



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 15, 2018 – 02:49 PM EST

PDB ID : 4E4F
Title : Crystal structure of enolase PC1_0802 (TARGET EFI-502240) from *Pectobacterium carotovorum* subsp. *carotovorum* PC1
Authors : Patskovsky, Y.; Toro, R.; Bhosle, R.; Hillerich, B.; Seidel, R.D.; Washington, E.; Scott Glenn, A.; Chowdhury, S.; Evans, B.; Hammonds, J.; Zencheck, W.D.; Imker, H.J.; Gerlt, J.A.; Almo, S.C.; Enzyme Function Initiative (EFI)
Deposited on : 2012-03-12
Resolution : 2.00 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030736
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

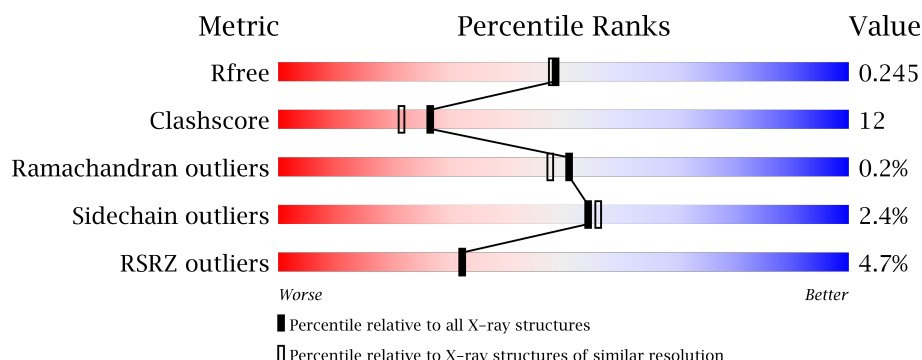
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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. 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	426	<div> <div>2%</div> <div> <div></div> <div>74%</div> <div>15%</div> <div>•</div> <div>9%</div> </div> </div>
1	B	426	<div> <div>6%</div> <div> <div></div> <div>69%</div> <div>19%</div> <div>•</div> <div>11%</div> </div> </div>
1	C	426	<div> <div>5%</div> <div> <div></div> <div>68%</div> <div>21%</div> <div>•</div> <div>11%</div> </div> </div>
1	D	426	<div> <div>4%</div> <div> <div></div> <div>69%</div> <div>20%</div> <div>•</div> <div>9%</div> </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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GOL	C	501	-	-	-	X
2	GOL	D	502	-	-	-	X
5	FMT	A	506	-	-	-	X
5	FMT	B	506	-	-	-	X
5	FMT	C	505	-	-	X	-
5	FMT	D	505	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13154 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 MANNONATE DEHYDRATASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	386	Total	C	N	O	S	0	1	0
			3092	1980	524	569	19			
1	B	381	Total	C	N	O	S	0	3	0
			3069	1966	521	563	19			
1	C	381	Total	C	N	O	S	0	1	0
			3060	1960	519	562	19			
1	D	388	Total	C	N	O	S	0	1	0
			3112	1994	527	572	19			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	EXPRESSION TAG	UNP C6D9S0
A	-20	HIS	-	EXPRESSION TAG	UNP C6D9S0
A	-19	HIS	-	EXPRESSION TAG	UNP C6D9S0
A	-18	HIS	-	EXPRESSION TAG	UNP C6D9S0
A	-17	HIS	-	EXPRESSION TAG	UNP C6D9S0
A	-16	HIS	-	EXPRESSION TAG	UNP C6D9S0
A	-15	HIS	-	EXPRESSION TAG	UNP C6D9S0
A	-14	SER	-	EXPRESSION TAG	UNP C6D9S0
A	-13	SER	-	EXPRESSION TAG	UNP C6D9S0
A	-12	GLY	-	EXPRESSION TAG	UNP C6D9S0
A	-11	VAL	-	EXPRESSION TAG	UNP C6D9S0
A	-10	ASP	-	EXPRESSION TAG	UNP C6D9S0
A	-9	LEU	-	EXPRESSION TAG	UNP C6D9S0
A	-8	GLY	-	EXPRESSION TAG	UNP C6D9S0
A	-7	THR	-	EXPRESSION TAG	UNP C6D9S0
A	-6	GLU	-	EXPRESSION TAG	UNP C6D9S0
A	-5	ASN	-	EXPRESSION TAG	UNP C6D9S0
A	-4	LEU	-	EXPRESSION TAG	UNP C6D9S0
A	-3	TYR	-	EXPRESSION TAG	UNP C6D9S0
A	-2	PHE	-	EXPRESSION TAG	UNP C6D9S0
A	-1	GLN	-	EXPRESSION TAG	UNP C6D9S0

