



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 6, 2023 – 08:41 pm GMT

PDB ID : 8PKW  
Title : Kelch domain of KEAP1 in complex with a ortho-dimethylbenzene linked cyclic peptide 5 (ortho-WRCDPETaEC).  
Authors : Braun, M.B.; Bischof, L.; Hartmann, M.D.  
Deposited on : 2023-06-27  
Resolution : 1.54 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

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

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

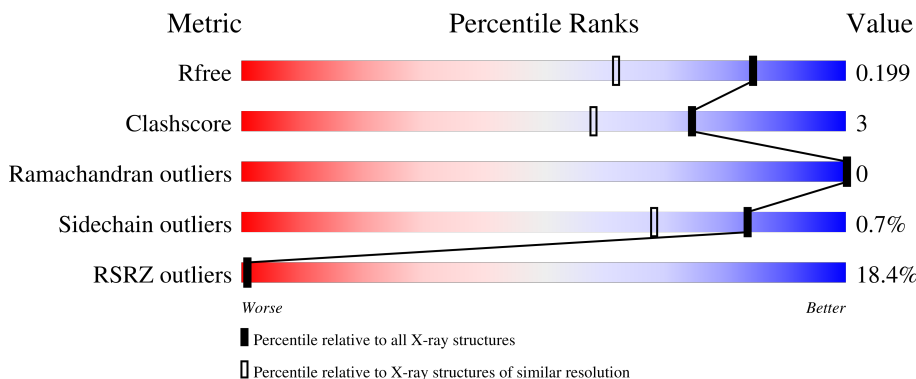
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.54 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	2556 (1.56-1.52)
Clashscore	141614	2634 (1.56-1.52)
Ramachandran outliers	138981	2580 (1.56-1.52)
Sidechain outliers	138945	2577 (1.56-1.52)
RSRZ outliers	127900	2524 (1.56-1.52)

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 of 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	316	
1	B	316	
2	P	12	

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 4957 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 Kelch-like ECH-associated protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	292	Total	C	N	O	S	0	18	0
			2334	1451	420	444	19			
1	B	287	Total	C	N	O	S	0	4	0
			2124	1319	381	408	16			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	309	GLY	-	expression tag	UNP Q14145
A	310	HIS	-	expression tag	UNP Q14145
A	311	MET	-	expression tag	UNP Q14145
A	319	SER	CYS	conflict	UNP Q14145
A	540	ALA	GLU	conflict	UNP Q14145
A	542	ALA	GLU	conflict	UNP Q14145
A	613	SER	CYS	conflict	UNP Q14145
A	622	SER	CYS	conflict	UNP Q14145
A	624	SER	-	expression tag	UNP Q14145
B	309	GLY	-	expression tag	UNP Q14145
B	310	HIS	-	expression tag	UNP Q14145
B	311	MET	-	expression tag	UNP Q14145
B	319	SER	CYS	conflict	UNP Q14145
B	540	ALA	GLU	conflict	UNP Q14145
B	542	ALA	GLU	conflict	UNP Q14145
B	613	SER	CYS	conflict	UNP Q14145
B	622	SER	CYS	conflict	UNP Q14145
B	624	SER	-	expression tag	UNP Q14145

- Molecule 2 is a protein called CP5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	P	12	Total	C	N	O	S	0	1	1
			83	46	15	19	3			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).

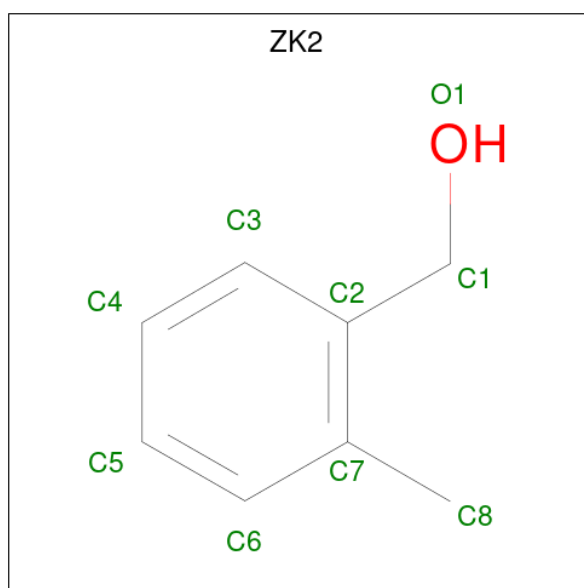


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	2	Total Na 2 2	0	0
7	B	1	Total Na 1 1	0	0

