



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 01:17 PM UTC

PDB ID : 8GEK / pdb_00008gek
Title : Dihydropicolinate 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 : 2023-03-06
Resolution : 1.93 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

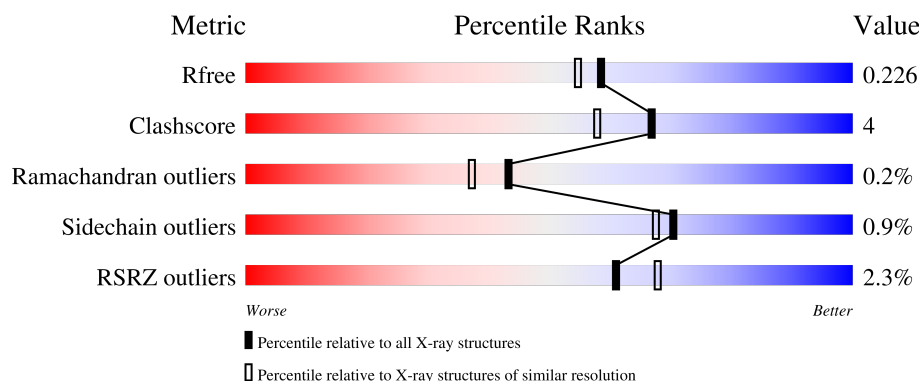
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.93 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}	180053	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (1.94-1.94)

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 $\leq 5\%$. 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	296	0% 94% 6%
1	B	296	2% 93% 6%
1	C	296	2% 91% 8%
1	D	296	3% 89% 11%
1	E	296	3% 90% 10%

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Mol	Chain	Length	Quality of chain
1	F	296	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: a small red segment at the beginning labeled '2%', a large green segment in the middle labeled '88%', and a small yellow segment at the end labeled '12%'.

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 27861 atoms, of which 13403 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	296	Total	C	H	N	O	S	0	2	0
			4497	1419	2243	379	443	13			
1	B	296	Total	C	H	N	O	S	0	0	0
			4476	1414	2230	378	442	12			
1	C	296	Total	C	H	N	O	S	0	1	0
			4490	1418	2239	378	442	13			
1	D	296	Total	C	H	N	O	S	0	0	0
			4476	1414	2230	378	442	12			
1	E	296	Total	C	H	N	O	S	0	0	0
			4476	1414	2230	378	442	12			
1	F	296	Total	C	H	N	O	S	0	0	0
			4477	1414	2231	378	442	12			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	255	Total	O	0	0
			255	255		
2	B	244	Total	O	0	0
			244	244		
2	C	132	Total	O	0	0
			132	132		
2	D	135	Total	O	0	0
			135	135		
2	E	97	Total	O	0	0
			97	97		
2	F	106	Total	O	0	0
			106	106		

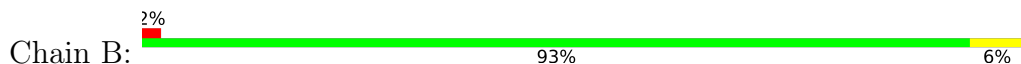
3 Residue-property plots

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



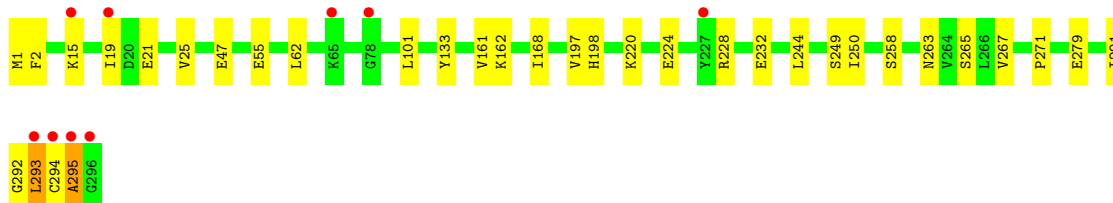
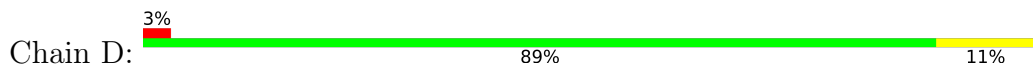
- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase



