Full wwPDB X-ray Structure Validation Report ⓘ

Oct 15, 2023 – 12:32 AM EDT

PDB ID	:	7LOY
Title	:	Dihydrodipicolinate synthase with pyruvate from Candidatus Liberibacter solanacearum
Authors	:	Gilkes, J.M.; Frampton, R.A.; Board, A.; Sheen, C.R.; Smith, G.R.; Dobson, R.C.J.
Deposited on	:	2021-02-11
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 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:

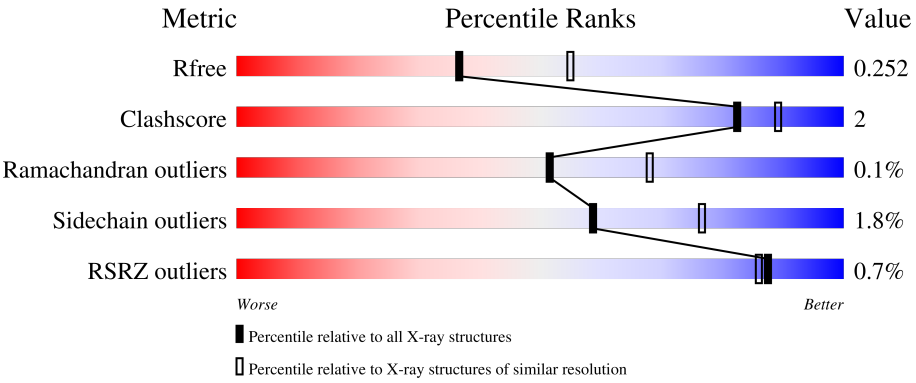
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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 of 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 <=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	295	93% 7%
1	B	295	% 92% 8%
1	C	295	92% 8%
1	D	295	92% 7%
1	E	295	2% 89% 11%

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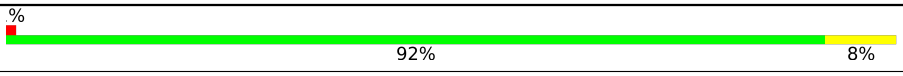
Mol	Chain	Length	Quality of chain
1	F	295	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 13864 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 4-hydroxy-tetrahydrodipicolinate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	S	0	0	0
			2236	1408	377	439	12			
1	B	295	Total	C	N	O	S	0	0	0
			2236	1408	377	439	12			
1	C	295	Total	C	N	O	S	0	0	0
			2236	1408	377	439	12			
1	D	295	Total	C	N	O	S	0	0	0
			2236	1408	377	439	12			
1	E	295	Total	C	N	O	S	0	0	0
			2236	1408	377	439	12			
1	F	295	Total	C	N	O	S	0	0	0
			2236	1408	377	439	12			

- Molecule 2 is water.

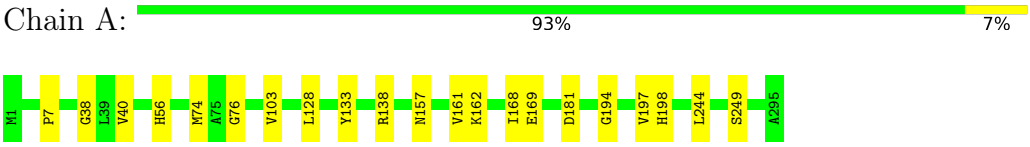
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	125	Total	O	0	0
			125	125		
2	B	108	Total	O	0	0
			108	108		
2	C	55	Total	O	0	0
			55	55		
2	D	64	Total	O	0	0
			64	64		
2	E	47	Total	O	0	0
			47	47		
2	F	49	Total	O	0	0
			49	49		

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.

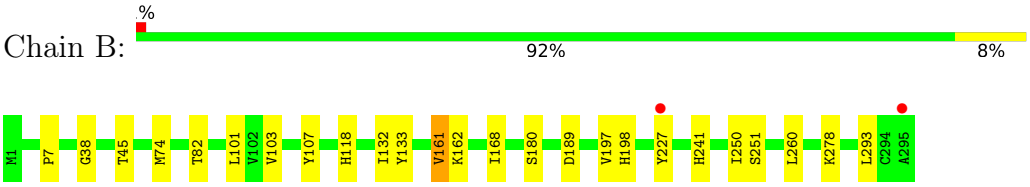
• Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain A:



