



# Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 05:40 am BST

PDB ID : 5GK1  
Title : Crystal structure of the ketosynthase SttD complexed with substrate  
Authors : Mori, T.; Saito, Y.; Morita, H.; Abe, I.  
Deposited on : 2016-07-03  
Resolution : 1.83 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 : 2.11  
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) : 2.11

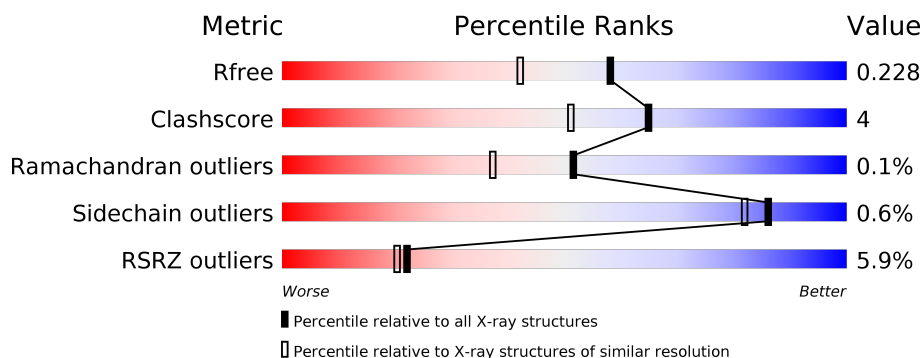
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.83 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	4003 (1.86-1.82)
Clashscore	141614	4233 (1.86-1.82)
Ramachandran outliers	138981	4185 (1.86-1.82)
Sidechain outliers	138945	4186 (1.86-1.82)
RSRZ outliers	127900	3957 (1.86-1.82)

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	402	<div> <div>0%</div> <div>88%</div> <div>6%</div> <div>6%</div> </div>
1	B	402	<div> <div>2%</div> <div>90%</div> <div>5%</div> <div>6%</div> </div>
1	C	402	<div> <div>8%</div> <div>80%</div> <div>14%</div> <div>6%</div> </div>
1	D	402	<div> <div>11%</div> <div>79%</div> <div>15%</div> <div>6%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12960 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 Ketosynthase StlD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	379	Total	C	N	O	S	0	0	0
			2964	1867	509	570	18			
1	B	379	Total	C	N	O	S	0	0	0
			2964	1867	509	570	18			
1	C	379	Total	C	N	O	S	0	0	0
			2964	1867	509	570	18			
1	D	379	Total	C	N	O	S	0	0	0
			2964	1867	509	570	18			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP Q7N4Z6
A	-18	GLY	-	expression tag	UNP Q7N4Z6
A	-17	SER	-	expression tag	UNP Q7N4Z6
A	-16	SER	-	expression tag	UNP Q7N4Z6
A	-15	HIS	-	expression tag	UNP Q7N4Z6
A	-14	HIS	-	expression tag	UNP Q7N4Z6
A	-13	HIS	-	expression tag	UNP Q7N4Z6
A	-12	HIS	-	expression tag	UNP Q7N4Z6
A	-11	HIS	-	expression tag	UNP Q7N4Z6
A	-10	HIS	-	expression tag	UNP Q7N4Z6
A	-9	SER	-	expression tag	UNP Q7N4Z6
A	-8	SER	-	expression tag	UNP Q7N4Z6
A	-7	GLY	-	expression tag	UNP Q7N4Z6
A	-6	LEU	-	expression tag	UNP Q7N4Z6
A	-5	VAL	-	expression tag	UNP Q7N4Z6
A	-4	PRO	-	expression tag	UNP Q7N4Z6
A	-3	ARG	-	expression tag	UNP Q7N4Z6
A	-2	GLY	-	expression tag	UNP Q7N4Z6
A	-1	SER	-	expression tag	UNP Q7N4Z6
A	0	HIS	-	expression tag	UNP Q7N4Z6
B	-19	MET	-	expression tag	UNP Q7N4Z6