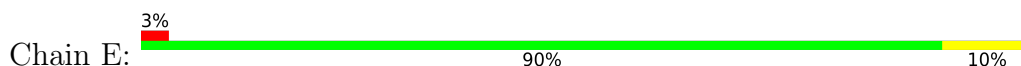
- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

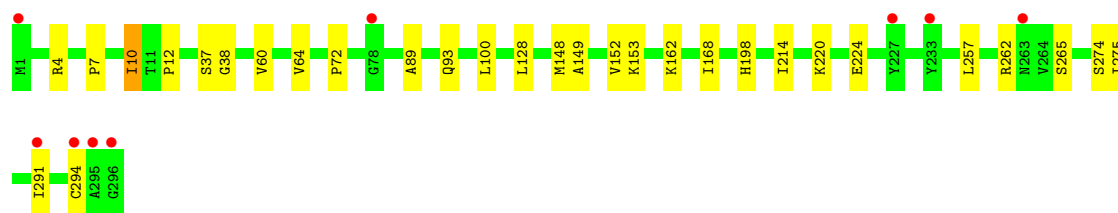


- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase

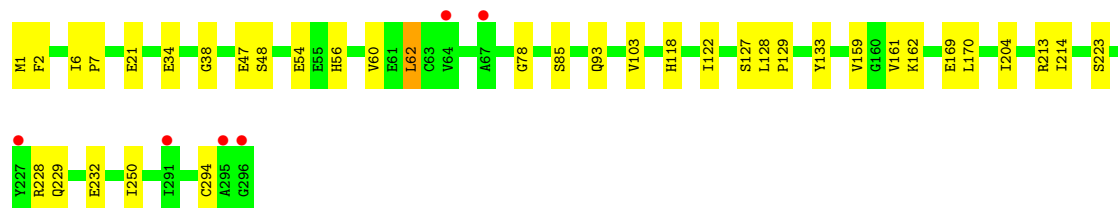
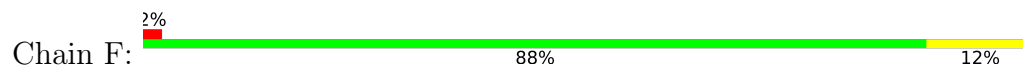


- Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase





● Molecule 1: 4-hydroxy-tetrahydrodipicolinate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	101.11Å 132.92Å 154.90Å 90.00° 99.79° 90.00°	Depositor
Resolution (Å)	45.81 – 1.93 45.81 – 1.93	Depositor EDS
% Data completeness (in resolution range)	99.5 (45.81-1.93) 99.9 (45.81-1.93)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.08 (at 1.92Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.185 , 0.225 0.186 , 0.226	Depositor DCC
R_{free} test set	4550 reflections (2.99%)	wwPDB-VP
Wilson B-factor (Å ²)	29.7	Xtriage
Anisotropy	0.197	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 36.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	27861	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% 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

5.1 Standard geometry

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

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	0.39	0/2283	0.58	0/3097
1	B	0.40	0/2263	0.58	0/3071
1	C	0.33	1/2271 (0.0%)	0.51	0/3081
1	D	0.33	0/2263	0.54	0/3071
1	E	0.28	0/2263	0.52	1/3071 (0.0%)
1	F	0.29	0/2263	0.51	0/3071
All	All	0.34	1/13606 (0.0%)	0.54	1/18462 (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	B	0	2
1	C	0	2
1	D	0	1
1	F	0	1
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	16	ASP	CG-OD1	-5.69	1.14	1.25

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	4	ARG	CB-CA-C	5.62	124.21	116.34

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	161	VAL	Mainchain,Peptide
1	C	204	ILE	Peptide
1	C	294	CYS	Peptide
1	D	161	VAL	Peptide
1	F	161	VAL	Peptide

5.2 Too-close contacts

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	2254	2243	2213	14	0
1	B	2246	2230	2211	15	0
1	C	2251	2239	2220	18	0
1	D	2246	2230	2211	21	0
1	E	2246	2230	2211	15	0
1	F	2246	2231	2211	19	0
2	A	255	0	0	6	0
2	B	244	0	0	3	0
2	C	132	0	0	3	0
2	D	135	0	0	1	0
2	E	97	0	0	0	0
2	F	106	0	0	1	0
All	All	14458	13403	13277	99	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 4.

