	ALA	TYR	ENGINEERED MUTATION	UNP A9JQL9

- Molecule 2 is ZARAGOZIC ACID A (three-letter code: ZGA) (formula: C<sub>35</sub>H<sub>46</sub>O<sub>14</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 49	C 35	O 14	0	0
2	B	1	Total 49	C 35	O 14	0	0

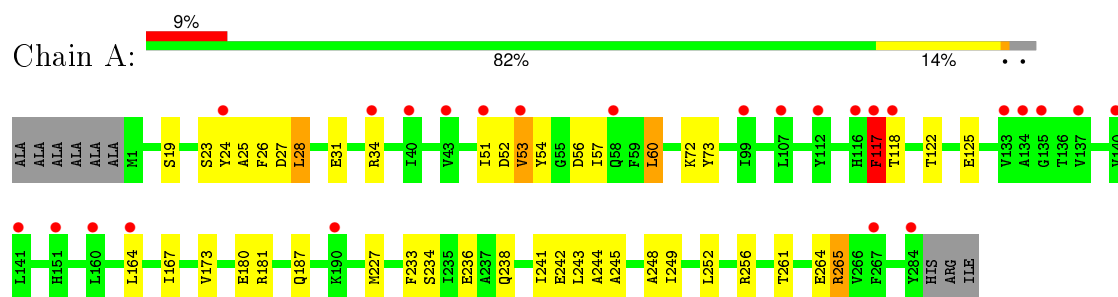
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	84	Total O 84 84	0	0
3	B	83	Total O 83 83	0	0

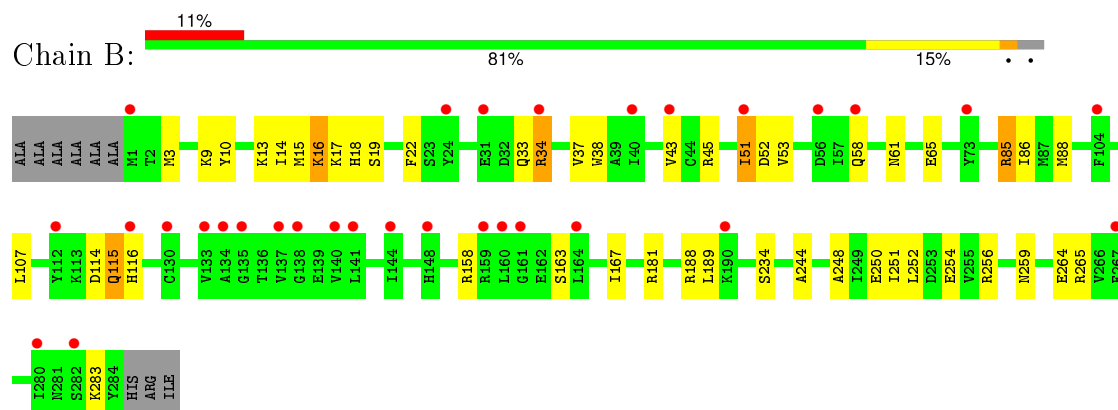
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ( $\text{RSRZ} > 2$ ). 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: Dehydrosqualene synthase



#### • Molecule 1: Dehydrosqualene synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.18Å 80.18Å 185.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.30 – 2.12 28.23 – 2.12	Depositor EDS
% Data completeness (in resolution range)	99.2 (28.30-2.12) 99.2 (28.23-2.12)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.67 (at 2.12Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.205 , 0.254 0.203 , 0.255	Depositor DCC
$R_{free}$ test set	1996 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	41.1	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 48.1	EDS
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 39812 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5035	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 66.59 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 5.9020e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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, 0.375 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: ZGA

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	0.39	0/2440	0.66	0/3290
1	B	0.36	0/2440	0.63	1/3290 (0.0%)
All	All	0.38	0/4880	0.64	1/6580 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	158	ARG	NE-CZ-NH2	-5.03	117.78	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	2385	0	2317	37	0
1	B	2385	0	2317	39	0
2	A	49	0	43	8	0
2	B	49	0	43	16	0
3	A	84	0	0	0	0
3	B	83	0	0	1	0
All	All	5035	0	4720	77	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 8.