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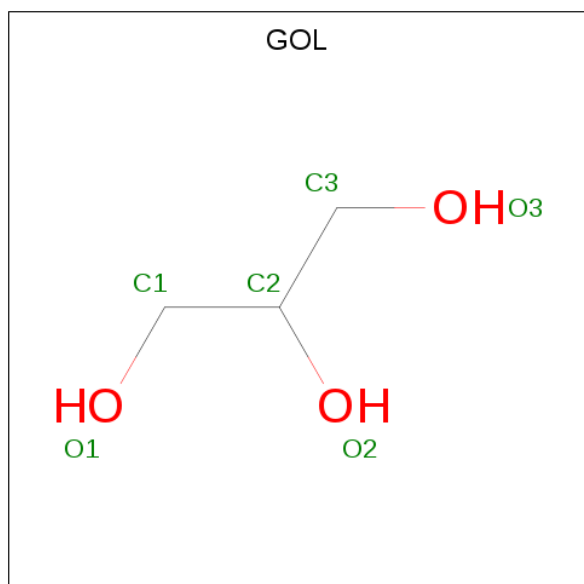
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	EXPRESSION TAG	UNP C6D9S0
B	-21	MET	-	EXPRESSION TAG	UNP C6D9S0
B	-20	HIS	-	EXPRESSION TAG	UNP C6D9S0
B	-19	HIS	-	EXPRESSION TAG	UNP C6D9S0
B	-18	HIS	-	EXPRESSION TAG	UNP C6D9S0
B	-17	HIS	-	EXPRESSION TAG	UNP C6D9S0
B	-16	HIS	-	EXPRESSION TAG	UNP C6D9S0
B	-15	HIS	-	EXPRESSION TAG	UNP C6D9S0
B	-14	SER	-	EXPRESSION TAG	UNP C6D9S0
B	-13	SER	-	EXPRESSION TAG	UNP C6D9S0
B	-12	GLY	-	EXPRESSION TAG	UNP C6D9S0
B	-11	VAL	-	EXPRESSION TAG	UNP C6D9S0
B	-10	ASP	-	EXPRESSION TAG	UNP C6D9S0
B	-9	LEU	-	EXPRESSION TAG	UNP C6D9S0
B	-8	GLY	-	EXPRESSION TAG	UNP C6D9S0
B	-7	THR	-	EXPRESSION TAG	UNP C6D9S0
B	-6	GLU	-	EXPRESSION TAG	UNP C6D9S0
B	-5	ASN	-	EXPRESSION TAG	UNP C6D9S0
B	-4	LEU	-	EXPRESSION TAG	UNP C6D9S0
B	-3	TYR	-	EXPRESSION TAG	UNP C6D9S0
B	-2	PHE	-	EXPRESSION TAG	UNP C6D9S0
B	-1	GLN	-	EXPRESSION TAG	UNP C6D9S0
B	0	SER	-	EXPRESSION TAG	UNP C6D9S0
C	-21	MET	-	EXPRESSION TAG	UNP C6D9S0
C	-20	HIS	-	EXPRESSION TAG	UNP C6D9S0
C	-19	HIS	-	EXPRESSION TAG	UNP C6D9S0
C	-18	HIS	-	EXPRESSION TAG	UNP C6D9S0
C	-17	HIS	-	EXPRESSION TAG	UNP C6D9S0
C	-16	HIS	-	EXPRESSION TAG	UNP C6D9S0
C	-15	HIS	-	EXPRESSION TAG	UNP C6D9S0
C	-14	SER	-	EXPRESSION TAG	UNP C6D9S0
C	-13	SER	-	EXPRESSION TAG	UNP C6D9S0
C	-12	GLY	-	EXPRESSION TAG	UNP C6D9S0
C	-11	VAL	-	EXPRESSION TAG	UNP C6D9S0
C	-10	ASP	-	EXPRESSION TAG	UNP C6D9S0
C	-9	LEU	-	EXPRESSION TAG	UNP C6D9S0
C	-8	GLY	-	EXPRESSION TAG	UNP C6D9S0
C	-7	THR	-	EXPRESSION TAG	UNP C6D9S0
C	-6	GLU	-	EXPRESSION TAG	UNP C6D9S0
C	-5	ASN	-	EXPRESSION TAG	UNP C6D9S0
C	-4	LEU	-	EXPRESSION TAG	UNP C6D9S0
C	-3	TYR	-	EXPRESSION TAG	UNP C6D9S0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	PHE	-	EXPRESSION TAG	UNP C6D9S0
C	-1	GLN	-	EXPRESSION TAG	UNP C6D9S0
C	0	SER	-	EXPRESSION TAG	UNP C6D9S0
D	-21	MET	-	EXPRESSION TAG	UNP C6D9S0
D	-20	HIS	-	EXPRESSION TAG	UNP C6D9S0
D	-19	HIS	-	EXPRESSION TAG	UNP C6D9S0
D	-18	HIS	-	EXPRESSION TAG	UNP C6D9S0
D	-17	HIS	-	EXPRESSION TAG	UNP C6D9S0
D	-16	HIS	-	EXPRESSION TAG	UNP C6D9S0
D	-15	HIS	-	EXPRESSION TAG	UNP C6D9S0
D	-14	SER	-	EXPRESSION TAG	UNP C6D9S0
D	-13	SER	-	EXPRESSION TAG	UNP C6D9S0
D	-12	GLY	-	EXPRESSION TAG	UNP C6D9S0
D	-11	VAL	-	EXPRESSION TAG	UNP C6D9S0
D	-10	ASP	-	EXPRESSION TAG	UNP C6D9S0
D	-9	LEU	-	EXPRESSION TAG	UNP C6D9S0
D	-8	GLY	-	EXPRESSION TAG	UNP C6D9S0
D	-7	THR	-	EXPRESSION TAG	UNP C6D9S0
D	-6	GLU	-	EXPRESSION TAG	UNP C6D9S0
D	-5	ASN	-	EXPRESSION TAG	UNP C6D9S0
D	-4	LEU	-	EXPRESSION TAG	UNP C6D9S0
D	-3	TYR	-	EXPRESSION TAG	UNP C6D9S0
D	-2	PHE	-	EXPRESSION TAG	UNP C6D9S0
D	-1	GLN	-	EXPRESSION TAG	UNP C6D9S0
D	0	SER	-	EXPRESSION TAG	UNP C6D9S0

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

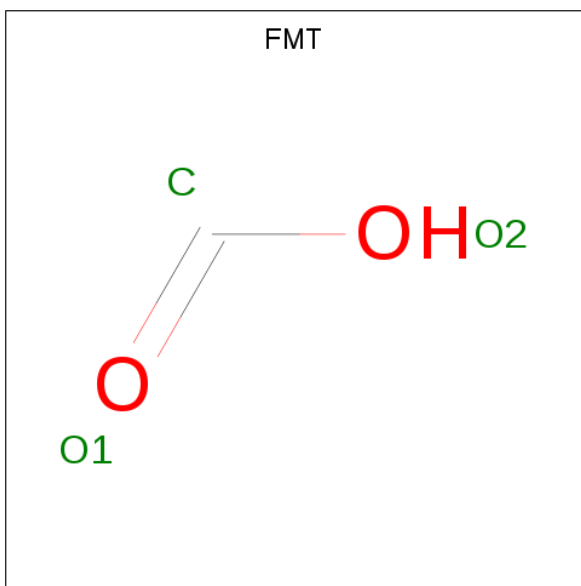
- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Cl 1 1	0	0
3	A	1	Total Cl 1 1	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Mg 1 1	0	0
4	A	1	Total Mg 1 1	0	0
4	D	1	Total Mg 1 1	0	0
4	C	1	Total Mg 1 1	0	0

- Molecule 5 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	208	Total	O	0	0
			208	208		
6	B	188	Total	O	0	1
			189	189		
6	C	173	Total	O	0	0
			173	173		
6	D	161	Total	O	0	0
			161	161		

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 ($\text{RSRZ} > 2$). 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 frequency in bits (0.00 to 0.15). The x-axis represents positions (1 to 200). The color scale indicates frequency percentages: 2% (red), 74% (green), 15% (yellow), and 9% (grey).