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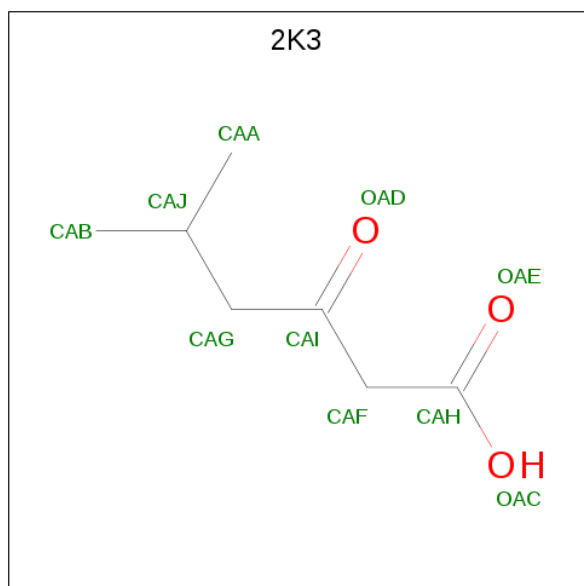
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP Q7N4Z6
B	-17	SER	-	expression tag	UNP Q7N4Z6
B	-16	SER	-	expression tag	UNP Q7N4Z6
B	-15	HIS	-	expression tag	UNP Q7N4Z6
B	-14	HIS	-	expression tag	UNP Q7N4Z6
B	-13	HIS	-	expression tag	UNP Q7N4Z6
B	-12	HIS	-	expression tag	UNP Q7N4Z6
B	-11	HIS	-	expression tag	UNP Q7N4Z6
B	-10	HIS	-	expression tag	UNP Q7N4Z6
B	-9	SER	-	expression tag	UNP Q7N4Z6
B	-8	SER	-	expression tag	UNP Q7N4Z6
B	-7	GLY	-	expression tag	UNP Q7N4Z6
B	-6	LEU	-	expression tag	UNP Q7N4Z6
B	-5	VAL	-	expression tag	UNP Q7N4Z6
B	-4	PRO	-	expression tag	UNP Q7N4Z6
B	-3	ARG	-	expression tag	UNP Q7N4Z6
B	-2	GLY	-	expression tag	UNP Q7N4Z6
B	-1	SER	-	expression tag	UNP Q7N4Z6
B	0	HIS	-	expression tag	UNP Q7N4Z6
C	-19	MET	-	expression tag	UNP Q7N4Z6
C	-18	GLY	-	expression tag	UNP Q7N4Z6
C	-17	SER	-	expression tag	UNP Q7N4Z6
C	-16	SER	-	expression tag	UNP Q7N4Z6
C	-15	HIS	-	expression tag	UNP Q7N4Z6
C	-14	HIS	-	expression tag	UNP Q7N4Z6
C	-13	HIS	-	expression tag	UNP Q7N4Z6
C	-12	HIS	-	expression tag	UNP Q7N4Z6
C	-11	HIS	-	expression tag	UNP Q7N4Z6
C	-10	HIS	-	expression tag	UNP Q7N4Z6
C	-9	SER	-	expression tag	UNP Q7N4Z6
C	-8	SER	-	expression tag	UNP Q7N4Z6
C	-7	GLY	-	expression tag	UNP Q7N4Z6
C	-6	LEU	-	expression tag	UNP Q7N4Z6
C	-5	VAL	-	expression tag	UNP Q7N4Z6
C	-4	PRO	-	expression tag	UNP Q7N4Z6
C	-3	ARG	-	expression tag	UNP Q7N4Z6
C	-2	GLY	-	expression tag	UNP Q7N4Z6
C	-1	SER	-	expression tag	UNP Q7N4Z6
C	0	HIS	-	expression tag	UNP Q7N4Z6
D	-19	MET	-	expression tag	UNP Q7N4Z6
D	-18	GLY	-	expression tag	UNP Q7N4Z6
D	-17	SER	-	expression tag	UNP Q7N4Z6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP Q7N4Z6
D	-15	HIS	-	expression tag	UNP Q7N4Z6
D	-14	HIS	-	expression tag	UNP Q7N4Z6
D	-13	HIS	-	expression tag	UNP Q7N4Z6
D	-12	HIS	-	expression tag	UNP Q7N4Z6
D	-11	HIS	-	expression tag	UNP Q7N4Z6
D	-10	HIS	-	expression tag	UNP Q7N4Z6
D	-9	SER	-	expression tag	UNP Q7N4Z6
D	-8	SER	-	expression tag	UNP Q7N4Z6
D	-7	GLY	-	expression tag	UNP Q7N4Z6
D	-6	LEU	-	expression tag	UNP Q7N4Z6
D	-5	VAL	-	expression tag	UNP Q7N4Z6
D	-4	PRO	-	expression tag	UNP Q7N4Z6
D	-3	ARG	-	expression tag	UNP Q7N4Z6
D	-2	GLY	-	expression tag	UNP Q7N4Z6
D	-1	SER	-	expression tag	UNP Q7N4Z6
D	0	HIS	-	expression tag	UNP Q7N4Z6