All (77) 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:301:ZGA:HAX	2:B:301:ZGA:CAR	1.78	1.13
1:A:53:VAL:HG11	1:B:17:LYS:HE2	1.39	1.04
2:B:301:ZGA:HAR	2:B:301:ZGA:HAX	1.05	1.03
2:B:301:ZGA:HAR	2:B:301:ZGA:CAX	1.94	0.93
2:B:301:ZGA:CAX	2:B:301:ZGA:CAR	2.48	0.90
1:A:227:MET:CE	1:A:242:GLU:HG3	2.04	0.87
1:A:227:MET:HE3	1:A:242:GLU:HG3	1.58	0.85
1:A:180:GLU:OE2	1:B:9:LYS:HE2	1.79	0.81
1:A:244:ALA:HB1	2:A:301:ZGA:HAEA	1.63	0.80
1:A:53:VAL:CG1	1:B:17:LYS:HE2	2.13	0.76
1:A:180:GLU:OE2	1:B:9:LYS:CE	2.42	0.67
1:A:227:MET:HE1	1:A:242:GLU:HG3	1.77	0.65
1:B:251:ILE:HD12	2:B:301:ZGA:HBBA	1.81	0.63
1:A:25:ALA:CB	2:A:301:ZGA:HAB	2.28	0.63
1:B:51:ILE:H	1:B:51:ILE:HD13	1.63	0.62
1:B:51:ILE:CD1	1:B:51:ILE:H	2.12	0.62
1:A:53:VAL:CG2	1:A:54:TYR:N	2.63	0.62
1:A:245:ALA:O	1:A:249:ILE:HG12	2.01	0.61
1:A:72:LYS:HD3	1:A:73:TYR:CE2	2.36	0.61
1:A:53:VAL:HG23	1:A:54:TYR:N	2.17	0.60
1:B:43:VAL:HG12	1:B:86:ILE:HG22	1.84	0.60
1:B:43:VAL:HG12	1:B:86:ILE:CG2	2.32	0.59
1:A:244:ALA:CB	2:A:301:ZGA:HAEA	2.33	0.59
1:B:51:ILE:HD13	1:B:52:ASP:H	1.66	0.59
1:B:167:ILE:HG13	1:B:248:ALA:HB1	1.86	0.57
1:A:51:ILE:HD13	1:A:60:LEU:HD12	1.88	0.56
1:A:122:THR:HG23	1:A:125:GLU:H	1.70	0.55
1:A:117:PHE:CG	1:A:181:ARG:HD3	2.41	0.55
1:A:31:GLU:HG3	1:A:34:ARG:HH21	1.73	0.52
1:B:115:GLN:O	1:B:116:HIS:CG	2.64	0.51
1:B:244:ALA:O	2:B:301:ZGA:CAE	2.58	0.51
1:B:10:TYR:CE1	1:B:14:ILE:HD11	2.46	0.50
1:A:261:THR:HG21	1:A:264:GLU:HG2	1.93	0.50
1:B:115:GLN:HG2	1:B:116:HIS:CD2	2.46	0.50
1:B:107:LEU:HD11	2:B:301:ZGA:HACB	1.94	0.50
1:B:33:GLN:O	1:B:37:VAL:HG23	2.10	0.50
1:B:14:ILE:HD13	1:B:86:ILE:HD11	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:ILE:HG13	1:A:248:ALA:HB1	1.95	0.49
1:A:164:LEU:HD22	2:A:301:ZGA:HAE	1.95	0.49
