



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 7, 2022 – 07:51 PM EST

PDB ID : 7KB3  
Title : The structure of a sensor domain of a histidine kinase (VxrA) from *Vibrio cholerae* O1 biovar eltor str. N16961, 2nd form  
Authors : Tan, K.; Wu, R.; Jedrzejczak, R.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases (CSGID)  
Deposited on : 2020-10-01  
Resolution : 2.25 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	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.2
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)	:	2.31.2

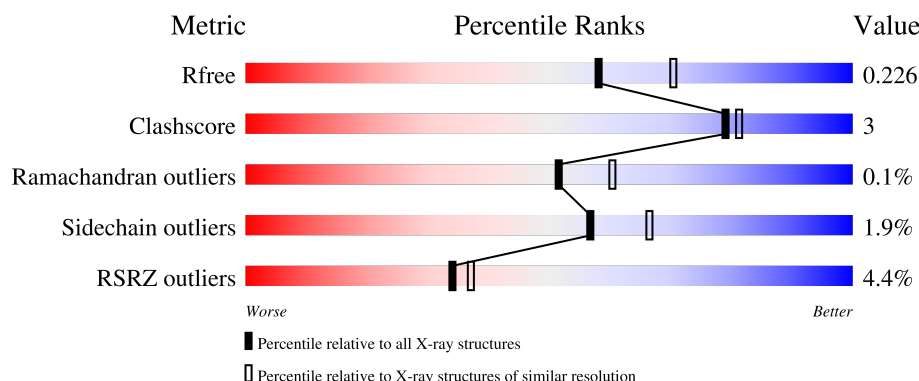
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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	222	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="width: 94%; height: 10px; background-color: green;"></div> <div style="width: 5%; height: 10px; background-color: yellow;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div>
1	B	222	<div> <div style="width: 12%; height: 10px; background-color: red;"></div> <div style="width: 87%; height: 10px; background-color: green;"></div> <div style="width: 9%; height: 10px; background-color: yellow;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div>
1	C	222	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="width: 89%; height: 10px; background-color: green;"></div> <div style="width: 8%; height: 10px; background-color: yellow;"></div> <div style="width: 3%; height: 10px; background-color: grey;"></div> </div>
1	D	222	<div> <div style="width: 3%; height: 10px; background-color: red;"></div> <div style="width: 95%; height: 10px; background-color: green;"></div> <div style="width: 5%; height: 10px; background-color: yellow;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GOL	D	302	-	-	-	X
3	ACT	B	302	-	-	X	-
3	ACT	D	305	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7135 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 Sensor histidine kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	2	0
			1748	1116	288	336	8			
1	B	216	Total	C	N	O	S	0	0	0
			1701	1085	280	328	8			
1	C	217	Total	C	N	O	S	0	0	0
			1710	1095	281	326	8			
1	D	220	Total	C	N	O	S	0	2	0
			1740	1112	284	336	8			

There are 12 discrepancies between the modelled and reference sequences:

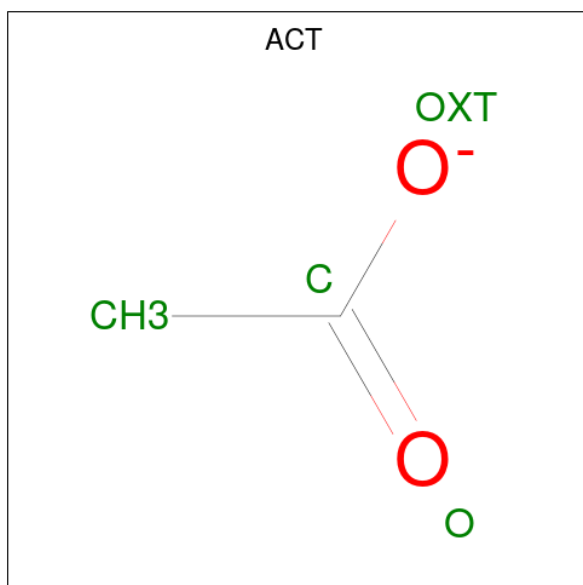
Chain	Residue	Modelled	Actual	Comment	Reference
A	35	SER	-	expression tag	UNP Q9KM24
A	36	ASN	-	expression tag	UNP Q9KM24
A	37	ALA	-	expression tag	UNP Q9KM24
B	35	SER	-	expression tag	UNP Q9KM24
B	36	ASN	-	expression tag	UNP Q9KM24
B	37	ALA	-	expression tag	UNP Q9KM24
C	35	SER	-	expression tag	UNP Q9KM24
C	36	ASN	-	expression tag	UNP Q9KM24
C	37	ALA	-	expression tag	UNP Q9KM24
D	35	SER	-	expression tag	UNP Q9KM24
D	36	ASN	-	expression tag	UNP Q9KM24
D	37	ALA	-	expression tag	UNP Q9KM24