- Molecule 2 is 3-OXO-5-METHYLHEXANOIC ACID (three-letter code: 2K3) (formula:  $C_7H_{12}O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			9	7	2		
2	C	1	Total	C	O	0	0
			9	7	2		

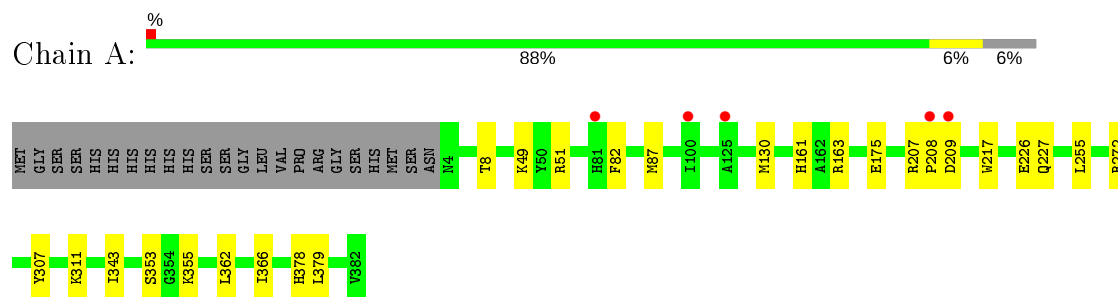
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	356	Total 356	O 356	0	0
3	B	325	Total 325	O 325	0	0
3	C	182	Total 182	O 182	0	0
3	D	223	Total 223	O 223	0	0

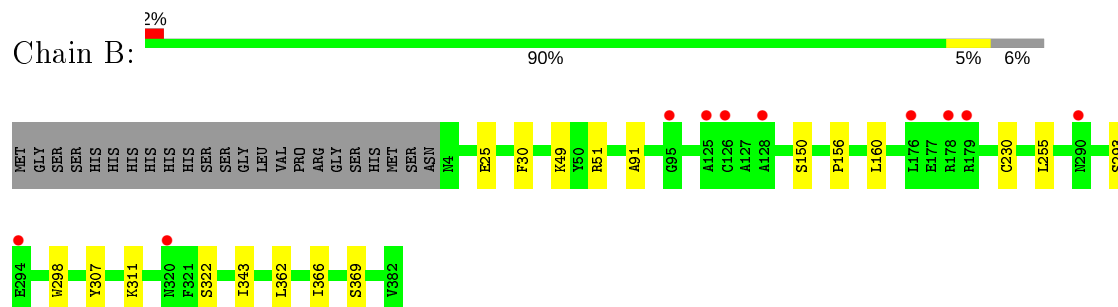
### 3 Residue-property plots [i](#)

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.

