



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 05:42 pm BST

PDB ID : 5Z72
Title : Crystal structure of CcpC regulatory domain in complex with citrate from *Bacillus amyloliquefaciens*
Authors : Chen, J.; Wang, L.; Shang, F.; Xu, Y.
Deposited on : 2018-01-26
Resolution : 2.40 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

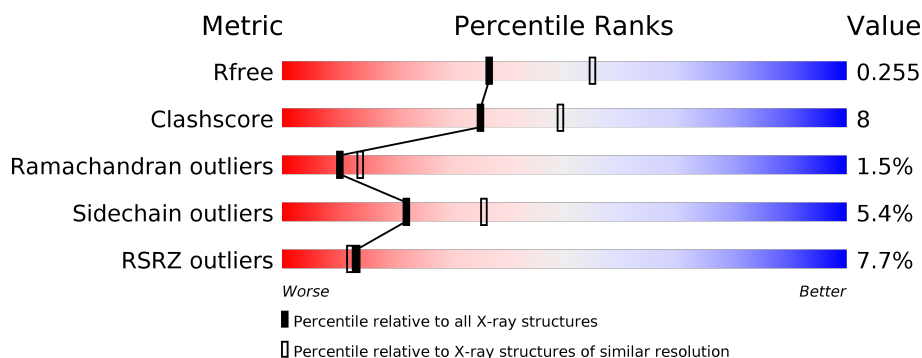
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 ≥ 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	293	<div> <div> <div>0%</div> <div>55%</div> <div>11%</div> <div>33%</div> </div> </div>
1	B	293	<div> <div>58%</div> <div>8%</div> <div>33%</div> </div>
1	C	293	<div> <div>3%</div> <div>53%</div> <div>12%</div> <div>33%</div> </div>
1	D	293	<div> <div>9%</div> <div>51%</div> <div>13%</div> <div>34%</div> </div>
1	E	293	<div> <div>12%</div> <div>40%</div> <div>18%</div> <div>39%</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	NA	E	301	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16114 atoms, of which 7875 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 CcpC.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	197	Total	C	H	N	O	S	0	1	0
			3230	1047	1610	268	298	7			
1	B	197	Total	C	H	N	O	S	0	0	0
			3213	1042	1602	266	296	7			
1	C	197	Total	C	H	N	O	S	0	0	0
			3213	1042	1602	266	296	7			
1	D	193	Total	C	H	N	O	S	0	0	0
			3163	1027	1582	261	286	7			
1	E	179	Total	C	H	N	O	S	0	0	0
			2901	941	1454	234	265	7			

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 3 is CITRATE ANION (three-letter code: FLC) (formula: C₆H₅O₇).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			18	6	5	7		
3	B	1	Total	C	H	O	0	0
			18	6	5	7		
3	C	1	Total	C	H	O	0	0
			18	6	5	7		
3	D	1	Total	C	H	O	0	0
			18	6	5	7		
3	E	1	Total	C	H	O	0	0
			18	6	5	7		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	85	Total	O	0	0
			85	85		
4	B	81	Total	O	0	0
			81	81		
4	C	69	Total	O	0	0
			69	69		
4	D	33	Total	O	0	0
			33	33		
4	E	24	Total	O	0	0
			24	24		

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.

Chain A:

Sequence logo for Chain A. The y-axis represents information content in bits (0.00 to 0.25). The x-axis lists amino acids. A color scale at the top indicates conservation levels: 0% (grey), 11% (yellow), 55% (green), and 33% (dark grey).