Position	Amino Acid	Frequency (bits)
1	W270	0.01
2	Y283	0.01
3	L284	0.01
4	R285	0.01
5	T286	0.01
6	T287	0.01
7	I288	0.01
8	T289	0.01
9	H290	0.01
10	I294	0.01
11	A304	0.01
12	V309	0.01
13	R310	0.01
14	T311	0.01
15	G312	0.01
16	S313	0.01
17	G314	0.01
18	G315	0.01
19	P316	0.01
20	L319	0.01
21	D331	0.01
22	V334	0.01
23	F337	0.01
24	Q340	0.01
25	S346	0.01
26	E347	0.01
27	Q348	0.01
28	M349	0.01
29	S356	0.01
30	K357	0.01
31	T358	0.01
32	F359	0.01
33	G367	0.01
34	G371	0.01
35	L372	0.01
36	G373	0.01
37	Y384	0.01
38	P385	0.01
39	E397	0.01
40	W402	0.01
41	M403	0.01
42	W404	0.01
43	K137	0.01
44	H138	0.01
45	R139	0.01
46	D140	0.01
47	V148	0.01
48	Q149	0.01
49	C150	0.01
50	GLY	0.01
51	VAL	0.01
52	PRQ	0.01
53	GLY	0.01
54	MET	0.01
55	GLU	0.01
56	THR	0.01
57	TVR	0.01
58	GLY	0.01
59	MET	0.01
60	ALA	0.01
61	LVS	0.01
62	GLY	0.01
63	LVS	0.01
64	GLY	0.01
65	LEU	0.01
66	ALA	0.01
67	TVR	0.01
68	E170	0.01
69	P171	0.01
70	A172	0.01
71	T173	0.01
72	K174	0.01
73	G175	0.01
74	S176	0.01
75	T185	0.01
76	Q348	0.01
77	F191	0.01
78	T192	0.01
79	P193	0.01
80	K194	0.01
81	L195	0.01
82	V199	0.01
83	E207	0.01
84	L217	0.01
85	W236	0.01
86	D239	0.01
87	P240	0.01
88	L251	0.01
89	Q254	0.01
90	E264	0.01
91	K137	0.01
92	H138	0.01
93	R139	0.01
94	D140	0.01
95	V148	0.01
96	Q149	0.01
97	C150	0.01
98	GLY	0.01
99	VAL	0.01
100	PRQ	0.01
101	GLY	0.01
102	MET	0.01
103	GLU	0.01
104	THR	0.01
105	TVR	0.01
106	GLY	0.01
107	MET	0.01
108	ALA	0.01
109	LVS	0.01
110	GLY	0.01
111	LVS	0.01
112	GLY	0.01
113	LEU	0.01
114	ALA	0.01
115	TVR	0.01
116	E170	0.01
117	P171	0.01
118	A172	0.01
119	T173	0.01
120	K174	0.01
121	G175	0.01
122	S176	0.01
123	T185	0.01
124	Q348	0.01
125	F191	0.01
126	T192	0.01
127	P193	0.01
128	K194	0.01
129	L195	0.01
130	V199	0.01
131	E207	0.01
132	L217	0.01
133	W236	0.01
134	D239	0.01
135	P240	0.01
136	L251	0.01
137	Q254	0.01
138	E264	0.01
139	K137	0.01
140	H138	

Chain B:

6% 69% 19% 11%

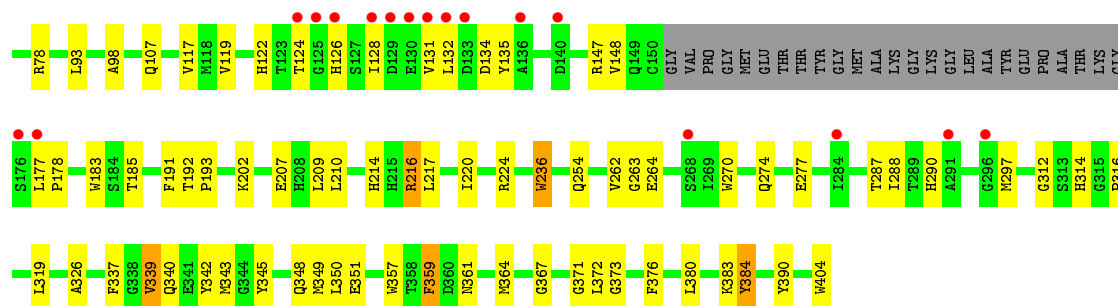
MET HIS HIS HIS HIS HIS HIS SER SER GLY GLY VAL ASP LEU THR GLU ASN LEU TYR PHE GLN S0 M1 V4 S5 A6 F9 V10 T11 C12 P13 G14 R15 T24 D25 S26 G27 L41 P42 Y46 E50 V51 C52 P53 I56 G57 R58 Y69 G73 P78

G79 P80 A101 Q107 L108 V110 G120 C121 H122 T123 T124 G125 H126 S127 I128 D129 E130 V131 L132 D133 D134 Y135 A136 K137 H138 R139 D140 Q141 I146 C150 GLY VAL PRO GLY MET GLU THR TYR GLY MET ALA LYS GLY LYS GLY LEU ALA TYR GLU PRO ALA THR LYS

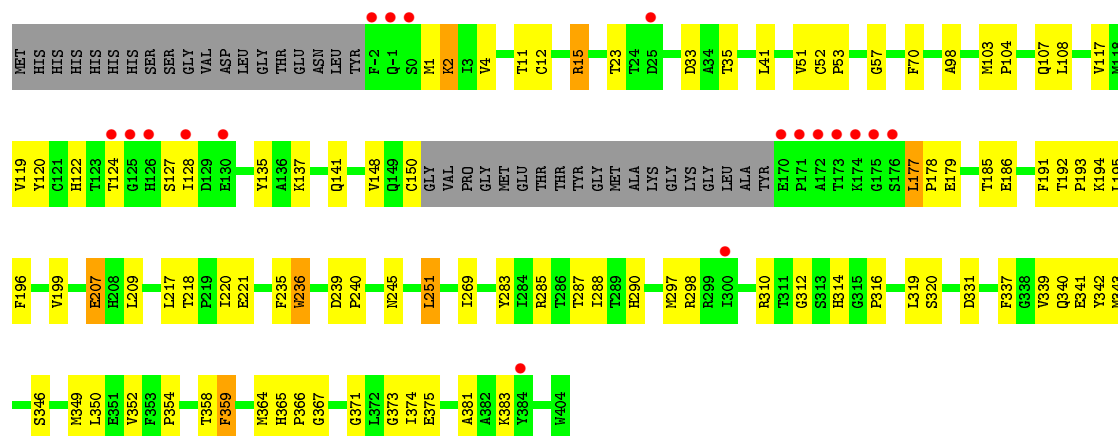
F337 G338 V339 Q340 M343 Q348 M349 F351 V352 F353 P354 H355 S356 K357 T358 F359 D360 M361 H365 P366 G367 I374 E375 F376 K379 Y384 H404

Chain C:

Position	Amino Acid	Information Content (bits)
1	MET	0.00
2	HIS	0.00
3	HIS	0.00
4	HIS	0.00
5	HIS	0.00
6	HIS	0.00
7	HIS	0.00
8	HIS	0.00
9	SER	0.00
10	SER	0.00
11	GLY	0.00
12	VAL	0.00
13	ASP	0.00
14	LEU	0.00
15	GLY	0.00
16	THR	0.00
17	GLU	0.00
18	ASN	0.00
19	LEU	0.00
20	PHE	0.00
21	Q-1	0.00
22	V4	0.00
23	S5	0.00
24	A6	0.00
25	E7	0.00
26	V8	0.00
27	T11	0.00
28	C12	0.00
29	P13	0.00
30	G14	0.00
31	R15	0.00
32	K21	0.00
33	L22	0.00
34	T23	0.00
35	G27	0.00
36	L28	0.00
37	L31	0.00
38	R39	0.00
39	P42	0.00
40	N48	0.00
41	R58	0.00
42	D59	0.00
43	A60	0.00
44	H61	0.00
45	Q62	0.00
46	I63	0.00
47	Y69	0.00
48	G73	0.00