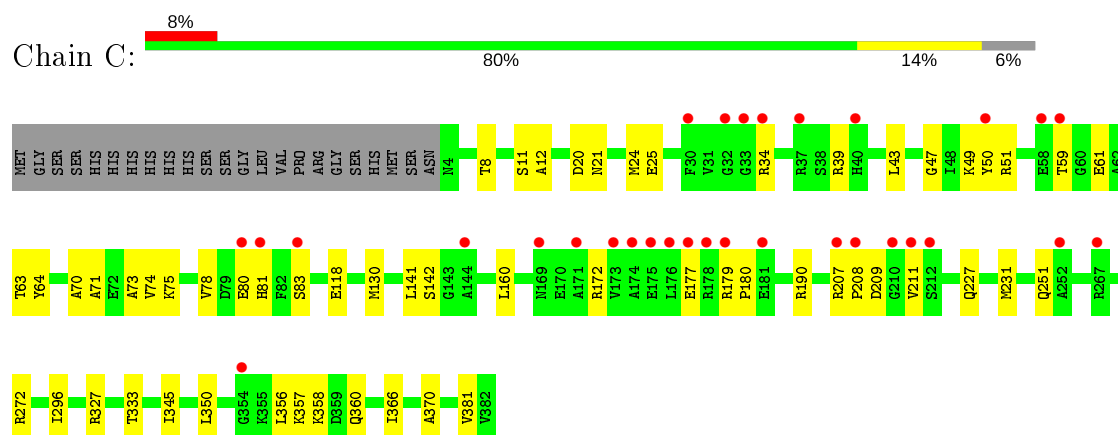
#### • Molecule 1: Ketosynthase StID



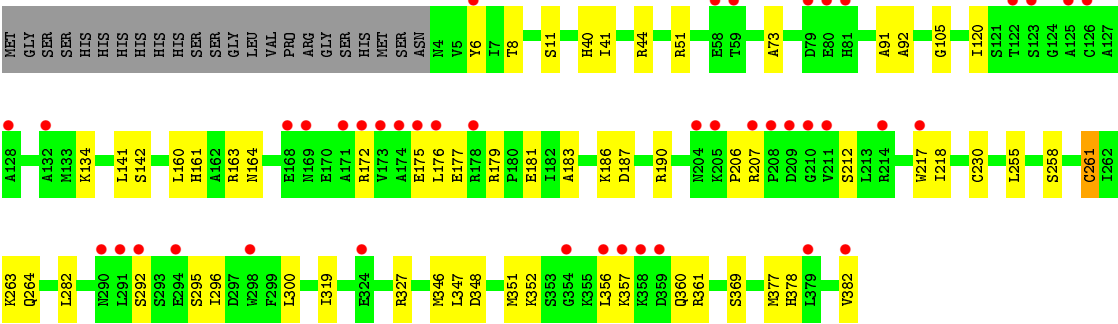
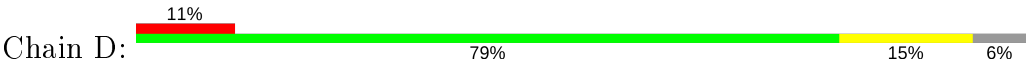
#### • Molecule 1: Ketosynthase StID



#### • Molecule 1: Ketosynthase StID



#### • Molecule 1: Ketosynthase StID





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.29 Å 127.64 Å 107.89 Å 90.00° 91.55° 90.00°	Depositor
Resolution (Å)	44.93 – 1.83 44.93 – 1.83	Depositor EDS
% Data completeness (in resolution range)	99.7 (44.93-1.83) 99.7 (44.93-1.83)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.45 (at 1.83 Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, $R_{free}$	0.198 , 0.231 0.196 , 0.228	Depositor DCC
$R_{free}$ test set	7448 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.6	Xtriage
Anisotropy	0.365	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 42.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.026 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	12960	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	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 [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: 2K3

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	0.41	0/3026	0.56	0/4092
1	B	0.39	0/3026	0.55	0/4092
1	C	0.38	0/3026	0.54	0/4092
1	D	0.39	1/3026 (0.0%)	0.54	0/4092
All	All	0.39	1/12104 (0.0%)	0.55	0/16368

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	261	CYS	CB-SG	-5.01	1.73	1.81

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	2964	0	2899	16	2
1	B	2964	0	2900	10	0
1	C	2964	0	2899	38	1
1	D	2964	0	2900	37	1
2	A	9	0	0	0	0
2	C	9	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	356	0	0	1	0
3	B	325	0	0	0	0
3	C	182	0	0	0	0
3	D	223	0	0	2	0
All	All	12960	0	11598	95	2

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 4.