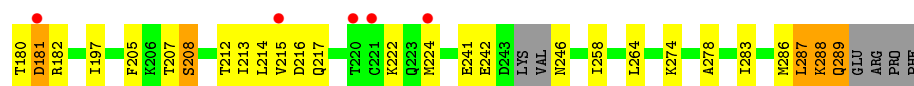
Amino Acid	Information Content (bits)
GLY	0.00
GLU	0.00
LYS	0.00
ILE	0.00
ILE	0.00
GLN	0.00
PHE	0.00
ALA	0.00
ASN	0.00
ASP	0.00
VAL	0.00
THR	0.00
ASP	0.00
ARG	0.00
GLN	0.00
ILE	0.00
ARG	0.00
ASN	0.00
ILE	0.00
ASP	0.00
GLU	0.00
LEU	0.00
GLY	0.00
GLY	0.00
ILE	0.00
THR	0.00
GLN	0.00
PRO	0.00
F279	0.00
I283	0.00
F284	0.00
D285	0.00
Q289	0.00
GLU	0.00
ARG	0.00
PRO	0.00
PHE	0.00

Chain B:

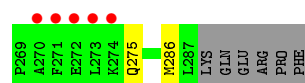
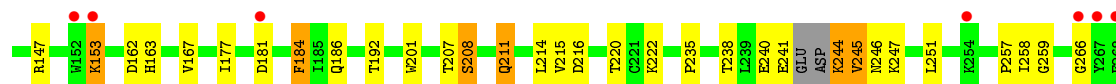
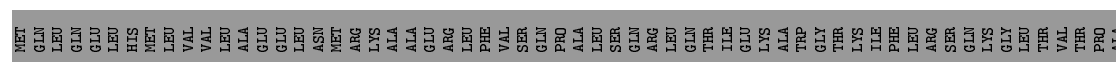
Sequence logo for Chain B. The y-axis represents information content in bits (0.00 to 0.08). The x-axis shows positions 1 to 100. A color key at the bottom identifies amino acids: S208 (orange), P209 (yellow), K210 (green), E240 (yellow), E241 (yellow), E242 (green), D243 (green), LYS (grey), VAL (grey), K246 (green), K247 (green), L264 (yellow), L265 (yellow), L266 (green), K274 (green), M286 (yellow), L287 (yellow), K288 (yellow), Q289 (green), GLU (green), PRO (grey), PRO (grey), PHE (grey).

Chain C:

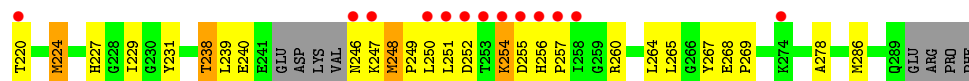
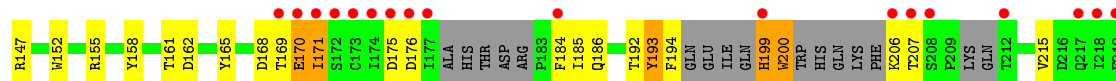
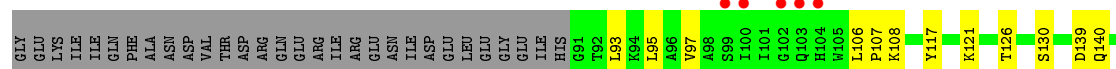
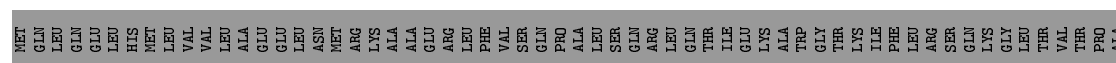
Amino Acid	Percentage
MET	3%
GLN	53%
LEU	12%
GLU	33%
HIS	0%
MET	0%
LEU	0%
VAL	0%
LEU	0%
ALA	0%
GLU	0%
LEU	0%
ASN	0%
MET	0%
ARG	0%
LYS	0%
ALA	0%
ALA	0%
GLU	0%
ARG	0%
LEU	0%
PHE	0%
VAL	0%
SER	0%
GLN	0%
PRO	0%
ALA	0%
LEU	0%
SER	0%
GLN	0%
ARG	0%
LEU	0%
GLN	0%
THR	0%
THR	0%
ILE	0%
GLU	0%
LYS	0%
ALA	0%
TRP	0%
GLY	0%
THR	0%
LYS	0%
ILE	0%
PHE	0%
LEU	0%
ARG	0%
SER	0%
GLN	0%
LYS	0%
GLY	0%
LEU	0%
THR	0%
VAL	0%
THR	0%
PRO	0%
ALA	0%