All (99) 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:C:295:ALA:HB1	2:C:415:HOH:O	1.54	1.07
1:F:294:CYS:SG	2:F:394:HOH:O	2.21	0.98
1:D:292:GLY:O	1:D:294:CYS:N	1.99	0.95
1:D:47:GLU:HG2	1:D:250:ILE:HD13	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:220:LYS:HE2	1:E:224:GLU:OE2	1.86	0.76
1:C:54:GLU:OE1	1:C:54:GLU:N	2.17	0.73
1:A:220:LYS:NZ	2:A:301:HOH:O	2.20	0.73
1:B:214:ILE:HD12	2:B:491:HOH:O	1.88	0.72
1:D:15:LYS:HD2	1:D:15:LYS:H	1.56	0.70
1:B:292:GLY:O	1:B:294:CYS:N	2.27	0.68
1:D:228:ARG:NH1	1:D:232:GLU:OE1	2.33	0.62
1:F:54:GLU:OE1	1:F:54:GLU:N	2.27	0.62
1:C:103:VAL:HA	1:C:133:TYR:HB3	1.84	0.59
1:A:228:ARG:HD2	1:A:228:ARG:C	2.27	0.59
1:D:265:SER:OG	1:D:267:VAL:HG23	2.04	0.58
1:F:103:VAL:HA	1:F:133:TYR:HB3	1.86	0.58
1:A:1[B]:MET:HG2	2:A:457:HOH:O	2.03	0.57
1:E:149:ALA:O	1:E:153:LYS:HD3	2.05	0.56
1:F:21:GLU:HB3	1:F:62:LEU:HD11	1.88	0.55
1:C:227:TYR:CD1	1:D:197:VAL:HG21	2.41	0.55
1:F:1:MET:HE2	1:F:2:PHE:CE2	2.42	0.55
1:B:291:ILE:HD12	1:B:293:LEU:HD22	1.89	0.53
1:E:168:ILE:C	1:E:168:ILE:HD12	2.35	0.52
1:D:294:CYS:O	1:D:295:ALA:HB3	2.09	0.52
1:C:142:GLU:OE1	1:C:167:ARG:NH2	2.42	0.52
1:B:78:GLY:HA3	2:B:418:HOH:O	2.08	0.51
1:D:101:LEU:HD11	1:D:133:TYR:HB2	1.92	0.51
1:B:250:ILE:HD11	1:B:272:MET:HG3	1.93	0.51
1:A:213:ARG:NH1	2:A:308:HOH:O	2.40	0.51
1:A:294:CYS:HB2	2:A:305:HOH:O	2.11	0.50
1:F:7:PRO:HD2	1:F:38:GLY:O	2.12	0.50
1:E:148:MET:O	1:E:152:VAL:HG23	2.11	0.50
1:E:93:GLN:HG3	1:E:128:LEU:HD13	1.93	0.49
1:B:291:ILE:CD1	1:B:293:LEU:HD22	2.42	0.49
1:F:47:GLU:HG3	1:F:250:ILE:HD13	1.94	0.49
1:E:7:PRO:HD2	1:E:38:GLY:O	2.13	0.49
1:B:19:ILE:HD11	1:B:55:GLU:HB3	1.93	0.49
1:C:168:ILE:HD12	1:C:198:HIS:CD2	2.48	0.49
1:D:291:ILE:CD1	1:D:293:LEU:HD12	2.43	0.48
1:A:294:CYS:SG	2:C:415:HOH:O	2.19	0.48
1:C:168:ILE:HD12	1:C:198:HIS:NE2	2.28	0.48
1:C:265:SER:OG	1:C:267:VAL:HG23	2.12	0.48
1:D:55:GLU:OE1	2:D:301:HOH:O	2.20	0.48
1:F:34:GLU:OE1	1:F:213:ARG:NH2	2.47	0.48
1:B:103:VAL:HA	1:B:133:TYR:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:54:GLU:H	1:C:54:GLU:CD	2.15	0.47
1:B:295:ALA:HB3	2:B:357:HOH:O	2.14	0.47
1:A:66:THR:O	1:A:70:ARG:NH2	2.46	0.46
1:B:291:ILE:O	1:B:293:LEU:N	2.38	0.46
1:F:93:GLN:HA	1:F:128:LEU:HD11	1.98	0.46
1:D:19:ILE:HD11	1:D:55:GLU:HB3	1.98	0.46
1:E:60:VAL:O	1:E:64:VAL:HG23	2.16	0.45
1:D:168:ILE:HD12	1:D:198:HIS:CD2	2.50	0.45