• Molecule 1: MANNONATE DEHYDRATASE



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	204.28 Å 86.34 Å 114.46 Å 90.00° 123.07° 90.00°	Depositor
Resolution (Å)	50.00 – 2.00 39.37 – 1.99	Depositor EDS
% Data completeness (in resolution range)	99.2 (50.00-2.00) 98.7 (39.37-1.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 2.00 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.188 , 0.245 0.192 , 0.245	Depositor DCC
R_{free} test set	3334 reflections (3.08%)	DCC
Wilson B-factor (Å ²)	39.5	Xtriage
Anisotropy	0.150	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 50.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.010 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	13154	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.00% 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: GOL, FMT, MG, CL

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	0/3184	0.54	0/4326
1	B	0.39	0/3166	0.54	0/4300
1	C	0.37	0/3151	0.53	0/4281
1	D	0.37	0/3205	0.53	0/4354
All	All	0.38	0/12706	0.53	0/17261

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3092	0	2982	55	0
1	B	3069	0	2963	70	0
1	C	3060	0	2949	86	0
1	D	3112	0	2999	71	0
2	A	18	0	24	1	0
2	B	18	0	24	1	0
2	C	18	0	24	3	0
2	D	18	0	24	1	0
3	A	1	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	3	0	1	1	0
5	B	3	0	1	1	0
5	C	3	0	1	2	0
5	D	3	0	1	0	0
6	A	208	0	0	8	0
6	B	189	0	0	6	0
6	C	173	0	0	16	0
6	D	161	0	0	5	0
All	All	13154	0	11993	282	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 12.