- Molecule 8 is (2-methylphenyl)methanol (three-letter code: ZK2) (formula: C<sub>8</sub>H<sub>10</sub>O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	P	1	Total C 8 8	0	0

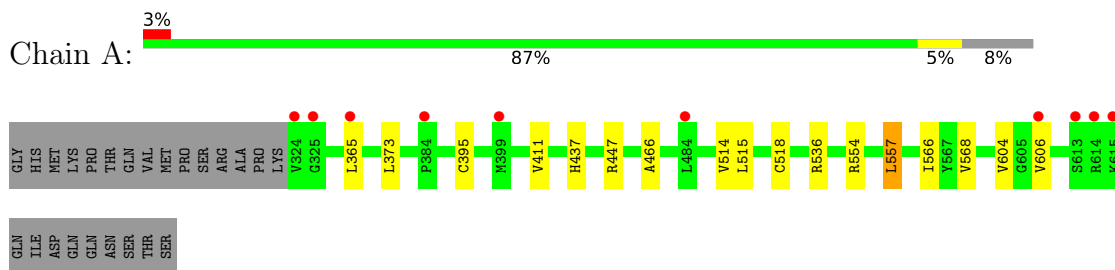
- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	257	Total O 257 257	0	0
9	B	106	Total O 106 106	0	0
9	P	6	Total O 6 6	0	0

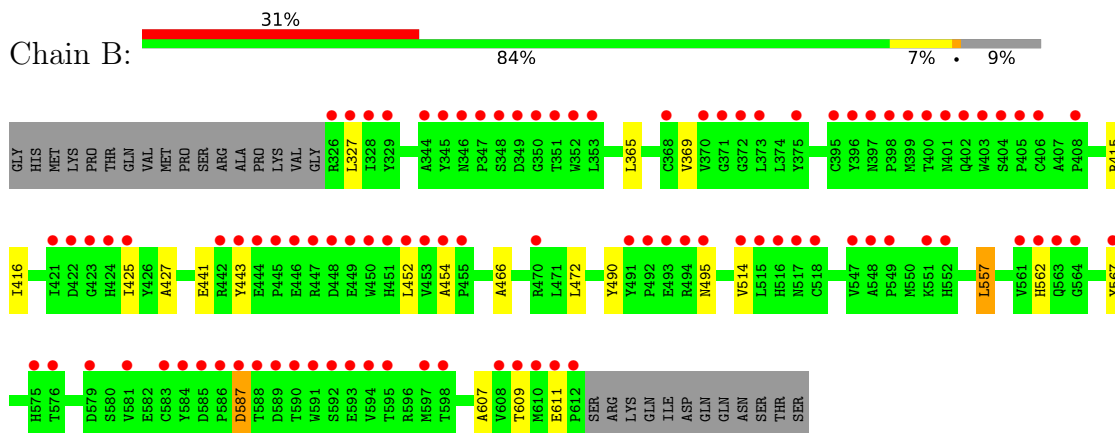
### 3 Residue-property plots [i](#)

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.