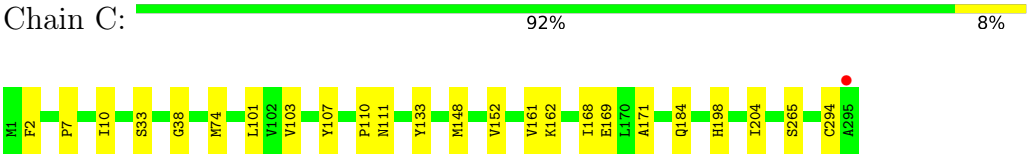
• Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain B:



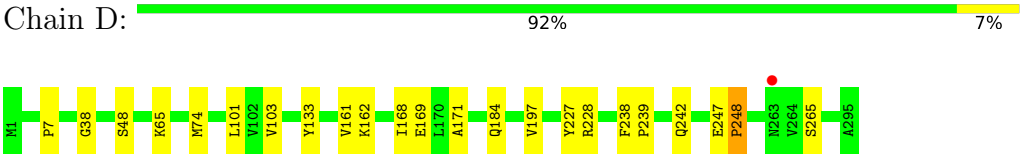
• Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain C:



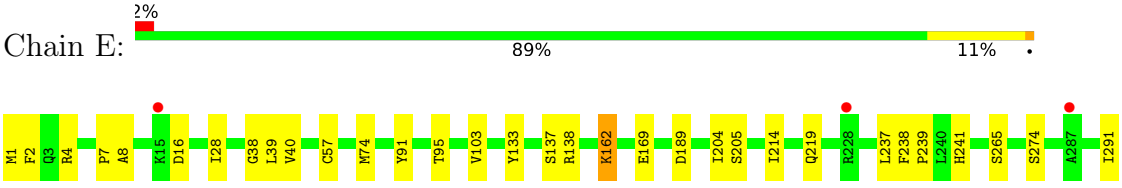
• Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain D:



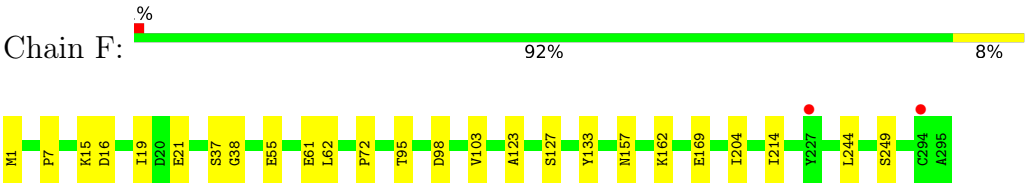
• Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain E:



• Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	101.78Å 133.58Å 155.99Å 90.00° 100.55° 90.00°	Depositor
Resolution (Å)	46.27 – 2.40 46.27 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.27-2.40) 99.9 (46.27-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.30 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.201 , 0.252 0.204 , 0.252	Depositor DCC
R_{free} test set	4050 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	33.8	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 28.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	13864	wwPDB-VP
Average B, all atoms (Å^2)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.70	0/2260	0.82	0/3066
1	B	0.68	0/2260	0.80	0/3066
1	C	0.69	0/2260	0.79	0/3066
1	D	0.70	0/2260	0.81	0/3066
1	E	0.70	0/2260	0.79	0/3066
1	F	0.70	0/2260	0.79	0/3066
All	All	0.69	0/13560	0.80	0/18396

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	A	0	2
1	B	0	1
1	C	0	4
1	D	0	1
1	E	0	2
1	F	0	1
All	All	0	11

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	161	VAL	Peptide,Mainchain

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Mol	Chain	Res	Type	Group
1	B	161	VAL	Mainchain
1	C	110	PRO	Peptide
1	C	161	VAL	Peptide
1	C	204	ILE	Peptide
1	C	294	CYS	Peptide
1	D	161	VAL	Peptide
1	E	162	KPI	Mainchain
1	E	204	ILE	Peptide
1	F	204	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	2236	0	2220	12	0
1	B	2236	0	2221	12	0
1	C	2236	0	2219	8	0
1	D	2236	0	2221	10	0
1	E	2236	0	2220	14	0
1	F	2236	0	2221	12	0
2	A	125	0	0	2	0
2	B	108	0	0	0	0
2	C	55	0	0	0	0
2	D	64	0	0	0	0
2	E	47	0	0	0	0
2	F	49	0	0	1	0
All	All	13864	0	13322	66	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 2.