1:A:7:PRO:HD2	1:A:38:GLY:O	2.16	0.45
1:B:250:ILE:HD11	1:B:272:MET:CG	2.46	0.45
1:C:238:PHE:HB3	1:C:239:PRO:HD3	1.99	0.45
1:D:220:LYS:NZ	1:D:224:GLU:OE2	2.49	0.45
1:F:56:HIS:O	1:F:60:VAL:HG23	2.16	0.44
1:A:103:VAL:HA	1:A:133:TYR:HB3	1.99	0.44
1:D:1:MET:HE3	1:D:2:PHE:CE2	2.51	0.44
1:F:169:GLU:HG3	1:F:170:LEU:N	2.33	0.44
1:C:1[A]:MET:HG3	2:C:357:HOH:O	2.18	0.44
1:A:228:ARG:HD2	1:A:228:ARG:O	2.18	0.43
1:C:54:GLU:N	1:C:54:GLU:CD	2.76	0.43
1:D:294:CYS:O	1:D:295:ALA:CB	2.66	0.43
1:C:292:GLY:C	1:C:293:LEU:O	2.61	0.43
1:D:263:ASN:O	1:D:263:ASN:CG	2.62	0.43
1:E:10:ILE:HD12	1:E:12:PRO:HD3	2.00	0.43
1:A:65:LYS:HD3	2:A:474:HOH:O	2.19	0.43
1:D:279:GLU:OE1	1:D:279:GLU:N	2.35	0.43
1:F:129:PRO:HB3	1:F:159:VAL:HG21	2.01	0.43
1:E:257:LEU:HD22	1:E:262:ARG:HG3	1.99	0.43
1:F:228:ARG:NH1	1:F:232:GLU:OE2	2.50	0.43
1:E:89:ALA:HB1	1:E:100:LEU:CD1	2.49	0.42
1:E:168:ILE:HD13	1:E:198:HIS:NE2	2.34	0.42
1:F:78:GLY:HA3	1:F:103:VAL:HG12	2.02	0.42
1:A:153:LYS:NZ	2:A:302:HOH:O	2.25	0.42
1:B:292:GLY:C	1:B:294:CYS:N	2.78	0.42
1:C:19:ILE:HD13	1:C:59:VAL:CG2	2.50	0.42
1:E:214:ILE:CD1	1:E:291:ILE:CG2	2.97	0.42
1:F:85:SER:HB2	1:F:122:ILE:HD11	2.02	0.42
1:F:228:ARG:HG3	1:F:229:GLN:N	2.33	0.42
1:B:167:ARG:NH2	1:B:170:LEU:HD11	2.35	0.41
1:C:7:PRO:HD2	1:C:38:GLY:O	2.21	0.41
1:D:21:GLU:O	1:D:25:VAL:HG23	2.20	0.41
1:A:19:ILE:HD11	1:A:55:GLU:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:113:LYS:HE3	1:E:275:ILE:O	2.21	0.41
1:D:271:PRO:HB3	1:F:118:HIS:HB2	2.01	0.41
1:C:167:ARG:HH11	1:C:167:ARG:HG3	1.86	0.40
1:E:168:ILE:HD13	1:E:198:HIS:CE1	2.56	0.40
1:F:6:ILE:O	1:F:204:ILE:HA	2.21	0.40
1:A:211:ALA:HB1	1:A:214:ILE:HG22	2.02	0.40
1:B:292:GLY:C	1:B:294:CYS:H	2.28	0.40
1:B:194:GLY:O	1:B:197:VAL:HG12	2.20	0.40
1:C:247:GLU:O	1:C:248:PRO:C	2.63	0.40
1:D:244:LEU:O	1:D:249:SER:HA	2.21	0.40
1:D:15:LYS:HD2	1:D:15:LYS:N	2.32	0.40
1:E:37:SER:O	1:E:72:PRO:HD2	2.22	0.40
1:F:47:GLU:O	1:F:48:SER:C	2.65	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	294/296 (99%)	289 (98%)	5 (2%)	0	100	100
1	B	293/296 (99%)	285 (97%)	7 (2%)	1 (0%)	36	30
1	C	293/296 (99%)	284 (97%)	8 (3%)	1 (0%)	36	30
1	D	293/296 (99%)	284 (97%)	7 (2%)	2 (1%)	18	9
1	E	293/296 (99%)	286 (98%)	7 (2%)	0	100	100
1	F	293/296 (99%)	288 (98%)	5 (2%)	0	100	100
All	All	1759/1776 (99%)	1716 (98%)	39 (2%)	4 (0%)	43	37