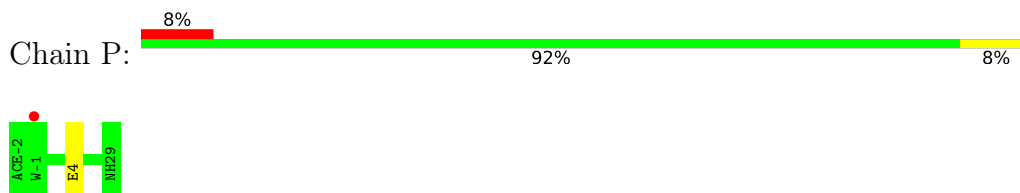
- Molecule 1: Kelch-like ECH-associated protein 1



- Molecule 1: Kelch-like ECH-associated protein 1



- Molecule 2: CP5



## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	162.68Å 68.97Å 77.97Å 90.00° 117.86° 90.00°	Depositor
Resolution (Å)	42.13 – 1.54 42.13 – 1.54	Depositor EDS
% Data completeness (in resolution range)	100.0 (42.13-1.54) 100.0 (42.13-1.54)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.06 (at 1.54Å)	Xtrriage
Refinement program	PHENIX 1.16_3549	Depositor
R, $R_{free}$	0.158 , 0.199 0.158 , 0.199	Depositor DCC
$R_{free}$ test set	2255 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.6	Xtrriage
Anisotropy	0.198	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 59.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.010 for -h-2*1,-k,l	Xtrriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	4957	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.69% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: DAL, NA, SO4, NH2, CL, ACE, ZK2, GOL, EDO

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	0.34	0/2396	0.56	0/3270
1	B	0.30	0/2176	0.52	0/2974
2	P	0.42	0/73	0.50	0/95
All	All	0.32	0/4645	0.54	0/6339

There are no bond length outliers.

There are no bond angle outliers.

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	2334	0	2190	12	0
1	B	2124	0	1916	16	0
2	P	83	0	65	1	0
3	A	10	0	0	0	0
3	B	5	0	0	0	0
4	A	1	0	0	0	0
5	A	8	0	12	0	0
6	A	6	0	8	0	0
6	B	6	0	8	0	0
7	A	2	0	0	0	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	1	0	0	0	0
8	P	8	0	0	0	0
9	A	257	0	0	0	0
9	B	106	0	0	0	0
9	P	6	0	0	0	0
All	All	4957	0	4199	28	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 3.

All (28) 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:B:441:GLU:HB3	1:B:452:LEU:HD23	1.60	0.82
1:A:466:ALA:HB1	1:A:514[A]:VAL:HG23	1.70	0.74
1:B:466:ALA:HB1	1:B:514:VAL:HG23	1.69	0.74
1:A:447:ARG:HG2	1:A:447:ARG:HH11	1.57	0.68
1:B:454:ALA:H	1:B:495:ASN:HD21	1.47	0.62
1:A:466:ALA:HB1	1:A:514[B]:VAL:HG13	1.82	0.60
1:B:425:ILE:HB	1:B:443:TYR:HB3	1.85	0.57
1:A:557:LEU:HD23	1:A:557:LEU:H	1.70	0.56
1:A:518:CYS:HB3	1:A:536:ARG:HG3	1.91	0.53
1:A:515:LEU:HD22	1:A:566:ILE:HG13	1.91	0.51
1:A:447:ARG:HG2	1:A:447:ARG:NH1	2.25	0.50
1:A:554:ARG:HD2	1:A:568[B]:VAL:HG11	1.94	0.49
1:B:365:LEU:H	1:B:365:LEU:HD23	1.80	0.47
1:A:411[B]:VAL:HG11	1:A:437:HIS:CE1	2.51	0.46
1:B:557:LEU:H	1:B:557:LEU:HD23	1.81	0.46
1:B:416:ILE:HD11	1:B:427:ALA:HB1	1.98	0.46
1:A:365:LEU:HD23	1:A:365:LEU:H	1.80	0.45
1:B:472:LEU:HB3	1:B:490:TYR:HB3	1.98	0.45
1:B:369:VAL:HG23	1:B:607:ALA:HB1	2.00	0.43
1:B:415:ARG:NH2	2:P:4:GLU:OE2	2.45	0.42
1:B:562:HIS:HB3	1:B:567:TYR:CE2	2.54	0.41
1:A:604:VAL:HG23	1:A:606[A]:VAL:HG13	2.01	0.41
1:B:327:LEU:CD1	1:B:611:GLU:HA	2.50	0.41
1:A:373:LEU:HB3	1:A:395[A]:CYS:SG	2.60	0.41
1:B:562:HIS:HB3	1:B:567:TYR:HE2	1.86	0.41
1:B:587:ASP:N	1:B:587:ASP:OD2	2.54	0.41
1:B:327:LEU:HD11	1:B:611:GLU:HA	2.03	0.40
1:B:369:VAL:HG21	1:B:609:THR:HB	2.03	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	308/316 (98%)	301 (98%)	7 (2%)	0	100	100
1	B	289/316 (92%)	280 (97%)	9 (3%)	0	100	100
2	P	10/12 (83%)	10 (100%)	0	0	100	100
All	All	607/644 (94%)	591 (97%)	16 (3%)	0	100	100