1:B:18:HIS:HB3	1:B:45:ARG:CZ	2.44	0.48
1:B:252:LEU:O	1:B:256:ARG:HG3	2.13	0.47
1:A:53:VAL:CG2	1:A:54:TYR:H	2.26	0.47
1:A:244:ALA:HB2	2:A:301:ZGA:HABB	1.98	0.46
1:A:27:ASP:HA	1:A:34:ARG:CD	2.46	0.46
1:B:15:MET:O	1:B:19:SER:HB3	2.15	0.46
1:B:114:ASP:HB3	1:B:181:ARG:NH2	2.31	0.46
1:B:88:MET:HG3	3:B:447:HOH:O	2.16	0.46
1:B:45:ARG:NH2	2:B:301:ZGA:OAP	2.47	0.45
1:A:25:ALA:HB2	2:A:301:ZGA:HAB	1.97	0.45
1:A:117:PHE:CB	1:A:181:ARG:HD3	2.47	0.45
1:A:117:PHE:HB3	1:A:181:ARG:CZ	2.46	0.45
1:B:85:ARG:HA	1:B:85:ARG:HD2	1.78	0.45
1:B:16:LYS:NZ	1:B:16:LYS:HA	2.32	0.44
1:A:233:PHE:CG	1:A:241:ILE:HD13	2.52	0.44
1:B:22:PHE:CE2	2:B:301:ZGA:HAQ	2.53	0.44
1:A:25:ALA:O	1:A:28:LEU:HB2	2.18	0.43
1:B:107:LEU:HD11	2:B:301:ZGA:CAC	2.48	0.43
1:A:19:SER:HB3	1:A:23:SER:HB2	2.01	0.43
1:A:181:ARG:HA	1:A:181:ARG:HD2	1.80	0.43
1:B:251:ILE:CD1	2:B:301:ZGA:HBBA	2.47	0.43
1:B:163:SER:O	1:B:167:ILE:HG12	2.19	0.43
1:B:61:ASN:O	1:B:65:GLU:HG3	2.19	0.43
1:B:22:PHE:CD2	2:B:301:ZGA:HAQ	2.54	0.42
1:A:234:SER:O	1:A:238:GLN:HG3	2.19	0.42
1:B:34:ARG:HD2	1:B:38:TRP:HZ2	1.84	0.42
1:B:188:ARG:HD3	1:B:188:ARG:HA	1.91	0.42
1:A:265:ARG:NH2	2:A:301:ZGA:OAJ	2.52	0.42
1:A:26:PHE:HE2	2:A:301:ZGA:HAU	1.85	0.41
1:A:252:LEU:O	1:A:256:ARG:HG3	2.20	0.41
1:B:248:ALA:HB2	2:B:301:ZGA:HAE	2.01	0.41
1:A:56:ASP:N	1:A:56:ASP:OD2	2.52	0.41
1:B:250:GLU:O	1:B:254:GLU:HG2	2.21	0.41
2:B:301:ZGA:HAA	2:B:301:ZGA:HAZA	1.89	0.41
1:B:88:MET:HE2	1:B:88:MET:HB2	1.92	0.41
1:B:248:ALA:N	2:B:301:ZGA:HAE	2.36	0.41
1:B:244:ALA:O	2:B:301:ZGA:HAEA	2.21	0.40
1:A:24:TYR:HE2	1:A:243:LEU:HD21	1.86	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	282/293 (96%)	274 (97%)	7 (2%)	1 (0%)	39	36
1	B	282/293 (96%)	275 (98%)	7 (2%)	0	100	100
All	All	564/586 (96%)	549 (97%)	14 (2%)	1 (0%)	52	52