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	293	LEU
1	C	293	LEU
1	D	293	LEU
1	D	295	ALA

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	245/243 (101%)	244 (100%)	1 (0%)	84	84
1	B	243/243 (100%)	242 (100%)	1 (0%)	84	84
1	C	244/243 (100%)	242 (99%)	2 (1%)	73	71
1	D	243/243 (100%)	241 (99%)	2 (1%)	73	71
1	E	243/243 (100%)	239 (98%)	4 (2%)	55	46
1	F	243/243 (100%)	239 (98%)	4 (2%)	55	46
All	All	1461/1458 (100%)	1447 (99%)	14 (1%)	70	64

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

Mol	Chain	Res	Type
1	A	65	LYS
1	B	265	SER
1	C	1[A]	MET
1	C	1[B]	MET
1	D	62	LEU
1	D	258	SER
1	E	10	ILE
1	E	265	SER
1	E	274	SER
1	E	294	CYS
1	F	62	LEU
1	F	127	SER
1	F	214	ILE
1	F	223	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	174	GLN
1	A	196	ASN
1	A	286	GLN
1	B	3	GLN
1	B	196	ASN
1	B	290	HIS
1	D	229	GLN
1	F	174	GLN
1	F	196	ASN
1	F	229	GLN
1	F	242	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	VPV	F	162	1	18,20,21	1.39	2 (11%)	13,24,26	1.58	1 (7%)
1	VPV	E	162	1	18,20,21	1.53	3 (16%)	13,24,26	0.87	0
1	VPV	D	162	1	18,20,21	1.67	2 (11%)	13,24,26	1.67	1 (7%)
1	VPV	C	162	1	18,20,21	1.46	1 (5%)	13,24,26	1.84	1 (7%)
1	VPV	B	162	1	18,20,21	1.47	3 (16%)	13,24,26	1.05	0
1	VPV	A	162	1	18,20,21	1.61	3 (16%)	13,24,26	2.44	2 (15%)

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	VPV	F	162	1	-	4/21/23/25	-
1	VPV	E	162	1	-	6/21/23/25	-
1	VPV	D	162	1	-	3/21/23/25	-
1	VPV	C	162	1	-	2/21/23/25	-
1	VPV	B	162	1	-	7/21/23/25	-
1	VPV	A	162	1	-	2/21/23/25	-

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	162	VPV	CB-CA	-4.85	1.46	1.53
1	C	162	VPV	CB-CA	-4.54	1.46	1.53
1	A	162	VPV	CB-CA	-4.47	1.46	1.53
1	E	162	VPV	CB-CA	-4.24	1.47	1.53
1	F	162	VPV	CB-CA	-3.54	1.48	1.53
1	A	162	VPV	CA-N	-3.13	1.39	1.48
1	B	162	VPV	CB-CA	-3.07	1.48	1.53
1	B	162	VPV	CA-N	-2.87	1.40	1.48
1	F	162	VPV	CA-N	-2.32	1.41	1.48
1	D	162	VPV	CA-N	-2.30	1.41	1.48
1	A	162	VPV	C1-NZ	-2.20	1.25	1.28
1	E	162	VPV	CA-N	-2.10	1.42	1.48
1	E	162	VPV	C5-C1	2.07	1.53	1.50
1	B	162	VPV	C5-C1	2.02	1.53	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	162	VPV	C8-C7-C6	-7.53	99.37	113.58
1	C	162	VPV	C8-C7-C6	-5.64	102.92	113.58
1	D	162	VPV	C8-C7-C6	-5.14	103.88	113.58
1	F	162	VPV	C8-C7-C6	-5.11	103.92	113.58
1	A	162	VPV	O10-C6-C5	-2.51	103.14	109.64