• Molecule 1: CcpC



• Molecule 1: CcpC



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	140.96Å 90.90Å 105.53Å 90.00° 106.18° 90.00°	Depositor
Resolution (Å)	29.71 – 2.40 39.34 – 2.29	Depositor EDS
% Data completeness (in resolution range)	98.1 (29.71-2.40) 96.5 (39.34-2.29)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.76 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.185 , 0.255 0.193 , 0.255	Depositor DCC
R_{free} test set	2000 reflections (3.59%)	wwPDB-VP
Wilson B-factor (Å ²)	48.6	Xtriage
Anisotropy	0.438	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 56.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16114	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: NA, FLC

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	0.82	1/1661 (0.1%)	0.80	1/2251 (0.0%)
1	B	0.82	0/1652	0.80	0/2239
1	C	0.70	0/1652	0.78	1/2239 (0.0%)
1	D	0.66	0/1622	0.75	1/2199 (0.0%)
1	E	0.66	0/1479	0.73	1/1999 (0.1%)
All	All	0.74	1/8066 (0.0%)	0.77	4/10927 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	221	CYS	CB-SG	-5.06	1.73	1.81

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	181	ASP	CB-CG-OD1	-9.23	110.00	118.30
1	E	246	ASN	CA-C-O	-6.21	107.07	120.10
1	A	252	ASP	CB-CG-OD1	5.82	123.54	118.30
1	C	154	GLY	N-CA-C	-5.07	100.42	113.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	179	HIS	Peptide
1	C	258	ILE	Peptide

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	1620	1610	1615	21	1
1	B	1611	1602	1608	17	0
1	C	1611	1602	1608	26	1
1	D	1581	1582	1589	28	0
1	E	1447	1454	1457	37	0
2	A	2	0	0	0	0
2	B	3	0	0	0	0
2	C	2	0	0	0	0
2	D	4	0	0	0	0
2	E	1	0	0	0	0
3	A	13	5	5	0	0
3	B	13	5	5	1	0
3	C	13	5	5	2	0
3	D	13	5	5	2	0
3	E	13	5	5	0	0
4	A	85	0	0	5	0
4	B	81	0	0	5	0
4	C	69	0	0	4	1
4	D	33	0	0	2	0
4	E	24	0	0	3	1
All	All	8239	7875	7902	130	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 8.