All (282) 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:D:135:TYR:OH	1:D:207:GLU:HG2	1.60	1.00
1:B:101:ALA:HB2	1:D:103:MET:CE	1.91	0.99
1:B:101:ALA:HB2	1:D:103:MET:HE3	1.49	0.95
1:C:148:VAL:HG21	1:C:209:LEU:HD11	1.59	0.85
1:C:359:PHE:C	1:C:359:PHE:CD2	2.52	0.82
1:D:150:CYS:HB2	1:D:195:LEU:HD22	1.59	0.82
1:A:135:TYR:OH	1:A:207:GLU:HG2	1.80	0.82
5:C:505:FMT:H	6:C:692:HOH:O	1.80	0.82
1:B:121:CYS:HB2	6:B:652:HOH:O	1.80	0.81
1:C:359:PHE:C	1:C:359:PHE:HD2	1.85	0.80
1:B:290:HIS:CE1	1:B:319:LEU:HD21	2.20	0.77
1:B:242:PRO:HB2	2:B:502:GOL:H31	1.66	0.77
1:D:137:LYS:HG2	1:D:141:GLN:HE21	1.50	0.77
1:C:11:THR:OG1	1:C:13:PRO:HD3	1.86	0.76
1:D:148:VAL:HG21	1:D:209:LEU:HD11	1.67	0.76
1:C:191:PHE:HB2	6:C:684:HOH:O	1.85	0.76
1:C:216:ARG:HH21	1:C:404:TRP:HA	1.49	0.76
1:B:139:ARG:HG3	1:B:140:ASP:N	2.01	0.75
1:B:365:HIS:ND1	1:B:366:PRO:HD2	2.01	0.75
5:A:506:FMT:H	6:A:649:HOH:O	1.88	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:148:VAL:CG2	1:C:209:LEU:HD11	2.17	0.73
1:A:98:ALA:HB3	1:A:371:GLY:HA2	1.71	0.73
1:D:135:TYR:OH	1:D:207:GLU:CG	2.36	0.72
1:C:98:ALA:HB3	1:C:371:GLY:HA2	1.72	0.71
1:A:135:TYR:OH	1:A:207:GLU:CG	2.39	0.71
1:C:348:GLN:O	1:C:351:GLU:HB2	1.92	0.70
1:C:359:PHE:O	1:C:359:PHE:HD2	1.75	0.69
1:C:288:ILE:HD13	1:C:297:MET:HG3	1.76	0.68
1:C:128:ILE:HD11	1:C:191:PHE:CE1	2.29	0.67
1:D:98:ALA:HB3	1:D:371:GLY:HA2	1.77	0.67
2:C:502:GOL:H11	6:C:750:HOH:O	1.94	0.67
1:C:15:ARG:HG2	1:C:349:MET:CE	2.23	0.67
1:D:314:HIS:CE1	1:D:316:PRO:HG3	2.30	0.66
1:C:348:GLN:NE2	1:C:384:TYR:CE1	2.62	0.66
1:B:359:PHE:CD2	1:B:359:PHE:C	2.69	0.66
1:C:124:THR:HG22	1:C:134:ASP:OD1	1.96	0.65
5:B:506:FMT:H	6:B:751:HOH:O	1.95	0.65
1:D:287:THR:CG2	1:D:314:HIS:HB3	2.26	0.65
1:D:122:HIS:CE1	1:D:343:MET:HG3	2.31	0.65
1:D:137:LYS:HG2	1:D:141:GLN:NE2	2.12	0.64
1:B:124:THR:HG22	1:B:134:ASP:OD1	1.98	0.63
1:D:148:VAL:CG2	1:D:209:LEU:HD11	2.28	0.63
1:B:122:HIS:CE1	1:B:343:MET:HG3	2.34	0.63
1:B:288:ILE:HD13	1:B:297:MET:HG3	1.81	0.62
1:C:314:HIS:CE1	1:C:316:PRO:HG3	2.33	0.62
1:B:375[A]:GLU:HG3	1:B:376:PHE:N	2.15	0.62
1:D:331:ASP:OD2	1:D:340:GLN:NE2	2.29	0.62
1:B:13:PRO:HB3	1:B:352:VAL:HG21	1.82	0.62
1:B:361:ASN:O	1:B:361:ASN:ND2	2.33	0.61
1:A:290:HIS:CE1	1:A:319:LEU:HD21	2.34	0.61
1:A:285:ARG:HG2	1:A:312:GLY:O	2.01	0.61
1:B:314:HIS:CE1	1:B:316:PRO:HG3	2.36	0.60
1:C:216:ARG:NH2	1:C:404:TRP:HA	2.14	0.60
1:D:352:VAL:HG13	1:D:381:ALA:HB2	1.83	0.60
1:C:216:ARG:HH21	1:C:404:TRP:CA	2.14	0.60
1:D:373:GLY:N	6:D:716:HOH:O	2.35	0.60
1:B:107:GLN:HA	1:B:107:GLN:OE1	2.02	0.59
1:C:15:ARG:HG2	1:C:349:MET:HE2	1.82	0.59
1:C:177:LEU:HG	1:C:178:PRO:HD2	1.83	0.59
1:D:236:TRP:C	1:D:236:TRP:CD1	2.74	0.59
1:A:348:GLN:NE2	1:A:384:TYR:CE1	2.71	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:12:CYS:O	1:B:14:GLY:N	2.35	0.59
1:D:288:ILE:HD13	1:D:297:MET:HG3	1.85	0.58
1:A:1:MET:HA	6:A:797:HOH:O	2.04	0.58
1:C:210:LEU:N	1:C:210:LEU:HD12	2.18	0.58
5:C:505:FMT:C	6:C:692:HOH:O	2.45	0.58
1:B:185:THR:HG23	1:B:217:LEU:HD22	1.85	0.58
1:D:185:THR:HG23	1:D:217:LEU:HD22	1.86	0.58
1:D:367:GLY:HA3	6:D:660:HOH:O	2.04	0.58
1:C:132:LEU:HD13	1:C:202:LYS:HD2	1.86	0.58
1:B:192:THR:N	1:B:193:PRO:CD	2.67	0.57
1:C:236:TRP:CD1	1:C:236:TRP:C	2.77	0.57
1:A:287:THR:CG2	1:A:314:HIS:HB3	2.33	0.57
1:A:123:THR:HG22	1:A:148:VAL:HA	1.85	0.57
1:B:365:HIS:CG	1:B:366:PRO:HD2	2.39	0.57
1:A:139:ARG:NH1	1:A:207:GLU:OE2	2.35	0.57
1:A:123:THR:HG23	1:A:131:VAL:HG13	1.87	0.57
1:D:192:THR:N	1:D:193:PRO:CD	2.68	0.56
1:A:195:LEU:O	1:A:195:LEU:HD12	2.05	0.56
1:C:117:VAL:HG13	1:C:337:PHE:CZ	2.40	0.56
1:C:128:ILE:HD11	1:C:191:PHE:CZ	2.40	0.56
1:D:359:PHE:C	1:D:359:PHE:CD2	2.79	0.56
1:C:290:HIS:CE1	1:C:319:LEU:HD21	2.42	0.55
1:A:119:VAL:HA	1:A:340:GLN:O	2.07	0.55
1:B:287:THR:CG2	1:B:314:HIS:HB3	2.36	0.55
1:C:312:GLY:HA2	1:C:339:VAL:O	2.05	0.55
1:D:290:HIS:CE1	1:D:319:LEU:HD21	2.42	0.55
1:A:128:ILE:HD11	1:A:191:PHE:CE1	2.41	0.55
1:C:119:VAL:HA	1:C:340:GLN:O	2.06	0.55
1:C:15:ARG:HG2	1:C:349:MET:HE1	1.88	0.55
1:B:123:THR:HG22	1:B:138:HIS:HD2	1.72	0.55
1:C:12:CYS:HA	1:C:15:ARG:O	2.07	0.54
1:A:127:SER:OG	1:A:130:GLU:HG3	2.07	0.54
1:C:316:PRO:HA	1:C:343:MET:HB2	1.90	0.54
1:D:120:TYR:CZ	1:D:341:GLU:HG3	2.42	0.54
1:C:254:GLN:NE2	6:C:729:HOH:O	2.40	0.54
1:B:375[A]:GLU:HG3	1:B:376:PHE:H	1.73	0.54
1:A:236:TRP:CD1	1:A:236:TRP:C	2.81	0.53
1:C:185:THR:HG23	1:C:217:LEU:HD22	1.89	0.53
1:A:195:LEU:O	1:A:199:VAL:HG23	2.09	0.53
1:B:339:VAL:HG22	1:B:340:GLN:H	1.73	0.53
1:A:314:HIS:CE1	1:A:316:PRO:HG3	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:192:THR:N	1:C:193:PRO:CD	2.72	0.53
1:D:287:THR:HG21	1:D:314:HIS:HB3	1.91	0.52
1:B:361:ASN:C	1:B:361:ASN:HD22	2.12	0.52
1:C:31:LEU:CD1	1:C:376:PHE:HB2	2.39	0.52
2:C:503:GOL:C3	6:C:773:HOH:O	2.58	0.52
1:A:385:PRO:HD2	6:A:693:HOH:O	2.09	0.52
1:D:352:VAL:CG1	1:D:381:ALA:HB2	2.40	0.52
1:B:236:TRP:C	1:B:236:TRP:CD1	2.83	0.52
1:C:224:ARG:NH2	6:C:634:HOH:O	2.43	0.51
1:B:339:VAL:HG22	1:B:340:GLN:N	2.26	0.51
1:C:359:PHE:O	1:C:359:PHE:CD2	2.58	0.51
1:C:361:ASN:O	1:C:361:ASN:CG	2.47	0.51
1:D:342:TYR:C	1:D:343:MET:O	2.43	0.51
1:B:41:LEU:N	1:B:42:PRO:CD	2.74	0.51
1:D:239:ASP:N	1:D:240:PRO:CD	2.74	0.51
1:C:342:TYR:HD2	6:C:708:HOH:O	1.93	0.51
1:D:119:VAL:HA	1:D:340:GLN:O	2.10	0.51
1:A:192:THR:N	1:A:193:PRO:CD	2.74	0.50
1:D:283:TYR:HA	1:D:310:ARG:O	2.11	0.50
1:B:123:THR:HG23	1:B:146:ILE:CG2	2.41	0.50
1:C:126:HIS:CD2	6:C:756:HOH:O	2.63	0.50
1:A:89:VAL:HG22	6:A:633:HOH:O	2.11	0.50
1:B:367:GLY:HA3	6:B:636:HOH:O	2.10	0.50
1:D:185:THR:HG23	1:D:217:LEU:CD2	2.41	0.50
1:D:177:LEU:HD22	1:D:178:PRO:HD2	1.94	0.50
1:D:236:TRP:C	1:D:236:TRP:HD1	2.13	0.50
1:B:288:ILE:HG12	6:B:642:HOH:O	2.12	0.50
1:C:287:THR:CG2	1:C:314:HIS:HB3	2.42	0.50
1:B:119:VAL:HA	1:B:340:GLN:O	2.11	0.49
1:B:11:THR:OG1	1:B:13:PRO:HD3	2.13	0.49
1:A:123:THR:CG2	1:A:131:VAL:HG13	2.42	0.49
1:B:150:CYS:HB2	1:B:195:LEU:HD22	1.94	0.49
1:C:4:VAL:HG22	1:C:23:THR:O	2.13	0.49
1:D:218:THR:OG1	1:D:221:GLU:HG3	2.13	0.48
1:D:122:HIS:ND1	1:D:343:MET:HG3	2.29	0.48
1:A:346:SER:OG	1:A:349:MET:HG3	2.13	0.48
1:B:311:THR:OG1	1:B:337:PHE:HA	2.14	0.48
1:D:12:CYS:HA	1:D:15:ARG:O	2.13	0.48
1:B:316:PRO:HA	1:B:343:MET:HB2	1.96	0.47
1:B:52:CYS:HB2	1:B:53:PRO:HD3	1.95	0.47