There are no Ramachandran outliers to report.

#### 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	245/258 (95%)	244 (100%)	1 (0%)	91	82
1	B	207/258 (80%)	205 (99%)	2 (1%)	76	55
2	P	9/9 (100%)	9 (100%)	0	100	100
All	All	461/525 (88%)	458 (99%)	3 (1%)	84	68

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	557	LEU
1	B	557	LEU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	587	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	469	ASN
1	B	495	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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
8	ZK2	P	101	2	8,8,9	0.23	0	10,10,11	0.24	0
3	SO4	B	701	-	4,4,4	0.14	0	6,6,6	0.26	0
6	GOL	A	705	-	5,5,5	0.84	0	5,5,5	1.11	0
6	GOL	B	703	-	5,5,5	0.74	0	5,5,5	1.04	0
3	SO4	A	702	-	4,4,4	0.14	0	6,6,6	0.05	0
3	SO4	A	701	-	4,4,4	0.14	0	6,6,6	0.17	0
5	EDO	A	706	-	3,3,3	0.48	0	2,2,2	0.29	0
5	EDO	A	704	-	3,3,3	0.46	0	2,2,2	0.38	0

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
8	ZK2	P	101	2	-	-	0/1/1/1
6	GOL	B	703	-	-	0/4/4/4	-
6	GOL	A	705	-	-	0/4/4/4	-
5	EDO	A	706	-	-	0/1/1/1	-
5	EDO	A	704	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