All (130) 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:E:286:MET:SD	4:E:421:HOH:O	2.22	0.97
1:B:286:MET:SD	4:B:457:HOH:O	2.45	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:185:ILE:HD13	1:E:224:MET:HB3	1.70	0.73
1:C:216:ASP:OD2	4:C:401:HOH:O	2.06	0.73
1:A:210:LYS:O	4:A:401:HOH:O	2.09	0.70
1:E:192:THR:OG1	1:E:260:ARG:NH2	2.25	0.69
1:A:211:GLN:O	1:C:121:LYS:NZ	2.25	0.69
1:C:217:GLN:OE1	4:C:402:HOH:O	2.10	0.68
1:A:207:THR:OG1	1:A:208:SER:N	2.28	0.67
3:D:305:FLC:OHB	3:D:305:FLC:OA2	2.14	0.66
1:A:264:LEU:C	1:A:265:LEU:HD12	2.16	0.65
1:C:159:LEU:HD21	1:C:283:ILE:HG21	1.79	0.64
1:D:147:ARG:NH2	1:D:162:ASP:OD2	2.33	0.62
1:E:224:MET:HG2	1:E:229:ILE:HD12	1.82	0.61
1:B:207:THR:OG1	1:B:208:SER:N	2.32	0.59
1:E:239:LEU:C	1:E:240:GLU:HG3	2.24	0.58
1:E:117:TYR:CE2	1:E:278:ALA:HB1	2.40	0.57
1:A:112:THR:HG23	4:A:430:HOH:O	2.04	0.56
1:E:268:GLU:N	1:E:269:PRO:CD	2.68	0.56
1:C:222:LYS:NZ	1:C:242:GLU:OE2	2.31	0.56
1:A:171:ILE:HD11	1:A:182:ARG:HD3	1.86	0.56
1:A:217[B]:GLN:OE1	1:A:220:THR:OG1	2.20	0.56
1:E:93:LEU:HD11	1:E:95:LEU:HD21	1.87	0.56
1:C:147:ARG:NH2	1:C:162:ASP:OD2	2.40	0.55
1:B:177:ILE:HG21	4:B:473:HOH:O	2.07	0.54
1:A:279:PHE:CE2	1:A:283:ILE:HD11	2.42	0.54
1:D:251:LEU:HD23	1:D:257:PRO:HA	1.90	0.54
1:C:197:ILE:HG13	4:C:436:HOH:O	2.08	0.54
1:D:207:THR:OG1	1:D:208:SER:N	2.40	0.54
1:D:235:PRO:HG2	1:D:238:THR:HG23	1.89	0.54
1:C:287:LEU:O	1:C:289:GLN:N	2.42	0.53
1:C:215:VAL:HG12	1:C:216:ASP:N	2.24	0.53
1:B:240:GLU:N	1:B:242:GLU:OE2	2.42	0.53
1:D:244:LYS:O	1:D:247:LYS:NZ	2.36	0.53
1:E:192:THR:O	1:E:194:PHE:N	2.42	0.53
1:E:155:ARG:NE	4:E:401:HOH:O	2.15	0.52
1:D:244:LYS:HG3	1:D:245:VAL:N	2.24	0.52
1:D:244:LYS:O	1:D:245:VAL:HG12	2.10	0.52
1:E:165:TYR:CE2	1:E:247:LYS:HE3	2.45	0.52
1:E:168:ASP:OD1	1:E:169:THR:N	2.43	0.52
3:D:305:FLC:OHB	3:D:305:FLC:OG2	2.18	0.51
1:D:121:LYS:NZ	1:D:275:GLN:OE1	2.19	0.51
1:D:215:VAL:HG12	1:D:216:ASP:N	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:147:ARG:HH22	1:C:162:ASP:CG	2.13	0.50
1:A:112:THR:HG22	4:A:420:HOH:O	2.12	0.50
1:C:117:TYR:CE2	1:C:278:ALA:HB1	2.46	0.49
1:D:163:HIS:HA	1:D:259:GLY:HA2	1.94	0.49
1:A:207:THR:HG21	4:A:404:HOH:O	2.12	0.49
1:C:167:VAL:HA	1:C:246:ASN:O	2.13	0.49
1:B:241:GLU:N	1:B:242:GLU:HA	2.28	0.48
1:C:178:ALA:HB2	1:C:205:PHE:CD1	2.49	0.48
1:D:110:LEU:HD12	1:E:224:MET:SD	2.53	0.48
1:C:286:MET:O	1:C:288:LYS:N	2.46	0.48
1:D:244:LYS:CG	1:D:245:VAL:N	2.77	0.47
1:D:162:ASP:O	1:D:259:GLY:HA2	2.14	0.47
1:A:116:ARG:HD2	1:A:117:TYR:CE1	2.49	0.47
1:E:171:ILE:HG22	1:E:248:MET:HE1	1.95	0.47
1:D:258:ILE:HG22	1:D:259:GLY:N	2.30	0.47
1:E:238:THR:HG22	1:E:239:LEU:HG	1.96	0.47
1:D:211:GLN:NE2	4:D:401:HOH:O	2.36	0.47
1:E:170:GLU:HB3	1:E:171:ILE:HD12	1.97	0.47
1:B:116:ARG:HD2	1:B:117:TYR:CE1	2.50	0.46
1:A:223:GLN:HG3	4:C:446:HOH:O	2.16	0.46
1:B:106:LEU:N	1:B:107:PRO:CD	2.78	0.46
3:B:304:FLC:OHB	3:B:304:FLC:OG1	2.24	0.46
1:D:244:LYS:CG	1:D:245:VAL:H	2.29	0.46