1:A:356:SER:OG	1:A:373:GLY:O	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:148:VAL:CG2	1:C:209:LEU:CD1	2.90	0.47
1:B:348:GLN:NE2	1:B:384:TYR:CE1	2.82	0.47
1:A:254:GLN:HG3	6:A:699:HOH:O	2.15	0.47
1:B:331:ASP:OD2	1:B:340:GLN:NE2	2.38	0.47
1:B:50:HIS:HD1	1:C:390:TYR:HE1	1.63	0.47
1:C:214:HIS:O	1:C:216:ARG:HD2	2.14	0.47
1:D:298:ARG:HD3	6:D:654:HOH:O	2.15	0.47
1:B:359:PHE:CD2	1:B:360:ASP:N	2.83	0.47
1:A:264:GLU:HB2	1:A:314:HIS:CG	2.51	0.46
1:D:374:ILE:HG13	1:D:375:GLU:N	2.31	0.46
1:B:239:ASP:N	1:B:240:PRO:CD	2.78	0.46
1:A:251:LEU:HB2	6:A:602:HOH:O	2.15	0.46
1:A:139:ARG:HG3	1:A:140:ASP:N	2.31	0.46
1:B:136:ALA:HA	1:B:139:ARG:HG2	1.98	0.46
1:C:39:ARG:O	1:C:42:PRO:HD2	2.16	0.46
1:D:51:VAL:HG13	1:D:70:PHE:CZ	2.51	0.46
1:C:185:THR:HG23	1:C:217:LEU:CD2	2.46	0.46
1:B:121:CYS:CB	6:B:652:HOH:O	2.51	0.46
1:C:236:TRP:C	1:C:236:TRP:HD1	2.18	0.46
1:D:269:ILE:HG22	2:D:502:GOL:H32	1.97	0.46
1:D:312:GLY:HA2	1:D:339:VAL:O	2.16	0.46
1:D:354:PRO:HB2	1:D:375:GLU:HB2	1.97	0.46
1:A:58:ARG:HB3	1:A:58:ARG:HE	1.62	0.45
1:B:128:ILE:O	1:B:132:LEU:HG	2.16	0.45
1:C:367:GLY:HA3	6:C:675:HOH:O	2.15	0.45
1:D:358:THR:O	1:D:364:MET:HA	2.15	0.45
1:D:236:TRP:O	1:D:236:TRP:HD1	2.00	0.45
1:B:69:TYR:O	1:B:73:GLY:HA3	2.16	0.45
1:D:107:GLN:HA	1:D:107:GLN:OE1	2.17	0.45
1:B:264:GLU:HB2	1:B:314:HIS:CG	2.52	0.45
1:C:177:LEU:HG	1:C:178:PRO:CD	2.47	0.45
1:C:148:VAL:HG23	1:C:209:LEU:CD1	2.47	0.45
1:A:192:THR:O	1:A:195:LEU:HB3	2.17	0.45
1:A:239:ASP:N	1:A:240:PRO:CD	2.79	0.45
1:C:107:GLN:HA	1:C:107:GLN:OE1	2.17	0.45
1:D:191:PHE:O	1:D:194:LYS:HB2	2.17	0.45
1:A:367:GLY:HA3	6:A:703:HOH:O	2.17	0.44
1:B:375[A]:GLU:CG	1:B:376:PHE:N	2.80	0.44
1:D:177:LEU:HA	1:D:177:LEU:HD23	1.74	0.44
1:A:270:TRP:CH2	1:D:245:ASN:HB2	2.53	0.44
1:A:49:ASP:HB3	1:D:41:LEU:HD12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:334:VAL:HG13	1:B:334:VAL:O	2.17	0.44
1:C:31:LEU:HD13	1:C:376:PHE:HB2	1.98	0.44
1:C:74:ALA:HB2	6:C:614:HOH:O	2.18	0.44
1:B:108:LEU:HD22	1:D:108:LEU:HD22	1.98	0.44
1:B:80:PRO:HB3	6:B:744:HOH:O	2.18	0.44
1:C:316:PRO:HD2	1:C:319:LEU:HD12	2.00	0.44
1:C:264:GLU:HB2	1:C:314:HIS:CG	2.53	0.44
1:B:123:THR:CG2	1:B:146:ILE:CG2	2.95	0.44
1:C:380:LEU:O	1:C:383:LYS:HB2	2.18	0.44
1:A:80:PRO:HD2	3:A:502:CL:CL	2.56	0.43
1:B:361:ASN:ND2	1:B:361:ASN:C	2.71	0.43
1:A:174:LYS:NZ	6:A:776:HOH:O	2.51	0.43
1:C:288:ILE:HG12	6:C:613:HOH:O	2.17	0.43
1:C:216:ARG:NH2	1:C:404:TRP:CD1	2.86	0.43
1:D:320:SER:CB	6:D:641:HOH:O	2.65	0.43
1:D:4:VAL:HG22	1:D:23:THR:O	2.18	0.43
1:B:223:ALA:O	1:B:227:LYS:HG3	2.18	0.43
1:D:103:MET:HB3	1:D:104:PRO:HD2	2.00	0.43
1:B:334:VAL:CG1	1:B:337:PHE:HB2	2.48	0.43
1:B:355:HIS:HA	1:B:374:ILE:HD12	1.99	0.43
1:B:285:ARG:HG2	1:B:312:GLY:O	2.18	0.43
1:D:316:PRO:HA	1:D:343:MET:HB2	2.00	0.43
1:A:283:TYR:HA	1:A:310:ARG:O	2.18	0.43
1:C:262:VAL:HG22	1:C:263:GLY:N	2.34	0.43
1:D:195:LEU:O	1:D:199:VAL:HG23	2.19	0.43
1:D:235:PHE:O	1:D:236:TRP:HB3	2.19	0.43
1:A:304:ALA:HB1	1:A:309:VAL:HB	2.00	0.43
1:A:331:ASP:OD2	1:A:340:GLN:NE2	2.46	0.43
1:B:137:LYS:O	1:B:141:GLN:HG3	2.19	0.43
1:C:131:VAL:HG11	1:C:148:VAL:HG13	2.01	0.43
1:D:128:ILE:HG12	1:D:128:ILE:H	1.69	0.43
1:A:313:SER:HB2	1:A:340:GLN:NE2	2.34	0.43
1:B:24:THR:C	1:B:26:SER:H	2.22	0.43
1:C:373:GLY:N	6:C:632:HOH:O	2.41	0.43
1:D:251:LEU:HB2	6:D:609:HOH:O	2.18	0.43
1:C:6:ALA:HA	1:C:21:LYS:O	2.18	0.42
1:C:31:LEU:HD11	1:C:376:PHE:HB2	2.01	0.42
1:C:351:GLU:HB3	1:C:380:LEU:HD21	2.01	0.42
1:B:210:LEU:HG	1:B:235:PHE:HB3	2.01	0.42
1:B:313:SER:HB2	1:B:340:GLN:HE22	1.83	0.42
1:A:357:TRP:CD1	1:A:357:TRP:C	2.92	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:TRP:CD1	1:A:294:ILE:HB	2.53	0.42
1:B:365:HIS:CE1	1:B:366:PRO:HD2	2.53	0.42
1:C:183:TRP:CE2	1:C:216:ARG:HG2	2.54	0.42
1:D:2:LYS:HZ2	1:D:57:GLY:HA2	1.85	0.42
1:C:135:TYR:OH	1:C:207:GLU:HB2	2.20	0.42
1:C:274:GLN:HA	1:C:277:GLU:HG2	2.00	0.42
1:B:245:ASN:HB2	1:C:270:TRP:CH2	2.54	0.42
1:D:52:CYS:HB2	1:D:53:PRO:HD3	2.00	0.42
1:A:334:VAL:O	1:A:334:VAL:HG13	2.19	0.42
1:C:350:LEU:HD23	1:C:350:LEU:HA	1.88	0.42
2:C:503:GOL:H31	6:C:773:HOH:O	2.18	0.42
1:D:346:SER:OG	1:D:349:MET:HG3	2.19	0.42
1:C:236:TRP:O	1:C:236:TRP:HD1	2.01	0.42
1:C:8:VAL:HB	1:C:48:ASN:ND2	2.35	0.42
1:B:350:LEU:O	1:B:353:PHE:N	2.50	0.42
1:D:365:HIS:ND1	1:D:366:PRO:HD2	2.35	0.42
1:B:46:TYR:O	1:B:50:HIS:HB2	2.20	0.42
1:B:58[A]:ARG:NH2	1:B:69:TYR:CE1	2.88	0.42
1:C:236:TRP:O	1:C:236:TRP:CD1	2.72	0.42
1:A:12:CYS:HA	1:A:15:ARG:O	2.20	0.41
1:B:359:PHE:C	1:B:359:PHE:HD2	2.18	0.41
1:C:58:ARG:HE	1:C:58:ARG:HB3	1.61	0.41
1:D:120:TYR:CE2	1:D:341:GLU:HA	2.55	0.41
1:D:236:TRP:CD1	1:D:236:TRP:O	2.74	0.41
1:C:126:HIS:HD2	6:C:756:HOH:O	2.02	0.41
1:C:326:ALA:HA	1:C:372:LEU:HD22	2.02	0.41
1:C:122:HIS:ND1	1:C:147:ARG:CZ	2.84	0.41
1:B:12:CYS:HA	1:B:15:ARG:O	2.21	0.41
1:C:63:ILE:HG12	1:C:93:LEU:HB3	2.03	0.41
1:A:170:GLU:HA	1:A:171:PRO:HD2	1.84	0.41
1:A:359:PHE:CD2	1:A:359:PHE:C	2.94	0.41
1:C:357:TRP:CD1	1:C:364:MET:CE	3.04	0.41
1:B:375[A]:GLU:CG	1:B:376:PHE:H	2.33	0.41
1:D:220:ILE:HD12	1:D:220:ILE:HA	1.90	0.41
1:D:186:GLU:OE1	1:D:186:GLU:N	2.40	0.41
1:A:311:THR:OG1	1:A:337:PHE:HA	2.21	0.40
1:A:114:ARG:CZ	1:A:337:PHE:HB3	2.51	0.40
1:A:402:TRP:CH2	2:A:505:GOL:H31	2.57	0.40
1:C:31:LEU:HD11	1:C:376:PHE:CB	2.51	0.40
1:C:59:ASP:C	1:C:61:HIS:H	2.22	0.40
1:D:350:LEU:HD23	1:D:350:LEU:HA	1.79	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:319:LEU:O	1:C:345:TYR:OH	2.32	0.40
1:C:69:TYR:O	1:C:73:GLY:HA3	2.21	0.40
1:D:192:THR:HG22	1:D:196:PHE:CE2	2.56	0.40
1:A:185:THR:HG23	1:A:217:LEU:CD2	2.51	0.40
1:A:34:ALA:HB2	1:A:88:ALA:HB2	2.03	0.40
1:C:128:ILE:O	1:C:132:LEU:HG	2.21	0.40
1:D:381:ALA:C	1:D:383:LYS:H	2.25	0.40
1:A:236:TRP:HD1	1:A:236:TRP:C	2.23	0.40
1:A:287:THR:HG21	1:A:314:HIS:HB3	2.02	0.40
1:D:117:VAL:HG13	1:D:337:PHE:CZ	2.56	0.40
1:D:33:ASP:OD1	1:D:35:THR:OG1	2.34	0.40
1:A:135:TYR:OH	1:A:207:GLU:HG3	2.17	0.40
1:A:313:SER:HB2	1:A:340:GLN:HE22	1.86	0.40
1:B:357:TRP:C	1:B:357:TRP:CD1	2.95	0.40
1:C:220:ILE:HA	1:C:220:ILE:HD12	1.97	0.40
1:C:348:GLN:HG3	6:C:671:HOH:O	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	383/426 (90%)	366 (96%)	16 (4%)	1 (0%)	44	40
1	B	380/426 (89%)	360 (95%)	19 (5%)	1 (0%)	44	40
1	C	378/426 (89%)	356 (94%)	21 (6%)	1 (0%)	44	40
1	D	385/426 (90%)	361 (94%)	24 (6%)	0	100	100
All	All	1526/1704 (90%)	1443 (95%)	80 (5%)	3 (0%)	51	48