All (66) 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:F:1:MET:N	2:F:301:HOH:O	2.04	0.89
1:D:74:MET:CE	1:D:101:LEU:HD13	2.13	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:74:MET:HE2	1:D:101:LEU:HD13	1.67	0.76
1:E:4:ARG:HA	1:E:219:GLN:HE21	1.57	0.69
1:B:168:ILE:HD12	1:B:198:HIS:CD2	2.29	0.68
1:B:74:MET:CE	1:B:101:LEU:HD13	2.23	0.68
1:F:123:ALA:O	1:F:157:ASN:ND2	2.31	0.62
1:E:103:VAL:HA	1:E:133:TYR:HB3	1.82	0.62
1:C:168:ILE:HD12	1:C:198:HIS:CD2	2.35	0.61
1:A:181:ASP:HB2	2:A:322:HOH:O	2.02	0.59
1:D:171:ALA:HA	1:D:184:GLN:HE22	1.68	0.58
1:A:56:HIS:HD2	2:A:366:HOH:O	1.86	0.57
1:B:197:VAL:HG12	1:B:227:TYR:CE1	2.39	0.57
1:C:103:VAL:HA	1:C:133:TYR:HB3	1.86	0.57
1:E:7:PRO:HD2	1:E:38:GLY:O	2.06	0.55
1:B:82:THR:OG1	1:B:118:HIS:HD2	1.89	0.55
1:B:7:PRO:HD2	1:B:38:GLY:O	2.07	0.55
1:E:291:ILE:HG22	1:E:293:LEU:HD23	1.89	0.54
1:C:171:ALA:HA	1:C:184:GLN:HE22	1.71	0.54
1:F:61:GLU:HA	1:F:95:THR:HG21	1.89	0.54
1:A:103:VAL:HA	1:A:133:TYR:HB3	1.91	0.53
1:F:103:VAL:HA	1:F:133:TYR:HB3	1.91	0.52
1:F:244:LEU:O	1:F:249:SER:HA	2.10	0.52
1:C:7:PRO:HD2	1:C:38:GLY:O	2.10	0.52
1:D:103:VAL:HA	1:D:133:TYR:HB3	1.91	0.52
1:E:57:CYS:HB3	1:E:91:TYR:CE2	2.45	0.51
1:B:103:VAL:HA	1:B:133:TYR:HB3	1.94	0.50
1:D:238:PHE:HB3	1:D:239:PRO:HD3	1.92	0.50
1:E:189:ASP:HB3	1:E:241:HIS:CE1	2.46	0.50
1:C:107:TYR:CD1	1:E:138:ARG:HB3	2.47	0.50
1:A:56:HIS:HE1	1:A:76:GLY:O	1.94	0.50
1:F:7:PRO:HD2	1:F:38:GLY:O	2.12	0.49
1:A:244:LEU:O	1:A:249:SER:HA	2.13	0.49
1:C:2:PHE:CZ	1:C:74:MET:HB2	2.49	0.48
1:F:95:THR:HG22	1:F:95:THR:O	2.14	0.48
1:E:189:ASP:OD1	1:E:205:SER:OG	2.16	0.48
1:F:1:MET:CE	1:F:98:ASP:HB3	2.44	0.48
1:F:214:ILE:H	1:F:214:ILE:HD12	1.79	0.47
1:E:238:PHE:HB3	1:E:239:PRO:HD3	1.97	0.46
1:D:197:VAL:HG12	1:D:227:TYR:CE1	2.51	0.45
1:D:7:PRO:HD2	1:D:38:GLY:O	2.17	0.45
1:B:189:ASP:HB3	1:B:241:HIS:CD2	2.52	0.45
1:E:28:ILE:HG23	1:E:39:LEU:HD11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:291:ILE:CG2	1:E:293:LEU:HD23	2.46	0.44
1:C:148:MET:O	1:C:152:VAL:HG23	2.16	0.44
1:B:45:THR:HA	1:B:250:ILE:HD11	1.99	0.44
1:E:214:ILE:HG23	1:E:237:LEU:HD21	2.00	0.44
1:A:194:GLY:O	1:A:197:VAL:HG12	2.18	0.43
1:A:128:LEU:O	1:A:157:ASN:OD1	2.35	0.43
1:A:56:HIS:CE1	1:A:76:GLY:O	2.71	0.43
1:A:168:ILE:HD12	1:A:198:HIS:CD2	2.53	0.43
1:D:228:ARG:NE	1:D:228:ARG:HA	2.34	0.42
1:F:21:GLU:HB3	1:F:62:LEU:HD21	2.01	0.42
1:B:132:ILE:O	1:B:161:VAL:HA	2.19	0.42
1:C:101:LEU:HD11	1:C:133:TYR:HB2	2.02	0.42
1:F:19:ILE:HD11	1:F:55:GLU:HB3	2.01	0.42
1:F:37:SER:O	1:F:72:PRO:HD2	2.20	0.41
1:A:7:PRO:HD2	1:A:38:GLY:O	2.19	0.41
1:B:260:LEU:HD23	1:B:293:LEU:HD13	2.02	0.41
1:B:74:MET:HE2	1:B:101:LEU:HD13	2.03	0.41
1:E:2:PHE:CZ	1:E:74:MET:HB2	2.56	0.41
1:A:40:VAL:HG22	1:A:74:MET:HB3	2.02	0.41
1:A:138:ARG:HB3	1:B:107:TYR:CD1	2.56	0.41
1:D:247:GLU:HB3	1:D:248:PRO:HD2	2.02	0.41
1:D:238:PHE:CE2	1:D:242:GLN:HG3	2.56	0.40
1:E:8:ALA:HA	1:E:40:VAL: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	292/295 (99%)	282 (97%)	10 (3%)	0	100	100
1	B	292/295 (99%)	283 (97%)	9 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	C	292/295 (99%)	284 (97%)	7 (2%)	1 (0%)	41 55
1	D	292/295 (99%)	278 (95%)	14 (5%)	0	100 100
1	E	292/295 (99%)	279 (96%)	13 (4%)	0	100 100
1	F	292/295 (99%)	280 (96%)	12 (4%)	0	100 100
All	All	1752/1770 (99%)	1686 (96%)	65 (4%)	1 (0%)	51 68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	111	ASN