1:C:212:THR:OG1	1:C:213:ILE:N	2.49	0.45
1:C:147:ARG:HD3	3:C:303:FLC:OG2	2.17	0.45
1:E:200:TRP:CH2	1:E:250:LEU:HG	2.51	0.45
1:D:167:VAL:HA	1:D:246:ASN:O	2.16	0.45
1:E:158:TYR:OH	1:E:161:THR:OG1	2.07	0.45
1:E:194:PHE:O	1:E:199:HIS:N	2.50	0.44
1:C:207:THR:OG1	1:C:208:SER:N	2.51	0.44
1:D:136:LEU:HD11	1:D:266:GLY:HA2	2.00	0.44
1:E:147:ARG:NH2	1:E:162:ASP:OD2	2.49	0.44
1:A:212:THR:OG1	1:A:213:ILE:N	2.51	0.44
1:B:264:LEU:C	1:B:265:LEU:HD12	2.37	0.44
1:C:168:ASP:O	1:C:246:ASN:HB2	2.18	0.44
1:E:200:TRP:CZ2	1:E:250:LEU:HG	2.52	0.44
1:D:184:PHE:CZ	1:D:186:GLN:HG2	2.53	0.44
1:E:93:LEU:HD11	1:E:95:LEU:CD2	2.47	0.44
1:B:171:ILE:HG21	1:B:177:ILE:HD12	2.00	0.43
1:D:244:LYS:HG3	1:D:245:VAL:H	1.83	0.43
1:E:106:LEU:N	1:E:107:PRO:CD	2.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:264:LEU:C	1:E:265:LEU:HD12	2.38	0.43
1:E:165:TYR:CE2	1:E:249:PRO:HG3	2.53	0.43
1:E:206:LYS:HG3	1:E:207:THR:N	2.34	0.43
1:E:152:TRP:CH2	1:E:267:TYR:CZ	3.06	0.43
1:B:192:THR:HG23	4:B:425:HOH:O	2.17	0.43
1:D:153:LYS:H	1:D:153:LYS:HD3	1.82	0.43
1:C:215:VAL:HG12	1:C:216:ASP:H	1.82	0.43
1:C:264:LEU:C	1:C:264:LEU:HD23	2.39	0.43
1:E:251:LEU:HD12	1:E:251:LEU:N	2.34	0.43
1:E:93:LEU:HD21	1:E:95:LEU:HD21	2.01	0.43
1:B:177:ILE:CG2	1:B:201:TRP:CH2	3.02	0.43
1:B:241:GLU:HB2	1:B:242:GLU:HA	2.01	0.43
1:D:100:ILE:O	1:D:104:HIS:HB2	2.19	0.43
1:E:184:PHE:CD1	1:E:231:TYR:CE2	3.07	0.43
1:D:177:ILE:HD13	1:D:177:ILE:HA	1.86	0.42
1:A:215:VAL:HG12	1:A:217[A]:GLN:H	1.84	0.42
1:A:265:LEU:N	1:A:265:LEU:HD12	2.34	0.42
1:C:180:THR:O	1:C:182:ARG:N	2.47	0.42
1:D:222:LYS:NZ	4:D:403:HOH:O	2.51	0.42
1:E:121:LYS:NZ	4:E:404:HOH:O	2.33	0.42
1:D:215:VAL:HG11	1:D:220:THR:HB	2.02	0.42
1:E:192:THR:O	1:E:193:TYR:C	2.58	0.42
1:A:212:THR:HA	1:C:121:LYS:HG2	2.00	0.42
1:E:215:VAL:HG11	1:E:220:THR:HB	2.02	0.42
1:B:286:MET:CG	4:B:457:HOH:O	2.67	0.42
1:C:92:THR:OG1	1:C:121:LYS:HB2	2.20	0.42
1:C:96:ALA:HB1	1:C:132:MET:HB3	2.01	0.41
1:E:140:GLN:HA	1:E:140:GLN:OE1	2.20	0.41
1:E:97:VAL:O	1:E:126:THR:HA	2.20	0.41
1:E:254:LYS:O	1:E:255:ASP:HB3	2.20	0.41
1:C:182:ARG:HH11	1:C:182:ARG:HG2	1.85	0.41
1:D:105:TRP:CH2	1:D:109:VAL:HG21	2.55	0.41
1:B:204:LYS:NZ	4:B:405:HOH:O	2.38	0.41
1:A:166:LEU:HD22	1:A:248:MET:HE1	2.02	0.41
1:A:268:GLU:N	1:A:269:PRO:CD	2.84	0.41
1:B:242:GLU:H	1:B:247:LYS:HZ1	1.67	0.41
1:B:122:VAL:HG12	1:B:123:SER:N	2.36	0.40
1:C:213:ILE:HG21	1:C:224:MET:CE	2.50	0.40
3:C:303:FLC:OHB	3:C:303:FLC:OA1	2.32	0.40
1:D:177:ILE:CG2	1:D:201:TRP:CH2	3.05	0.40
1:D:244:LYS:CD	1:D:245:VAL:H	2.34	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:112:THR:O	1:B:113:TYR:C	2.57	0.40
1:E:251:LEU:HA	1:E:257:PRO:HA	2.02	0.40
1:A:116:ARG:HB3	1:A:117:TYR:CE1	2.55	0.40
1:A:105:TRP:CD2	1:A:160:MET:HE1	2.56	0.40
1:A:210:LYS:HB2	4:A:401:HOH:O	2.21	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)
4:C:430:HOH:O	4:E:402:HOH:O[2_455]	2.17	0.03
1:A:180:THR:O	1:C:208:SER:OG[4_455]	2.17	0.03