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0

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

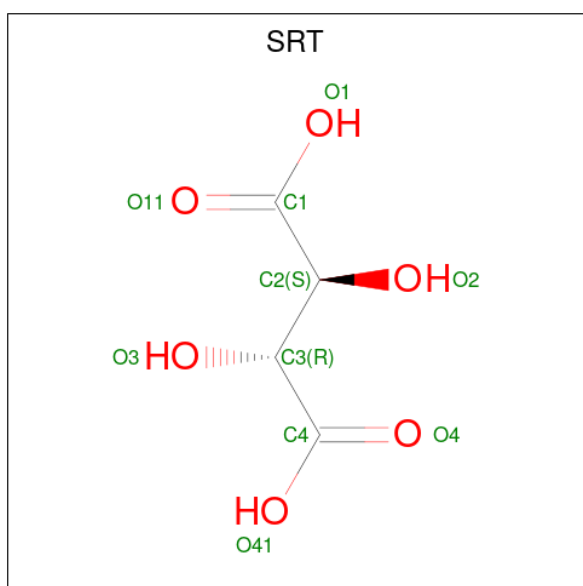
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	7	Total Cl 7 7	0	0
4	B	4	Total Cl 4 4	0	0
4	C	3	Total Cl 3 3	0	0
4	D	7	Total Cl 8 8	0	1

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			7	4	3		
5	D	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is S,R MESO-TARTARIC ACID (three-letter code: SRT) (formula:  $C_4H_6O_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	O	0	0
			10	4	6		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	40	Total 40	O 40	0	0
7	B	11	Total 11	O 11	0	0
7	C	46	Total 46	O 46	0	0
7	D	31	Total 33	O 33	0	2



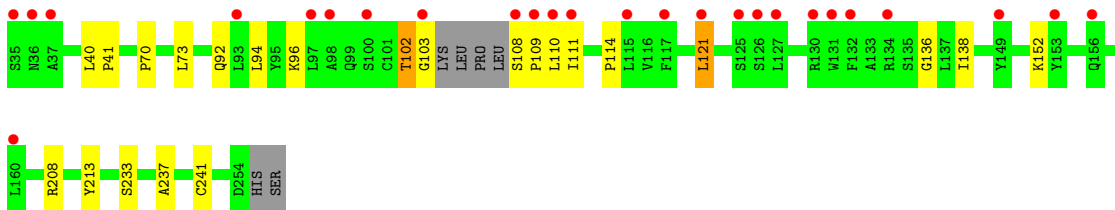
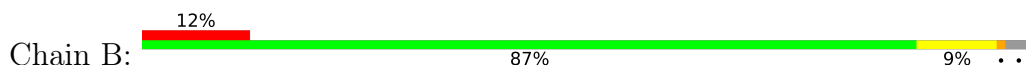
### 3 Residue-property plots [i](#)

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.

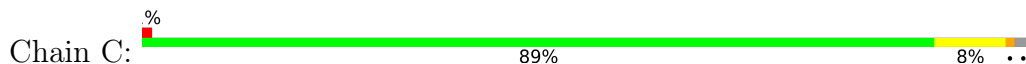
- Molecule 1: Sensor histidine kinase



- Molecule 1: Sensor histidine kinase



- Molecule 1: Sensor histidine kinase



- Molecule 1: Sensor histidine kinase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	112.08Å 116.68Å 120.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.07 – 2.25 41.07 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.6 (41.07-2.25) 99.6 (41.07-2.25)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.72 (at 2.24Å)	Xtriage
Refinement program	PHENIX (1.18.2_3874: ???)	Depositor
R, $R_{free}$	0.205 , 0.227 0.205 , 0.226	Depositor DCC
$R_{free}$ test set	3721 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	55.5	Xtriage
Anisotropy	0.364	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 41.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.012 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7135	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% 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: GOL, ACT, PEG, CL, SRT