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	243/243 (100%)	242 (100%)	1 (0%)	91 96
1	B	243/243 (100%)	240 (99%)	3 (1%)	71 85
1	C	243/243 (100%)	239 (98%)	4 (2%)	62 79
1	D	243/243 (100%)	237 (98%)	6 (2%)	47 67
1	E	243/243 (100%)	235 (97%)	8 (3%)	38 57
1	F	243/243 (100%)	239 (98%)	4 (2%)	62 79
All	All	1458/1458 (100%)	1432 (98%)	26 (2%)	59 76

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

Mol	Chain	Res	Type
1	A	169	GLU
1	B	180	SER
1	B	251	SER
1	B	278	LYS
1	C	10	ILE
1	C	33	SER

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Mol	Chain	Res	Type
1	C	169	GLU
1	C	265	SER
1	D	48	SER
1	D	65	LYS
1	D	168	ILE
1	D	169	GLU
1	D	248	PRO
1	D	265	SER
1	E	1	MET
1	E	16	ASP
1	E	95	THR
1	E	137	SER
1	E	169	GLU
1	E	265	SER
1	E	274	SER
1	E	293	LEU
1	F	15	LYS
1	F	16	ASP
1	F	127	SER
1	F	169	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	HIS
1	B	118	HIS
1	B	135	ASN
1	B	229	GLN
1	B	241	HIS
1	C	135	ASN
1	C	174	GLN
1	C	184	GLN
1	C	242	GLN
1	D	27	HIS
1	D	135	ASN
1	D	174	GLN
1	D	184	GLN
1	E	27	HIS
1	E	196	ASN
1	E	219	GLN
1	E	229	GLN
1	F	27	HIS

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Mol	Chain	Res	Type
1	F	229	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

6 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	KPI	B	162	1	11,13,14	1.12	1 (9%)	10,15,17	2.18	6 (60%)
1	KPI	D	162	1	11,13,14	1.08	0	10,15,17	3.10	7 (70%)
1	KPI	E	162	1	11,13,14	1.41	1 (9%)	10,15,17	2.49	3 (30%)
1	KPI	F	162	1	11,13,14	1.32	2 (18%)	10,15,17	2.11	2 (20%)
1	KPI	C	162	1	11,13,14	1.20	1 (9%)	10,15,17	2.45	3 (30%)
1	KPI	A	162	1	11,13,14	1.34	1 (9%)	10,15,17	1.85	1 (10%)

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
1	KPI	B	162	1	-	0/13/14/16	-
1	KPI	D	162	1	-	8/13/14/16	-
1	KPI	E	162	1	-	0/13/14/16	-
1	KPI	F	162	1	-	0/13/14/16	-
1	KPI	C	162	1	-	1/13/14/16	-
1	KPI	A	162	1	-	1/13/14/16	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	162	KPI	CX2-CX1	-3.68	1.45	1.49
1	A	162	KPI	CX2-CX1	-3.24	1.45	1.49
1	F	162	KPI	CX2-CX1	-2.82	1.46	1.49
1	C	162	KPI	O-C	2.42	1.29	1.19
1	B	162	KPI	O-C	2.13	1.28	1.19
1	F	162	KPI	O-C	2.02	1.28	1.19