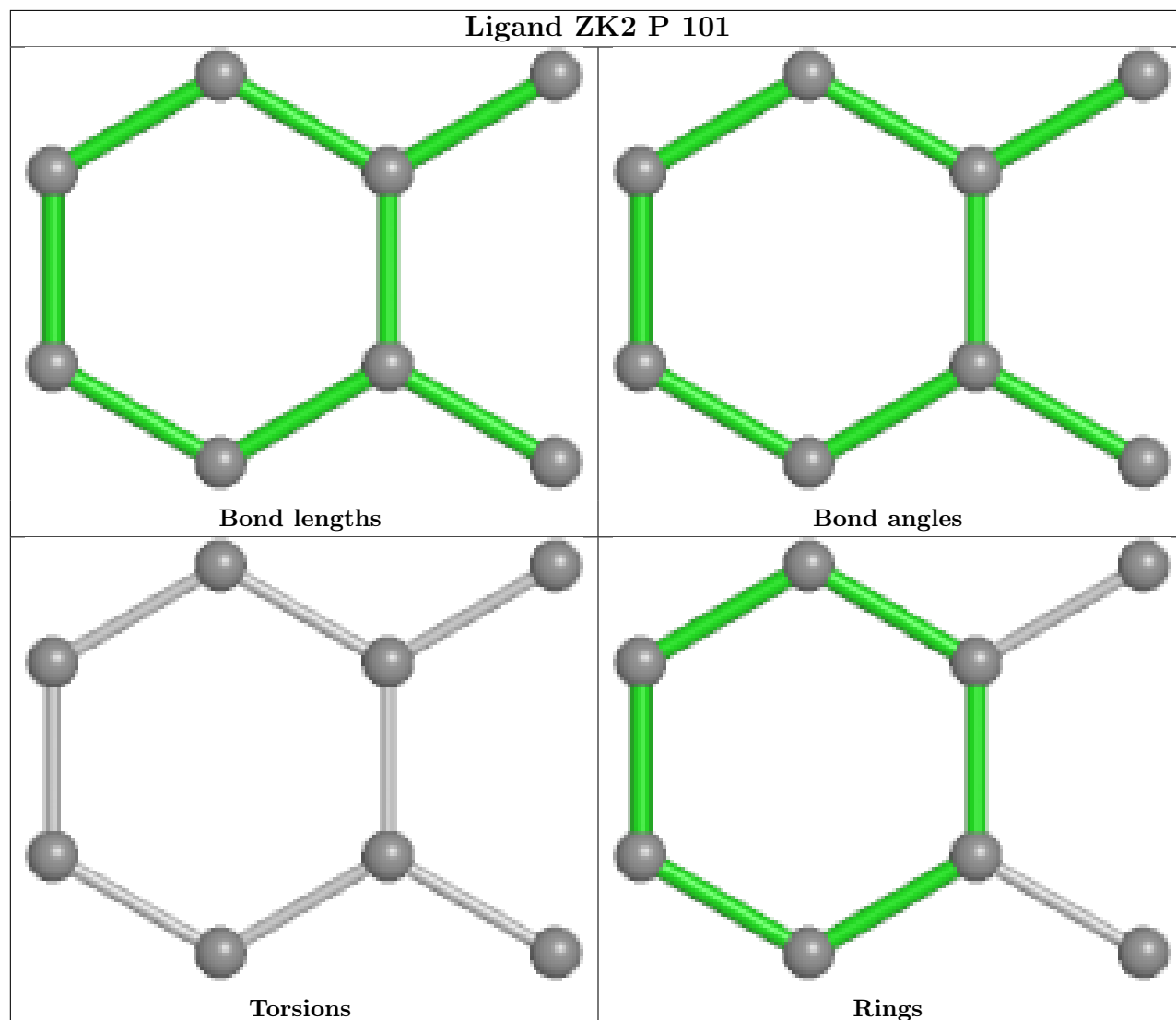
Mol	Chain	Res	Type	Atoms
5	A	704	EDO	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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 [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, 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	292/316 (92%)	0.38	10 (3%) 45 51	24, 32, 58, 107	0
1	B	287/316 (90%)	1.73	97 (33%) 0 0	27, 57, 91, 115	0
2	P	9/12 (75%)	0.54	1 (11%) 5 5	36, 44, 69, 80	0
All	All	588/644 (91%)	1.04	108 (18%) 1 1	24, 40, 86, 115	0

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	595	THR	8.9
1	B	351	THR	8.6
1	B	352	TRP	8.5
1	B	346	ASN	8.5
1	B	610	MET	8.1
1	A	324	VAL	7.5
1	A	615	LYS	7.2
1	B	452	LEU	7.0
1	B	591	TRP	6.5
1	B	446	GLU	6.3
1	B	345	TYR	6.3
1	B	399	MET	6.1
1	B	592	SER	6.0
1	B	327	LEU	6.0
1	B	349	ASP	6.0
1	B	612	PRO	5.6
1	B	608	VAL	5.6
1	B	370	VAL	5.5
1	B	562	HIS	5.3
1	B	353	LEU	5.2
1	B	373	LEU	5.2
1	B	590	THR	5.2
1	B	423	GLY	5.1