All (95) 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:8:THR:HB	1:A:207:ARG:HG2	1.68	0.73
1:C:211:VAL:HG11	1:C:381:VAL:HG13	1.74	0.69
1:C:142:SER:HB2	1:D:141:LEU:HD23	1.76	0.68
1:D:258:SER:HB3	1:D:261:CYS:SG	2.37	0.65
1:A:307:TYR:CE1	1:A:311:LYS:HE3	2.35	0.61
1:A:207:ARG:HD3	1:A:208:PRO:HD2	1.81	0.61
1:C:24:MET:HE1	1:C:43:LEU:HD11	1.81	0.61
1:C:358:LYS:HA	1:C:381:VAL:HG12	1.82	0.60
1:D:217:TRP:CZ2	1:D:378:HIS:HB2	2.37	0.60
1:C:8:THR:HB	1:C:207:ARG:HG2	1.83	0.59
1:D:361:ARG:HB3	1:D:378:HIS:HE1	1.68	0.58
1:A:227:GLN:OE1	1:A:272:ARG:HD3	2.03	0.58
1:C:21:ASN:HB3	1:C:43:LEU:HD13	1.87	0.56
1:B:307:TYR:CE1	1:B:311:LYS:HE3	2.41	0.56
1:D:183:ALA:HB3	1:D:186:LYS:HE3	1.88	0.56
1:D:217:TRP:CE2	1:D:378:HIS:HB2	2.41	0.56
1:C:34:ARG:NH2	1:C:180:PRO:HG2	2.22	0.55
1:D:361:ARG:HB3	1:D:378:HIS:CE1	2.42	0.54
1:D:212:SER:O	1:D:382:VAL:HG22	2.08	0.53
1:C:160:LEU:HD22	1:C:190:ARG:HA	1.90	0.53
1:D:11:SER:OG	1:D:73:ALA:O	2.25	0.53
1:A:161:HIS:ND1	1:A:163:ARG:HG2	2.24	0.53
1:D:172:ARG:O	1:D:175:GLU:HG2	2.10	0.52
1:D:300:LEU:HB3	1:D:346:MET:HE1	1.89	0.52
1:D:261:CYS:HB2	3:D:495:HOH:O	2.09	0.52
1:D:6:TYR:CZ	1:D:206:PRO:HD3	2.45	0.51
1:C:211:VAL:CG1	1:C:381:VAL:HG13	2.40	0.51
1:D:357:LYS:O	1:D:360:GLN:HB2	2.11	0.51
1:C:80:GLU:HG2	1:C:81:HIS:ND1	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:230:CYS:HB3	1:D:369:SER:O	2.11	0.50
1:A:226:GLU:HB2	3:A:769:HOH:O	2.12	0.50
1:C:251:GLN:HG3	1:D:164:ASN:OD1	2.11	0.50
1:A:255:LEU:HD22	1:B:255:LEU:HD22	1.92	0.50
1:D:160:LEU:HD22	1:D:190:ARG:HA	1.93	0.49
1:D:6:TYR:CE2	1:D:206:PRO:HD3	2.46	0.49
1:C:20:ASP:HB3	1:C:50:TYR:CE1	2.48	0.49
1:A:82:PHE:HZ	1:A:87:MET:HB3	1.78	0.48
1:D:172:ARG:HG3	1:D:172:ARG:HH11	1.78	0.48
1:C:227:GLN:OE1	1:C:272:ARG:HD3	2.15	0.47
1:C:172:ARG:NH1	1:C:180:PRO:O	2.47	0.47
1:C:63:THR:HG1	1:C:64:TYR:HD1	1.60	0.47
1:D:177:GLU:HB2	1:D:179:ARG:HG2	1.97	0.47
1:B:343:ILE:HG12	1:B:366:ILE:HD11	1.97	0.47
1:A:343:ILE:HG12	1:A:366:ILE:HD11	1.97	0.46
1:B:230:CYS:HB3	1:B:369:SER:O	2.15	0.46
1:C:350:LEU:HD21	1:C:356:LEU:HD21	1.97	0.46
1:D:348:ASP:OD1	1:D:352:LYS:NZ	2.47	0.46
1:D:351:MET:HA	1:D:356:LEU:HD12	1.98	0.46