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	0.23	0/1793	0.39	0/2440
1	B	0.25	0/1744	0.40	0/2372
1	C	0.24	0/1755	0.40	0/2390
1	D	0.24	0/1785	0.40	0/2432
All	All	0.24	0/7077	0.40	0/9634

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	1748	0	1688	6	0
1	B	1701	0	1634	17	0
1	C	1710	0	1652	14	0
1	D	1740	0	1661	6	0
2	A	6	0	8	0	0
2	D	18	0	24	1	0
3	A	8	0	5	0	0
3	B	8	0	6	3	0
3	C	12	0	9	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	8	0	6	0	0
4	A	7	0	0	0	0
4	B	4	0	0	0	0
4	C	3	0	0	0	0
4	D	8	0	0	0	0
5	B	7	0	10	0	0
5	D	7	0	10	0	0
6	C	10	0	4	1	0
7	A	40	0	0	0	0
7	B	11	0	0	0	0
7	C	46	0	0	0	0
7	D	33	0	0	0	0
All	All	7135	0	6717	38	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 (38) 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:108:SER:HB3	1:B:109:PRO:CD	1.92	0.99
1:B:108:SER:HB3	1:B:109:PRO:HD2	1.45	0.96
1:B:108:SER:CB	1:B:109:PRO:HD2	2.01	0.90
1:B:108:SER:CB	1:B:109:PRO:CD	2.54	0.83
1:B:108:SER:HB3	1:B:109:PRO:HD3	1.80	0.63
1:C:40:LEU:HD23	1:D:243:ILE:HG13	1.82	0.61
1:B:70:PRO:HD2	1:B:73:LEU:HD12	1.81	0.60
1:D:170:PRO:HA	2:D:303:GOL:H32	1.86	0.58
1:D:94:LEU:HD22	1:D:111:ILE:HD11	1.90	0.54
1:B:108:SER:HB2	1:B:109:PRO:HD2	1.88	0.54
1:B:237:ALA:HB3	1:D:186:GLU:HG2	1.93	0.51
1:B:94:LEU:HD11	1:B:111:ILE:HG21	1.91	0.50
1:D:70:PRO:HD2	1:D:73:LEU:HD12	1.95	0.49
1:C:208:ARG:HH22	6:C:304:SRT:C4	2.25	0.48
1:C:251:ASP:OD1	1:C:252:VAL:N	2.46	0.48
1:C:70:PRO:HD2	1:C:73:LEU:HD12	1.95	0.48
1:B:121:LEU:O	1:B:152:LYS:NZ	2.45	0.47
3:B:302:ACT:H3	1:C:239:ASN:HD22	1.80	0.47
1:C:239:ASN:O	1:C:240:THR:HG22	2.16	0.46
1:B:111:ILE:HG23	1:B:114:PRO:HG2	1.97	0.46
1:A:239:ASN:N	1:A:239:ASN:OD1	2.48	0.46

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:208:ARG:HB2	1:C:213:TYR:CE1	2.51	0.46
1:C:180:HIS:O	1:C:184:MET:HG3	2.16	0.45
1:B:233:SER:HB3	1:D:84:SER:HB3	1.98	0.45
1:A:208:ARG:HB2	1:A:213:TYR:CE1	2.53	0.44
1:B:92:GLN:O	1:B:96:LYS:HG2	2.18	0.44
1:C:106:PRO:HB2	1:C:111:ILE:HD11	2.01	0.43
3:B:302:ACT:H3	1:C:239:ASN:ND2	2.33	0.43
1:A:80:LEU:HD13	1:C:234:LEU:HD12	2.01	0.42
1:A:180:HIS:O	1:A:184:MET:HG3	2.20	0.41
1:B:208:ARG:HB2	1:B:213:TYR:CE1	2.56	0.41
1:B:102:THR:HG23	1:B:103:GLY:H	1.85	0.41
1:B:136:GLY:O	1:B:138:ILE:N	2.48	0.41
1:A:234:LEU:HD12	1:C:80:LEU:HD13	2.03	0.41
1:A:190:ASN:HB2	3:B:302:ACT:H2	2.04	0.40
1:C:123:LYS:HE2	1:C:123:LYS:HB3	1.86	0.40
1:B:40:LEU:HB3	1:B:41:PRO:HD3	2.03	0.40
1:C:147:PHE:O	1:C:151:GLU:HG3	2.21	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	219/222 (99%)	216 (99%)	3 (1%)	0	100	100
1	B	212/222 (96%)	203 (96%)	9 (4%)	0	100	100
1	C	215/222 (97%)	208 (97%)	6 (3%)	1 (0%)	29	29
1	D	220/222 (99%)	217 (99%)	3 (1%)	0	100	100
All	All	866/888 (98%)	844 (98%)	21 (2%)	1 (0%)	51	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	239	ASN