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	400	THR	5.1
1	B	350	GLY	5.0
1	B	328	ILE	5.0
1	B	552	HIS	5.0
1	A	613	SER	4.9
1	B	451	HIS	4.9
1	B	516	HIS	4.8
1	B	444	GLU	4.8
1	B	348	SER	4.7
1	B	347	PRO	4.7
1	B	583	CYS	4.6
1	B	448	ASP	4.6
1	B	584	TYR	4.6
1	B	576	THR	4.6
1	B	408	PRO	4.6
1	B	587	ASP	4.4
1	B	375	TYR	4.4
1	B	609	THR	4.4
1	B	405	PRO	4.3
1	B	567	TYR	4.2
1	B	425	ILE	4.2
1	B	371	GLY	4.2
1	B	611	GLU	4.1
1	B	397	ASN	4.1
1	B	401	ASN	4.1
1	B	561	VAL	4.0
1	B	575	HIS	4.0
1	B	494	ARG	4.0
1	B	445	PRO	4.0
1	B	515	LEU	4.0
1	B	447	ARG	3.9
1	B	450	TRP	3.9
1	B	443	TYR	3.9
1	B	518	CYS	3.8
1	B	449	GLU	3.7
1	B	594	VAL	3.7
1	B	395	CYS	3.7
1	B	442	ARG	3.7
1	A	614	ARG	3.6
1	B	581	VAL	3.6
1	B	406	CYS	3.6
1	B	491	TYR	3.6

*Continued on next page...*



*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	579	ASP	3.5
1	B	593	GLU	3.5
1	B	422	ASP	3.4
1	B	563	GLN	3.4
1	B	372	GLY	3.4
1	B	403	TRP	3.3
1	B	453	VAL	3.3
1	B	402	GLN	3.2
1	A	399[A]	MET	3.2
1	B	398	PRO	3.2
1	B	455	PRO	3.2
1	B	326	ARG	3.1
1	B	344	ALA	3.1
1	B	495	ASN	3.0
1	B	517	ASN	3.0
1	B	329	TYR	3.0
1	B	396	TYR	3.0
1	B	470	ARG	3.0
1	B	421	ILE	2.9
1	B	586	PRO	2.9
1	B	551	LYS	2.9
1	A	484	LEU	2.8
1	B	588	THR	2.7
1	B	493	GLU	2.7
1	B	368	CYS	2.7
1	B	585	ASP	2.6
1	A	325	GLY	2.6
1	B	564	GLY	2.6
1	B	589	ASP	2.6
2	P	-1	TRP	2.6
1	A	606[A]	VAL	2.5
1	B	549	PRO	2.5
1	B	598	THR	2.5
1	B	597	MET	2.4
1	B	492	PRO	2.3
1	A	384	PRO	2.3
1	B	404	SER	2.3
1	B	424	HIS	2.3
1	B	454	ALA	2.2
1	B	548	ALA	2.2
1	A	365	LEU	2.2
1	B	514	VAL	2.1

*Continued on next page...*

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	547	VAL	2.1

## 6.2 Non-standard residues in protein, DNA, RNA chains [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
2	DAL	P	6	5/6	0.94	0.09	37,38,39,43	0