1:C:118:GLU:OE2	1:D:134:LYS:NZ	2.38	0.45
1:D:190:ARG:NH1	3:D:406:HOH:O	2.45	0.45
1:D:40:HIS:CE1	1:D:41:ILE:HG13	2.52	0.45
1:C:357:LYS:O	1:C:360:GLN:HB2	2.16	0.45
1:D:8:THR:HB	1:D:207:ARG:HG2	1.98	0.45
1:C:207:ARG:HA	1:C:207:ARG:HD3	1.83	0.45
1:C:80:GLU:HG2	1:C:81:HIS:CE1	2.52	0.45
1:A:207:ARG:HD3	1:A:207:ARG:HA	1.72	0.44
1:C:71:ALA:O	1:C:75:LYS:HG3	2.17	0.44
1:C:231:MET:HB3	1:C:370:ALA:HA	2.00	0.44
1:D:218:ILE:HG12	1:D:377:MET:HG3	1.99	0.44
1:D:347:LEU:O	1:D:351:MET:HB2	2.18	0.44
1:C:130:MET:HG3	1:C:366:ILE:HD13	1.99	0.44
1:B:293:SER:OG	1:B:322:SER:O	2.27	0.43
1:D:292:SER:O	1:D:295:SER:OG	2.26	0.43
1:A:343:ILE:HD12	1:A:343:ILE:HA	1.90	0.43
1:C:24:MET:HE1	1:C:43:LEU:HD21	1.99	0.43
1:D:91:ALA:HA	1:D:120:ILE:HG13	2.00	0.43
1:A:130:MET:HG3	1:A:366:ILE:HD13	2.00	0.43
1:A:217:TRP:CZ2	1:A:378:HIS:HB2	2.54	0.43
1:A:49:LYS:HA	1:A:49:LYS:HD3	1.93	0.43
1:C:209:ASP:N	1:C:209:ASP:OD1	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:296:ILE:O	1:D:327:ARG:NH1	2.51	0.43
1:B:25:GLU:HG2	1:B:30:PHE:HE1	1.84	0.43
1:C:296:ILE:O	1:C:327:ARG:NH1	2.47	0.43
1:C:49:LYS:HA	1:C:49:LYS:HD3	1.80	0.43
1:C:59:THR:HB	1:C:61:GLU:HG2	2.01	0.42
1:A:353:SER:HB2	1:A:355:LYS:HE3	2.01	0.42
1:C:177:GLU:HG3	1:C:179:ARG:H	1.84	0.42
1:D:179:ARG:NH1	1:D:181:GLU:HG2	2.34	0.42
1:D:161:HIS:ND1	1:D:163:ARG:HB2	2.34	0.42
1:C:70:ALA:O	1:C:74:VAL:HG23	2.20	0.42
1:C:141:LEU:HD23	1:D:142:SER:HB2	2.02	0.41
1:B:49:LYS:HD3	1:B:49:LYS:HA	1.91	0.41
1:D:92:ALA:HB3	1:D:105:GLY:HA2	2.03	0.41
1:B:91:ALA:O	1:B:150:SER:HA	2.21	0.41
1:B:298:TRP:HB2	1:B:362:LEU:HG	2.03	0.41
1:C:47:GLY:O	1:C:333:THR:HG23	2.20	0.41
1:C:251:GLN:HB3	1:D:255:LEU:HD11	2.03	0.41
1:A:362:LEU:HB2	1:A:379:LEU:HB2	2.02	0.41
1:C:12:ALA:HB1	1:C:345:ILE:HG12	2.02	0.41
1:B:156:PRO:O	1:B:160:LEU:HG	2.20	0.41
1:C:78:VAL:HG13	1:C:83:SER:HA	2.02	0.40
1:D:282:LEU:HD23	1:D:319:ILE:HD11	2.03	0.40
1:C:34:ARG:HH21	1:C:180:PRO:HG2	1.87	0.40
1:C:11:SER:OG	1:C:73:ALA:O	2.31	0.40
1:C:25:GLU:HB2	1:C:39:ARG:HD3	2.03	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:GLU:OE1	1:D:44:ARG:NH2[2_555]	1.91	0.29
1:A:209:ASP:OD1	1:C:34:ARG:CD[1_556]	2.13	0.07