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	78	ARG
1	B	78	ARG
1	C	78	ARG

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	327/357 (92%)	320 (98%)	7 (2%)	59	62
1	B	325/357 (91%)	319 (98%)	6 (2%)	64	68
1	C	324/357 (91%)	319 (98%)	5 (2%)	70	74
1	D	329/357 (92%)	316 (96%)	13 (4%)	36	32
All	All	1305/1428 (91%)	1274 (98%)	31 (2%)	54	56

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	89	VAL
1	A	123	THR
1	A	139	ARG
1	A	207	GLU
1	A	236	TRP
1	A	251	LEU
1	A	397	GLU
1	B	15	ARG
1	B	139	ARG
1	B	236	TRP
1	B	251	LEU
1	B	359	PHE
1	B	361	ASN
1	C	216	ARG
1	C	236	TRP
1	C	339	VAL
1	C	359	PHE
1	C	384	TYR
1	D	1	MET

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Mol	Chain	Res	Type
1	D	2	LYS
1	D	11	THR
1	D	15	ARG
1	D	124	THR
1	D	127	SER
1	D	177	LEU
1	D	179	GLU
1	D	207	GLU
1	D	236	TRP
1	D	251	LEU
1	D	285	ARG
1	D	359	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	254	GLN
1	B	138	HIS
1	B	279	GLN
1	B	361	ASN
1	C	48	ASN
1	C	254	GLN
1	D	102	ASN
1	D	141	GLN