### 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	191/192 (100%)	187 (98%)	4 (2%)	53	62
1	B	185/192 (96%)	181 (98%)	4 (2%)	52	61
1	C	186/192 (97%)	182 (98%)	4 (2%)	52	61
1	D	187/192 (97%)	185 (99%)	2 (1%)	73	82
All	All	749/768 (98%)	735 (98%)	14 (2%)	57	66

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	ASP
1	A	85	GLU
1	A	239	ASN
1	A	241	CYS
1	B	102	THR
1	B	110	LEU
1	B	121	LEU
1	B	241	CYS
1	C	38	ASP
1	C	72	ARG
1	C	240	THR
1	C	252	VAL
1	D	58	THR
1	D	235	LEU

Sometimes 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 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 38 ligands modelled in this entry, 22 are monoatomic - leaving 16 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	$\# Z  > 2$
5	PEG	D	306	-	6,6,6	0.12	0	5,5,5	0.07	0
3	ACT	B	301	-	3,3,3	1.32	0	3,3,3	1.53	0
6	SRT	C	304	-	9,9,9	1.01	0	12,12,12	1.03	0
2	GOL	D	302	-	5,5,5	0.90	0	5,5,5	1.01	0
2	GOL	D	303	-	5,5,5	0.89	0	5,5,5	1.03	0
3	ACT	B	302	-	3,3,3	1.32	0	3,3,3	1.49	0
3	ACT	C	301	-	3,3,3	1.28	0	3,3,3	1.37	0
3	ACT	C	302	-	3,3,3	1.31	0	3,3,3	1.52	0
3	ACT	D	305	-	3,3,3	1.37	0	3,3,3	1.51	0
5	PEG	B	303	-	6,6,6	0.12	0	5,5,5	0.07	0
2	GOL	A	301	-	5,5,5	0.91	0	5,5,5	1.01	0
3	ACT	D	304	-	3,3,3	1.30	0	3,3,3	1.52	0
3	ACT	C	303	-	3,3,3	1.33	0	3,3,3	1.38	0
2	GOL	D	301	-	5,5,5	0.90	0	5,5,5	1.01	0
3	ACT	A	302	-	3,3,3	1.31	0	3,3,3	1.52	0
3	ACT	A	303	1	3,3,3	1.28	0	3,3,3	1.42	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
5	PEG	D	306	-	-	0/4/4/4	-
6	SRT	C	304	-	-	6/12/12/12	-
2	GOL	D	302	-	-	2/4/4/4	-
2	GOL	D	303	-	-	4/4/4/4	-
5	PEG	B	303	-	-	0/4/4/4	-
2	GOL	A	301	-	-	0/4/4/4	-
2	GOL	D	301	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	302	GOL	C1-C2-C3-O3
2	D	302	GOL	O2-C2-C3-O3
2	D	303	GOL	O1-C1-C2-C3
6	C	304	SRT	O2-C2-C3-C4
6	C	304	SRT	C1-C2-C3-C4
6	C	304	SRT	O3-C3-C4-O4
6	C	304	SRT	O3-C3-C4-O41
2	D	303	GOL	C1-C2-C3-O3
2	D	303	GOL	O2-C2-C3-O3
6	C	304	SRT	O2-C2-C3-O3
2	D	303	GOL	O1-C1-C2-O2
6	C	304	SRT	C1-C2-C3-O3