## 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	377/402 (94%)	368 (98%)	9 (2%)	0	100	100
1	B	377/402 (94%)	366 (97%)	11 (3%)	0	100	100
1	C	377/402 (94%)	360 (96%)	16 (4%)	1 (0%)	41	27
1	D	377/402 (94%)	361 (96%)	16 (4%)	0	100	100
All	All	1508/1608 (94%)	1455 (96%)	52 (3%)	1 (0%)	51	37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	208	PRO

### 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	321/341 (94%)	320 (100%)	1 (0%)	92	90
1	B	321/341 (94%)	320 (100%)	1 (0%)	92	90
1	C	321/341 (94%)	320 (100%)	1 (0%)	92	90
1	D	321/341 (94%)	316 (98%)	5 (2%)	62	49
All	All	1284/1364 (94%)	1276 (99%)	8 (1%)	86	82

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	ARG
1	B	51	ARG
1	C	51	ARG
1	D	51	ARG
1	D	176	LEU
1	D	187	ASP
1	D	263	LYS

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Mol	Chain	Res	Type
1	D	264	GLN

Some 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 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	2K3	A	401	1	7,8,9	1.47	1 (14%)	7,9,11	1.08	1 (14%)
2	2K3	C	401	1	7,8,9	1.15	0	7,9,11	0.97	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
2	2K3	A	401	1	-	0/6/7/8	-
2	2K3	C	401	1	-	0/6/7/8	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	2K3	CAG-CAI	3.17	1.55	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	2K3	OAD-CAI-CAG	2.11	124.56	121.55

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	379/402 (94%)	-0.02	5 (1%) 77 77	18, 27, 43, 72	0
1	B	379/402 (94%)	0.08	10 (2%) 56 53	16, 28, 44, 73	0
1	C	379/402 (94%)	0.53	31 (8%) 11 10	23, 38, 67, 93	0
1	D	379/402 (94%)	0.72	43 (11%) 5 4	20, 38, 63, 87	0
All	All	1516/1608 (94%)	0.33	89 (5%) 22 20	16, 32, 60, 93	0

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	178	ARG	7.4
1	C	176	LEU	7.0
1	C	210	GLY	6.4
1	C	178	ARG	5.4
1	D	209	ASP	4.6
1	C	175	GLU	4.5
1	C	173	VAL	4.2
1	C	81	HIS	4.2
1	D	208	PRO	4.2
1	C	37	ARG	4.2
1	D	174	ALA	4.2
1	C	177	GLU	4.0
1	D	6	TYR	4.0
1	C	33	GLY	3.9
1	D	172	ARG	3.9
1	C	208	PRO	3.9
1	C	211	VAL	3.8
1	D	291	LEU	3.8
1	D	176	LEU	3.8
1	B	176	LEU	3.7
1	D	354	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	179	ARG	3.6
1	C	181	GLU	3.6
1	C	174	ALA	3.5
1	C	179	ARG	3.5
1	D	178	ARG	3.5
1	D	126	CYS	3.4
1	D	290	ASN	3.4
1	D	173	VAL	3.3
1	D	81	HIS	3.3
1	D	211	VAL	3.2
1	D	128	ALA	3.2
1	C	32	GLY	3.2
1	D	171	ALA	3.2
1	D	175	GLU	3.2
1	C	212	SER	3.2
1	D	122	THR	3.1
1	C	30	PHE	3.0
1	C	207	ARG	3.0
1	C	83	SER	3.0
1	D	80	GLU	2.9
1	D	79	ASP	2.9
1	D	294	GLU	2.9
1	A	100	ILE	2.9
1	D	292	SER	2.9
1	C	58	GLU	2.8
1	C	171	ALA	2.8
1	C	34	ARG	2.8
1	A	81	HIS	2.8
1	A	209	ASP	2.8
1	D	169	ASN	2.8
1	D	59	THR	2.7
1	D	356	LEU	2.7
1	D	58	GLU	2.7
1	C	252	ALA	2.7
1	D	358	LYS	2.7
1	D	168	GLU	2.7
1	D	217	TRP	2.7
1	B	125	ALA	2.7
1	D	204	ASN	2.7
1	D	205	LYS	2.6
1	B	126	CYS	2.6
1	B	290	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	128	ALA	2.5
1	D	125	ALA	2.5
1	D	210	GLY	2.5
1	B	95	GLY	2.5
1	A	208	PRO	2.5
1	C	50	TYR	2.4
1	D	207	ARG	2.4
1	D	379	LEU	2.4
1	D	298	TRP	2.4
1	C	354	GLY	2.4
1	B	294	GLU	2.3
1	C	80	GLU	2.3
1	C	169	ASN	2.3
1	C	267	ARG	2.3
1	C	144	ALA	2.3
1	D	382	VAL	2.2
1	D	123	SER	2.2
1	C	59	THR	2.2
1	D	132	ALA	2.1
1	D	357	LYS	2.1
1	B	320	ASN	2.1
1	D	324	GLU	2.1
1	D	214	ARG	2.1
1	A	125	ALA	2.1
1	D	359	ASP	2.1
1	C	40	HIS	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](#)

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( $\text{\AA}^2$ )	Q<0.9
2	2K3	A	401	9/10	0.91	0.15	25,30,34,35	0
2	2K3	C	401	9/10	0.91	0.15	31,36,41,42	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.