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	162	VPV	C6-C7-C8-C9
1	D	162	VPV	O-C-CA-CB
1	E	162	VPV	C5-C1-C2-O4
1	E	162	VPV	C6-C7-C8-C9
1	F	162	VPV	O-C-CA-CB
1	F	162	VPV	C6-C7-C8-C9
1	B	162	VPV	O10-C6-C7-C8
1	E	162	VPV	O10-C6-C7-C8
1	B	162	VPV	C5-C6-C7-C8
1	B	162	VPV	C1-C5-C6-O10
1	E	162	VPV	C5-C6-C7-C8
1	C	162	VPV	C7-C8-C9-O11
1	D	162	VPV	C7-C8-C9-O12
1	C	162	VPV	C7-C8-C9-O12
1	D	162	VPV	C7-C8-C9-O11
1	B	162	VPV	C7-C8-C9-O12
1	F	162	VPV	C7-C8-C9-O12
1	A	162	VPV	C7-C8-C9-O11
1	F	162	VPV	C7-C8-C9-O11
1	A	162	VPV	C7-C8-C9-O12
1	B	162	VPV	C7-C8-C9-O11
1	E	162	VPV	C7-C8-C9-O11
1	E	162	VPV	C7-C8-C9-O12
1	B	162	VPV	C1-C5-C6-C7

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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 ⓘ

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	295/296 (99%)	-0.24	4 (1%)	73 79	15, 31, 45, 70	1 (0%)
1	B	295/296 (99%)	-0.23	5 (1%)	69 75	20, 30, 48, 83	0
1	C	295/296 (99%)	0.14	7 (2%)	59 67	24, 41, 58, 82	1 (0%)
1	D	295/296 (99%)	0.25	9 (3%)	51 57	30, 42, 62, 107	0
1	E	295/296 (99%)	0.43	9 (3%)	51 57	37, 49, 65, 100	0
1	F	295/296 (99%)	0.47	6 (2%)	65 72	32, 47, 64, 96	0
All	All	1770/1776 (99%)	0.14	40 (2%)	61 68	15, 41, 61, 107	2 (0%)

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	293	LEU	6.7
1	C	1[A]	MET	6.1
1	D	293	LEU	5.5
1	C	293	LEU	5.2
1	B	294	CYS	5.1
1	D	296	GLY	4.6
1	C	294	CYS	4.1
1	A	1[A]	MET	3.9
1	D	15	LYS	3.5
1	F	296	GLY	3.5
1	D	294	CYS	3.4
1	A	295	ALA	3.4
1	E	295	ALA	3.3
1	C	296	GLY	3.1
1	E	1	MET	3.1
1	E	78	GLY	3.1
1	F	227	TYR	2.9
1	B	296	GLY	2.8
1	E	296	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	295	ALA	2.7
1	D	78	GLY	2.7
1	F	295	ALA	2.6
1	B	227	TYR	2.6
1	A	296	GLY	2.6
1	C	227	TYR	2.6
1	E	291	ILE	2.5
1	A	228	ARG	2.5
1	E	294	CYS	2.5
1	E	227	TYR	2.4
1	F	67	ALA	2.4
1	B	263	ASN	2.3
1	D	19	ILE	2.3
1	F	64	VAL	2.3
1	E	263	ASN	2.3
1	C	295	ALA	2.2
1	D	227	TYR	2.1
1	D	65	LYS	2.1
1	E	233	TYR	2.1
1	F	291	ILE	2.0
1	C	78	GLY	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, 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
1	VPV	F	162	21/22	0.90	0.11	34,48,63,75	0
1	VPV	E	162	21/22	0.91	0.12	31,49,68,73	0
1	VPV	C	162	21/22	0.93	0.09	28,42,56,63	0
1	VPV	D	162	21/22	0.93	0.10	24,38,58,61	0
1	VPV	A	162	21/22	0.95	0.10	18,25,48,68	0
1	VPV	B	162	21/22	0.95	0.09	17,27,52,57	0

6.3 Carbohydrates ⓘ

There are no oligosaccharides 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.