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	117	PHE

### 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	256/259 (99%)	245 (96%)	11 (4%)	35	33
1	B	256/259 (99%)	241 (94%)	15 (6%)	24	20
All	All	512/518 (99%)	486 (95%)	26 (5%)	29	26

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LEU
1	A	52	ASP
1	A	53	VAL
1	A	57	ILE
1	A	60	LEU

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Mol	Chain	Res	Type
1	A	117	PHE
1	A	118	THR
1	A	173	VAL
1	A	187	GLN
1	A	236	GLU
1	A	265	ARG
1	B	3	MET
1	B	13	LYS
1	B	16	LYS
1	B	34	ARG
1	B	51	ILE
1	B	53	VAL
1	B	58	GLN
1	B	85	ARG
1	B	115	GLN
1	B	189	LEU
1	B	234	SER
1	B	259	ASN
1	B	264	GLU
1	B	265	ARG
1	B	283	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	HIS
1	A	62	GLN
1	A	238	GLN
1	B	61	ASN
1	B	95	GLN
1	B	116	HIS
1	B	179	ASN
1	B	187	GLN
1	B	238	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 ⓘ

2 ligands are modelled in this entry.

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	$\# Z  > 2$
2	ZGA	A	301	-	39,51,51	1.23	2 (5%)	40,76,76	1.43	10 (25%)
2	ZGA	B	301	-	39,51,51	1.22	2 (5%)	40,76,76	1.32	5 (12%)

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
2	ZGA	A	301	-	-	0/37/95/95	0/1/3/3
2	ZGA	B	301	-	-	0/37/95/95	0/1/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	ZGA	OBC-CBG	4.40	1.45	1.35
2	A	301	ZGA	OBC-CBG	4.42	1.45	1.35
2	B	301	ZGA	OBD-CBH	5.32	1.46	1.34
2	A	301	ZGA	OBD-CBH	5.37	1.46	1.34

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	B	301	ZGA	OBF-CBV-CBQ	-3.50	100.42	104.05
2	B	301	ZGA	CBM-CBA-CBP	-2.73	110.14	113.52
2	A	301	ZGA	CAZ-CBV-CBQ	-2.49	105.91	114.95
2	A	301	ZGA	CBR-OBC-CBG	-2.29	113.17	116.77
2	A	301	ZGA	OBF-CBV-CBQ	-2.13	101.84	104.05
2	A	301	ZGA	CBT-OBH-CBH	-2.05	113.55	117.88
2	A	301	ZGA	OBH-CBH-OAH	-2.05	120.11	123.30
2	A	301	ZGA	CAD-CBN-CBB	2.38	115.38	111.01
2	B	301	ZGA	OBC-CBR-CBI	2.43	114.12	109.29
2	A	301	ZGA	OBE-CBV-CAZ	2.69	111.93	104.59
2	A	301	ZGA	OBH-CBH-CAQ	2.73	118.19	111.42
2	A	301	ZGA	OBC-CBG-CAC	3.19	117.12	111.10
2	A	301	ZGA	CAF-CBP-CBA	3.24	114.34	110.92
2	B	301	ZGA	CAR-CAQ-CBH	3.29	130.85	122.71
2	B	301	ZGA	OBC-CBG-CAC	3.50	117.70	111.10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	ZGA	8	0
2	B	301	ZGA	16	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 ⓘ

### 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	284/293 (96%)	0.44	25 (8%) 12 17	23, 46, 68, 104	0
1	B	284/293 (96%)	0.42	31 (10%) 7 10	26, 48, 66, 86	0
All	All	568/586 (96%)	0.43	56 (9%) 9 13	23, 47, 67, 104	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	117	PHE	6.1
1	A	267	PHE	5.2
1	B	137	VAL	5.1
1	B	56	ASP	4.7
1	B	141	LEU	4.5
1	A	140	VAL	4.3
1	A	190	LYS	4.1
1	A	137	VAL	4.0
1	A	133	VAL	3.9
1	B	267	PHE	3.8
1	B	133	VAL	3.8
1	A	141	LEU	3.7
1	B	112	TYR	3.7
1	B	134	ALA	3.6
1	B	140	VAL	3.6
1	A	164	LEU	3.5
1	B	164	LEU	3.4
1	A	134	ALA	3.4
1	A	51	ILE	3.2
1	B	51	ILE	3.2
1	A	40	ILE	3.1
1	B	73	TYR	3.1
1	A	151	HIS	3.1
1	A	112	TYR	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	135	GLY	2.9
1	B	280	ILE	2.9
1	A	43	VAL	2.9
1	B	40	ILE	2.8
1	A	116	HIS	2.7
1	B	135	GLY	2.6
1	B	190	LYS	2.5
1	B	58	GLN	2.5
1	A	53	VAL	2.5
1	A	34	ARG	2.5
1	B	104	PHE	2.5
1	B	31	GLU	2.5
1	B	24	TYR	2.4
1	A	107	LEU	2.3
1	B	138	GLY	2.3
1	B	282	SER	2.3
1	A	284	TYR	2.3
1	B	116	HIS	2.3
1	B	160	LEU	2.3
1	A	24	TYR	2.3
1	B	148	HIS	2.2
1	B	161	GLY	2.2
1	A	118	THR	2.2
1	B	144	ILE	2.2
1	B	130	CYS	2.1
1	B	43	VAL	2.1
1	A	160	LEU	2.1
1	B	34	ARG	2.0
1	A	58	GLN	2.0
1	B	1	MET	2.0
1	A	99	ILE	2.0
1	B	159	ARG	2.0

## 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 [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, 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ZGA	B	301	49/49	0.92	0.17	0.05	33,54,59,61	0
2	ZGA	A	301	49/49	0.94	0.14	-0.36	32,51,63,65	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.