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	194/293 (66%)	183 (94%)	10 (5%)	1 (0%)	29	41
1	B	193/293 (66%)	180 (93%)	12 (6%)	1 (0%)	29	41
1	C	193/293 (66%)	180 (93%)	10 (5%)	3 (2%)	9	13
1	D	189/293 (64%)	170 (90%)	14 (7%)	5 (3%)	5	5
1	E	167/293 (57%)	151 (90%)	12 (7%)	4 (2%)	6	6
All	All	936/1465 (64%)	864 (92%)	58 (6%)	14 (2%)	10	14

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	181	ASP
1	C	288	LYS
1	D	245	VAL

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Mol	Chain	Res	Type
1	E	170	GLU
1	E	171	ILE
1	E	193	TYR
1	C	287	LEU
1	D	184	PHE
1	D	211	GLN
1	A	92	THR
1	B	288	LYS
1	D	240	GLU
1	E	176	ASP
1	D	117	TYR

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	180/264 (68%)	171 (95%)	9 (5%)	24	40
1	B	179/264 (68%)	171 (96%)	8 (4%)	27	44
1	C	179/264 (68%)	171 (96%)	8 (4%)	27	44
1	D	176/264 (67%)	168 (96%)	8 (4%)	27	44
1	E	162/264 (61%)	148 (91%)	14 (9%)	10	16
All	All	876/1320 (66%)	829 (95%)	47 (5%)	22	36

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	123	SER
1	A	147	ARG
1	A	208	SER
1	A	211	GLN
1	A	223	GLN
1	A	243	ASP
1	A	247	LYS
1	A	274	LYS