## 6.3 Carbohydrates [i](#)

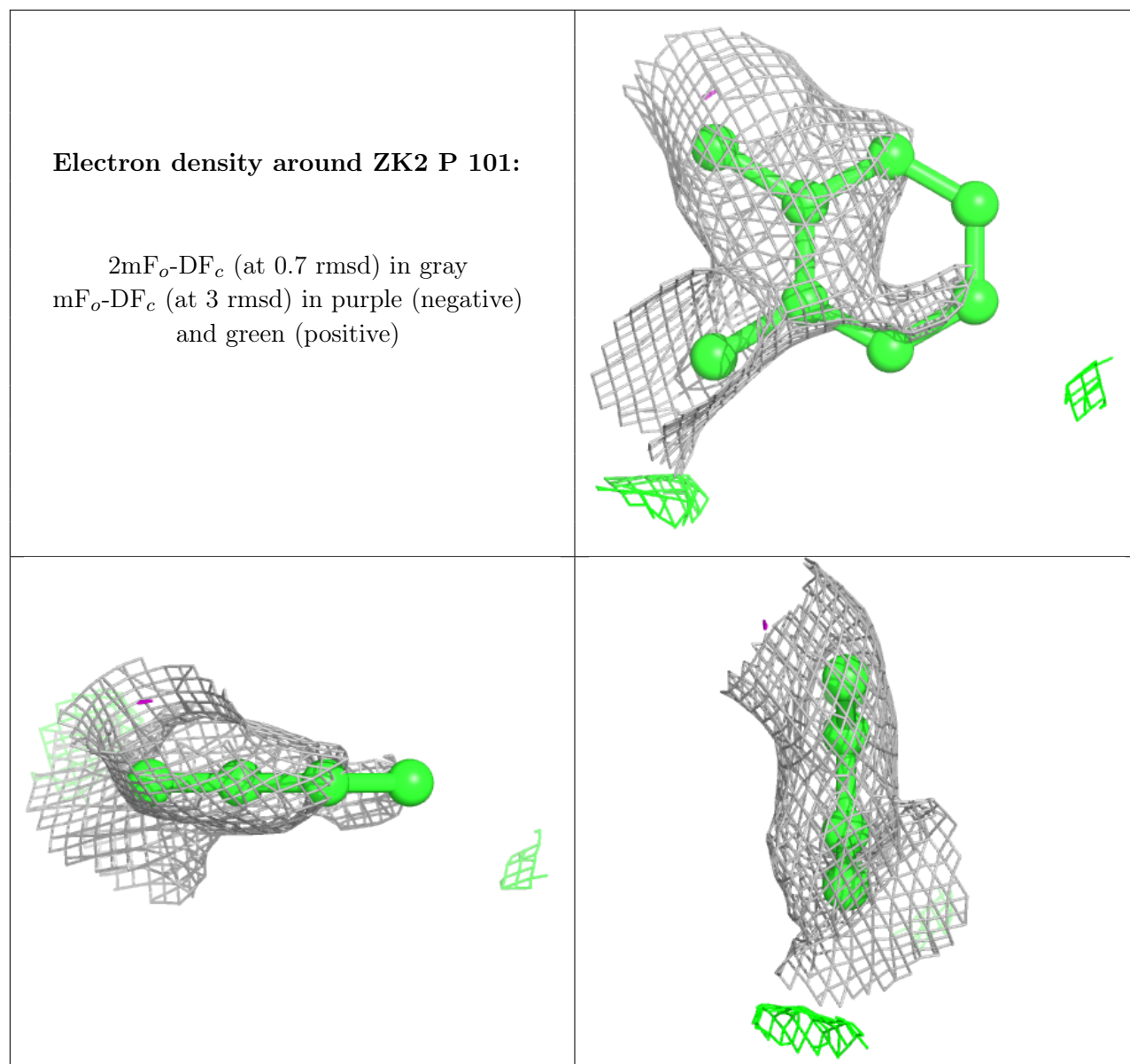
There are no monosaccharides in this entry.

## 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
5	EDO	A	706	4/4	0.75	0.17	68,73,73,74	0
8	ZK2	P	101	8/9	0.83	0.19	63,72,78,78	0
3	SO4	A	702	5/5	0.85	0.32	132,132,133,134	0
6	GOL	B	703	6/6	0.89	0.27	38,40,41,41	6
4	CL	A	703	1/1	0.89	0.10	80,80,80,80	0
7	NA	A	708	1/1	0.91	0.12	67,67,67,67	0
6	GOL	A	705	6/6	0.91	0.16	35,54,61,66	0
5	EDO	A	704	4/4	0.96	0.10	41,53,59,64	0
7	NA	A	707	1/1	0.96	0.28	63,63,63,63	0
3	SO4	A	701	5/5	0.98	0.12	33,34,40,42	5
7	NA	B	702	1/1	0.99	0.17	46,46,46,46	0
3	SO4	B	701	5/5	0.99	0.14	39,40,45,49	5

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.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.