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	304	SRT	1	0
2	D	303	GOL	1	0
3	B	302	ACT	3	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	219/222 (98%)	0.07	3 (1%) 75 77	46, 61, 94, 142	0
1	B	216/222 (97%)	0.67	26 (12%) 4 3	46, 85, 140, 167	0
1	C	217/222 (97%)	0.02	2 (0%) 84 85	43, 59, 102, 146	0
1	D	220/222 (99%)	0.10	7 (3%) 47 50	42, 65, 103, 137	0
All	All	872/888 (98%)	0.22	38 (4%) 34 37	42, 65, 123, 167	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	36	ASN	6.5
1	B	37	ALA	6.2
1	B	108	SER	5.6
1	B	109	PRO	5.2
1	B	110	LEU	5.0
1	A	37	ALA	4.9
1	B	160	LEU	4.8
1	B	127	LEU	4.6
1	B	149	TYR	4.4
1	B	36	ASN	3.8
1	D	237	ALA	3.7
1	D	35	SER	3.7
1	B	35	SER	3.7
1	D	106	PRO	3.5
1	B	98	ALA	3.5
1	B	117	PHE	3.4
1	B	125	SER	3.3
1	C	240	THR	3.1
1	B	134	ARG	3.1
1	B	93	LEU	3.0
1	B	126	SER	2.9

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	115	LEU	2.8
1	B	121	LEU	2.8
1	B	103	GLY	2.7
1	B	153	TYR	2.7
1	D	238	ASP	2.6
1	B	156	GLN	2.6
1	B	100	SER	2.5
1	A	238	ASP	2.4
1	B	97	LEU	2.4
1	B	130	ARG	2.3
1	B	111	ILE	2.2
1	D	240	THR	2.2
1	D	242	PHE	2.2
1	B	132	PHE	2.1
1	B	131	TRP	2.1
1	C	242	PHE	2.0
1	D	235	LEU	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 monosaccharides 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. 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	GOL	A	301	6/6	0.40	0.24	85,96,104,108	0
3	ACT	D	305	4/4	0.49	0.46	64,64,75,78	0
5	PEG	B	303	7/7	0.57	0.20	89,90,93,94	0
2	GOL	D	303	6/6	0.62	0.30	63,69,78,79	0
6	SRT	C	304	10/10	0.67	0.28	66,81,83,86	10
4	CL	A	306	1/1	0.74	0.09	89,89,89,89	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	ACT	A	302	4/4	0.76	0.35	74,80,83,86	0
4	CL	D	311	1/1	0.76	0.19	111,111,111,111	0
2	GOL	D	302	6/6	0.77	0.45	77,83,89,94	0
3	ACT	A	303	4/4	0.78	0.38	65,70,73,73	0
5	PEG	D	306	7/7	0.79	0.39	82,84,90,91	0
4	CL	C	305	1/1	0.80	0.14	104,104,104,104	0
3	ACT	B	302	4/4	0.82	0.27	65,69,71,73	0
4	CL	D	309	1/1	0.82	0.24	67,67,67,67	1
3	ACT	C	301	4/4	0.82	0.21	81,82,91,92	0
4	CL	B	306	1/1	0.83	0.27	92,92,92,92	0
3	ACT	C	303	4/4	0.83	0.20	62,68,70,75	0
4	CL	D	312	1/1	0.83	0.08	100,100,100,100	0
3	ACT	B	301	4/4	0.85	0.15	74,79,82,85	0
4	CL	C	307	1/1	0.85	0.14	91,91,91,91	0
4	CL	D	308	1/1	0.85	0.16	98,98,98,98	0
3	ACT	D	304	4/4	0.86	0.18	84,93,97,97	0
3	ACT	C	302	4/4	0.88	0.13	76,84,85,92	0
4	CL	A	307	1/1	0.88	0.12	93,93,93,93	0
4	CL	D	307	1/1	0.90	0.10	102,102,102,102	0
4	CL	A	310	1/1	0.91	0.06	68,68,68,68	1
4	CL	D	313[A]	1/1	0.91	0.25	46,46,46,46	1
4	CL	D	313[B]	1/1	0.91	0.25	52,52,52,52	1
4	CL	A	308	1/1	0.92	0.13	77,77,77,77	1
4	CL	C	306	1/1	0.93	0.15	68,68,68,68	0
4	CL	B	307	1/1	0.93	0.09	56,56,56,56	1
4	CL	D	310	1/1	0.94	0.16	94,94,94,94	0
2	GOL	D	301	6/6	0.94	0.16	62,67,71,74	0
4	CL	A	305	1/1	0.96	0.16	57,57,57,57	0
4	CL	B	304	1/1	0.96	0.15	52,52,52,52	1
4	CL	A	309	1/1	0.97	0.06	67,67,67,67	1
4	CL	A	304	1/1	0.98	0.14	58,58,58,58	0
4	CL	B	305	1/1	0.99	0.17	54,54,54,54	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.