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Mol	Chain	Res	Type
1	A	285	ASP
1	B	108	LYS
1	B	112	THR
1	B	123	SER
1	B	173	CYS
1	B	186	GLN
1	B	207	THR
1	B	208	SER
1	B	210	LYS
1	C	123	SER
1	C	162	ASP
1	C	181	ASP
1	C	208	SER
1	C	214	LEU
1	C	241	GLU
1	C	274	LYS
1	C	289	GLN
1	D	112	THR
1	D	153	LYS
1	D	192	THR
1	D	208	SER
1	D	214	LEU
1	D	241	GLU
1	D	244	LYS
1	D	286	MET
1	E	108	LYS
1	E	130	SER
1	E	139	ASP
1	E	175	ASP
1	E	186	GLN
1	E	199	HIS
1	E	200	TRP
1	E	224	MET
1	E	227	HIS
1	E	238	THR
1	E	248	MET
1	E	252	ASP
1	E	254	LYS
1	E	256	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	186	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 12 are monoatomic - leaving 5 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$
3	FLC	D	305	2	3,12,12	1.62	1 (33%)	3,17,17	3.37	2 (66%)
3	FLC	B	304	2	3,12,12	2.62	2 (66%)	3,17,17	2.28	1 (33%)
3	FLC	C	303	2	3,12,12	1.41	0	3,17,17	2.41	1 (33%)
3	FLC	A	303	2	3,12,12	1.95	2 (66%)	3,17,17	2.40	2 (66%)
3	FLC	E	302	2	3,12,12	1.39	0	3,17,17	1.29	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
3	FLC	D	305	2	-	3/6/16/16	-
3	FLC	B	304	2	-	2/6/16/16	-
3	FLC	C	303	2	-	0/6/16/16	-
3	FLC	A	303	2	-	0/6/16/16	-
3	FLC	E	302	2	-	3/6/16/16	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	304	FLC	OHB-CB	-2.95	1.38	1.43
3	B	304	FLC	CA-CB	-2.90	1.50	1.54
3	D	305	FLC	CA-CB	-2.49	1.51	1.54
3	A	303	FLC	CG-CB	-2.41	1.51	1.54
3	A	303	FLC	OHB-CB	-2.09	1.39	1.43

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	305	FLC	CB-CG-CGC	-4.59	107.63	114.98
3	C	303	FLC	CB-CA-CAC	-4.05	108.51	114.98
3	B	304	FLC	CB-CA-CAC	-3.46	109.45	114.98
3	A	303	FLC	CB-CA-CAC	-3.35	109.62	114.98
3	D	305	FLC	CB-CA-CAC	-3.15	109.94	114.98
3	A	303	FLC	CB-CG-CGC	-2.41	111.13	114.98

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	305	FLC	CAC-CA-CB-CBC
3	D	305	FLC	CAC-CA-CB-CG
3	D	305	FLC	CAC-CA-CB-OHB
3	B	304	FLC	CAC-CA-CB-CG
3	E	302	FLC	CAC-CA-CB-CBC
3	E	302	FLC	OHB-CB-CG-CGC
3	B	304	FLC	CAC-CA-CB-OHB
3	E	302	FLC	CAC-CA-CB-OHB