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	162	KPI	C1-CX1-CX2	6.66	124.64	118.17
1	C	162	KPI	C1-CX1-CX2	6.05	124.05	118.17
1	F	162	KPI	C1-CX1-CX2	5.43	123.44	118.17
1	D	162	KPI	CE-NZ-CX1	5.15	135.73	121.70
1	A	162	KPI	C1-CX1-CX2	4.98	123.00	118.17
1	D	162	KPI	CX2-CX1-NZ	4.86	126.83	114.98
1	D	162	KPI	C1-CX1-NZ	-3.95	112.78	123.11
1	B	162	KPI	C1-CX1-CX2	3.89	121.94	118.17
1	C	162	KPI	CE-NZ-CX1	3.31	130.71	121.70
1	D	162	KPI	O1-CX2-CX1	2.75	122.33	116.35
1	D	162	KPI	O2-CX2-CX1	-2.68	117.95	121.38
1	E	162	KPI	CD-CE-NZ	-2.68	105.79	110.66
1	B	162	KPI	CE-NZ-CX1	2.56	128.68	121.70
1	D	162	KPI	CD-CE-NZ	-2.39	106.31	110.66
1	D	162	KPI	C1-CX1-CX2	2.29	120.39	118.17
1	C	162	KPI	O2-CX2-CX1	-2.21	118.55	121.38
1	B	162	KPI	CX2-CX1-NZ	2.19	120.31	114.98
1	B	162	KPI	O1-CX2-CX1	2.18	121.09	116.35
1	B	162	KPI	CD-CE-NZ	-2.07	106.90	110.66
1	B	162	KPI	C1-CX1-NZ	-2.06	117.72	123.11
1	F	162	KPI	CE-NZ-CX1	2.02	127.20	121.70
1	E	162	KPI	CE-NZ-CX1	2.01	127.17	121.70

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	162	KPI	N-CA-CB-CG
1	D	162	KPI	C-CA-CB-CG
1	D	162	KPI	O-C-CA-CB
1	D	162	KPI	CG-CD-CE-NZ

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Mol	Chain	Res	Type	Atoms
1	D	162	KPI	CA-CB-CG-CD
1	D	162	KPI	C1-CX1-NZ-CE
1	D	162	KPI	CE-CD-CG-CB
1	D	162	KPI	CX2-CX1-NZ-CE
1	A	162	KPI	CG-CD-CE-NZ
1	C	162	KPI	CG-CD-CE-NZ

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)

There are no ligands in this entry.

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^{th} 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	294/295 (99%)	-0.42	0 100 100	19, 27, 42, 64	0
1	B	294/295 (99%)	-0.36	2 (0%) 87 86	19, 29, 46, 65	0
1	C	294/295 (99%)	-0.34	1 (0%) 94 93	25, 37, 54, 74	0
1	D	294/295 (99%)	-0.30	1 (0%) 94 93	25, 39, 57, 77	0
1	E	294/295 (99%)	-0.12	6 (2%) 65 63	32, 44, 60, 111	0
1	F	294/295 (99%)	-0.07	2 (0%) 87 86	31, 46, 64, 81	0
All	All	1764/1770 (99%)	-0.27	12 (0%) 87 86	19, 38, 58, 111	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	294	CYS	5.5
1	E	295	ALA	3.9
1	F	227	TYR	3.4
1	B	295	ALA	3.4
1	E	293	LEU	3.4
1	E	228	ARG	2.8
1	C	295	ALA	2.5
1	E	15	LYS	2.4
1	E	287	ALA	2.4
1	F	294	CYS	2.2
1	D	263	ASN	2.2
1	B	227	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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^{th} 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
1	KPI	C	162	14/15	0.94	0.14	30,32,40,40	0
1	KPI	F	162	14/15	0.94	0.17	39,41,48,49	0
1	KPI	E	162	14/15	0.96	0.13	33,35,41,43	0
1	KPI	B	162	14/15	0.97	0.16	19,22,24,25	0
1	KPI	D	162	14/15	0.97	0.13	24,30,39,39	0
1	KPI	A	162	14/15	0.98	0.13	20,22,33,36	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.