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	305	FLC	2	0
3	B	304	FLC	1	0
3	C	303	FLC	2	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, 95th 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 ²)	Q<0.9
1	A	197/293 (67%)	0.01	2 (1%) 82 80	37, 55, 84, 109	0
1	B	197/293 (67%)	-0.07	1 (0%) 91 89	39, 52, 85, 107	0
1	C	197/293 (67%)	0.16	8 (4%) 37 36	45, 62, 94, 117	0
1	D	193/293 (65%)	0.66	27 (13%) 2 2	50, 74, 121, 152	0
1	E	179/293 (61%)	0.79	36 (20%) 1 0	46, 80, 148, 185	0
All	All	963/1465 (65%)	0.30	74 (7%) 13 12	37, 62, 117, 185	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	253	THR	6.2
1	D	153	LYS	5.8
1	D	152	TRP	4.8
1	E	174	ILE	4.7
1	E	199	HIS	4.6
1	E	173	CYS	4.6
1	E	208	SER	4.6
1	D	102	GLY	4.4
1	E	175	ASP	4.3
1	E	258	ILE	4.2
1	E	169	THR	4.2
1	E	250	LEU	4.0
1	D	273	LEU	3.9
1	E	207	THR	3.9
1	D	118	PRO	3.9
1	E	212	THR	3.7
1	E	254	LYS	3.7
1	A	217[A]	GLN	3.6
1	C	220	THR	3.5
1	D	139	ASP	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	267	TYR	3.5
1	D	103	GLN	3.5
1	E	251	LEU	3.4
1	D	272	GLU	3.3
1	D	137	TYR	3.3
1	E	172	SER	3.2
1	D	112	THR	3.2
1	C	221	CYS	3.1
1	D	116	ARG	3.0
1	E	255	ASP	3.0
1	E	176	ASP	3.0
1	E	103	GLN	2.8
1	E	100	ILE	2.8
1	E	171	ILE	2.7
1	E	177	ILE	2.7
1	E	184	PHE	2.7
1	D	99	SER	2.7
1	C	137	TYR	2.7
1	D	271	PHE	2.6
1	E	102	GLY	2.6
1	D	254	LYS	2.6
1	E	256	HIS	2.6
1	B	274	LYS	2.6
1	D	106	LEU	2.6
1	E	220	THR	2.6
1	D	105	TRP	2.6
1	E	99	SER	2.5
1	C	215	VAL	2.5
1	E	246	ASN	2.5
1	D	266	GLY	2.5
1	D	101	ILE	2.5
1	E	274	LYS	2.5
1	C	181	ASP	2.4
1	E	247	LYS	2.4
1	D	181	ASP	2.4
1	D	117	TYR	2.4
1	D	274	LYS	2.3
1	C	224	MET	2.3
1	D	270	ALA	2.3
1	E	217	GLN	2.3
1	E	257	PRO	2.3
1	E	170	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	E	206	LYS	2.3
1	C	112	THR	2.2
1	E	219	GLU	2.2
1	A	106	LEU	2.2
1	D	98	ALA	2.1
1	E	218	ILE	2.1
1	D	93	LEU	2.1
1	C	179	HIS	2.1
1	D	135	SER	2.1
1	D	268	GLU	2.0
1	E	252	ASP	2.0
1	E	104	HIS	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 ⓘ

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, 95th 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 ²)	Q<0.9
2	NA	E	301	1/1	0.79	0.42	85,85,85,85	0
3	FLC	D	305	13/13	0.85	0.22	67,76,97,97	0
3	FLC	E	302	13/13	0.86	0.22	85,94,115,122	0
2	NA	D	302	1/1	0.88	0.12	84,84,84,84	0
3	FLC	B	304	13/13	0.90	0.22	45,54,75,75	0
2	NA	A	302	1/1	0.91	0.18	66,66,66,66	0
2	NA	D	301	1/1	0.92	0.24	63,63,63,63	0
2	NA	B	302	1/1	0.93	0.20	54,54,54,54	0
2	NA	D	304	1/1	0.93	0.75	93,93,93,93	0
2	NA	C	302	1/1	0.93	0.74	78,78,78,78	0
2	NA	D	303	1/1	0.94	0.17	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NA	A	301	1/1	0.94	0.19	55,55,55,55	0
3	FLC	C	303	13/13	0.95	0.17	47,58,70,70	0
2	NA	C	301	1/1	0.96	0.21	53,53,53,53	0
3	FLC	A	303	13/13	0.96	0.17	42,48,60,60	0
2	NA	B	303	1/1	0.98	0.07	58,58,58,58	0
2	NA	B	301	1/1	0.98	0.11	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.