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

Of 22 ligands modelled in this entry, 6 are monoatomic - leaving 16 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	GOL	A	501	-	5,5,5	0.38	0	5,5,5	0.25	0
2	GOL	A	503	-	5,5,5	0.26	0	5,5,5	0.69	0
2	GOL	A	505	-	5,5,5	0.29	0	5,5,5	0.31	0
5	FMT	A	506	4	0,2,2	0.00	-	0,1,1	0.00	-
2	GOL	B	501	-	5,5,5	0.38	0	5,5,5	0.21	0
2	GOL	B	502	-	5,5,5	0.37	0	5,5,5	0.39	0
2	GOL	B	504	-	5,5,5	0.30	0	5,5,5	0.36	0
5	FMT	B	506	4	0,2,2	0.00	-	0,1,1	0.00	-
2	GOL	C	501	-	5,5,5	0.38	0	5,5,5	0.19	0
2	GOL	C	502	-	5,5,5	0.51	0	5,5,5	0.49	0
2	GOL	C	503	-	5,5,5	0.35	0	5,5,5	0.19	0
5	FMT	C	505	4	0,2,2	0.00	-	0,1,1	0.00	-
2	GOL	D	501	-	5,5,5	0.38	0	5,5,5	0.34	0
2	GOL	D	502	-	5,5,5	0.36	0	5,5,5	0.29	0
2	GOL	D	504	-	5,5,5	0.31	0	5,5,5	0.58	0
5	FMT	D	505	4	0,2,2	0.00	-	0,1,1	0.00	-

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	GOL	A	501	-	-	0/4/4/4	0/0/0/0
2	GOL	A	503	-	-	0/4/4/4	0/0/0/0
2	GOL	A	505	-	-	0/4/4/4	0/0/0/0
5	FMT	A	506	4	-	0/0/0/0	0/0/0/0
2	GOL	B	501	-	-	0/4/4/4	0/0/0/0
2	GOL	B	502	-	-	0/4/4/4	0/0/0/0
2	GOL	B	504	-	-	0/4/4/4	0/0/0/0
5	FMT	B	506	4	-	0/0/0/0	0/0/0/0
2	GOL	C	501	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	C	502	-	-	0/4/4/4	0/0/0/0
2	GOL	C	503	-	-	0/4/4/4	0/0/0/0
5	FMT	C	505	4	-	0/0/0/0	0/0/0/0
2	GOL	D	501	-	-	0/4/4/4	0/0/0/0
2	GOL	D	502	-	-	0/4/4/4	0/0/0/0
2	GOL	D	504	-	-	0/4/4/4	0/0/0/0
5	FMT	D	505	4	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	505	GOL	1	0
5	A	506	FMT	1	0
2	B	502	GOL	1	0
5	B	506	FMT	1	0
2	C	502	GOL	1	0
2	C	503	GOL	2	0
5	C	505	FMT	2	0
2	D	502	GOL	1	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	386/426 (90%)	-0.19	7 (1%) 69 68	27, 40, 67, 85	0
1	B	381/426 (89%)	0.10	27 (7%) 17 17	26, 43, 70, 91	0
1	C	381/426 (89%)	0.17	20 (5%) 28 28	28, 46, 74, 99	0
1	D	388/426 (91%)	0.13	18 (4%) 33 33	27, 45, 74, 107	0
All	All	1536/1704 (90%)	0.05	72 (4%) 32 32	26, 43, 71, 107	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	-2	PHE	8.1
1	C	124	THR	6.9
1	B	124	THR	5.5
1	D	-1	GLN	5.5
1	C	125	GLY	4.8
1	D	171	PRO	4.8
1	B	125	GLY	4.6
1	D	124	THR	4.2
1	A	172	ALA	4.2
1	D	126	HIS	3.9
1	D	172	ALA	3.8
1	D	173	THR	3.7
1	B	126	HIS	3.6
1	C	126	HIS	3.5
1	A	173	THR	3.4
1	C	-1	GLN	3.4
1	B	4	VAL	3.4
1	A	126	HIS	3.2
1	C	136	ALA	3.1
1	B	176	SER	3.1
1	C	129	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	177	LEU	3.0
1	B	131	VAL	3.0
1	A	0	SER	2.9
1	C	128	ILE	2.9
1	D	0	SER	2.9
1	C	28	LEU	2.8
1	B	288	ILE	2.8
1	B	175	GLY	2.7
1	D	125	GLY	2.7
1	B	361	ASN	2.6
1	B	133	ASP	2.6
1	C	130	GLU	2.6
1	C	268	SER	2.6
1	C	140	ASP	2.5
1	D	130	GLU	2.5
1	B	1	MET	2.5
1	D	174	LYS	2.5
1	A	137	LYS	2.4
1	B	24	THR	2.4
1	C	133	ASP	2.4
1	B	27	GLY	2.4
1	B	129	ASP	2.4
1	B	0	SER	2.4
1	C	131	VAL	2.3
1	D	300	ILE	2.3
1	B	296	GLY	2.3
1	B	265	VAL	2.3
1	B	291	ALA	2.3
1	C	27	GLY	2.3
1	B	297	MET	2.2
1	A	176	SER	2.2
1	D	128	ILE	2.2
1	B	56	ILE	2.2
1	D	176	SER	2.2
1	D	384	TYR	2.2
1	D	170	GLU	2.2
1	B	295	THR	2.1
1	B	300	ILE	2.1
1	B	6	ALA	2.1
1	C	291	ALA	2.1
1	C	296	GLY	2.1
1	B	9	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	140	ASP	2.1
1	D	25	ASP	2.1
1	C	284	ILE	2.1
1	C	132	LEU	2.1
1	B	301	ALA	2.1
1	D	175	GLY	2.1
1	B	379	LYS	2.0
1	C	176	SER	2.0
1	A	288	ILE	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	GOL	D	502	6/6	0.78	0.36	5.08	54,61,72,78	0
5	FMT	A	506	3/3	0.90	0.19	2.95	39,39,43,51	0
5	FMT	D	505	3/3	0.94	0.16	2.92	52,52,54,55	0
5	FMT	B	506	3/3	0.94	0.19	2.69	37,37,52,60	0
2	GOL	C	501	6/6	0.90	0.20	2.59	46,49,63,68	0
2	GOL	A	503	6/6	0.91	0.19	1.89	28,51,59,59	0
2	GOL	B	501	6/6	0.92	0.15	1.43	42,53,58,74	0
2	GOL	B	504	6/6	0.93	0.14	1.34	50,67,74,77	0
2	GOL	A	505	6/6	0.88	0.15	1.12	45,58,66,67	0
2	GOL	C	502	6/6	0.88	0.16	0.77	44,50,57,65	0
2	GOL	D	504	6/6	0.90	0.14	0.72	34,60,64,65	0
2	GOL	C	503	6/6	0.92	0.13	0.64	52,69,72,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	GOL	B	502	6/6	0.91	0.14	0.48	39,50,56,59	0
5	FMT	C	505	3/3	0.89	0.15	0.46	37,37,50,51	0
2	GOL	A	501	6/6	0.94	0.13	0.33	39,45,59,60	0
2	GOL	D	501	6/6	0.97	0.13	0.04	46,51,58,69	0
3	CL	A	502	1/1	0.97	0.15	-0.32	46,46,46,46	0
4	MG	A	504	1/1	0.95	0.10	-1.07	34,34,34,34	0
4	MG	D	503	1/1	0.98	0.06	-1.58	40,40,40,40	0
4	MG	C	504	1/1	0.94	0.07	-1.91	43,43,43,43	0
4	MG	B	505	1/1	0.92	0.03	-2.36	38,38,38,38	0
3	CL	B	503	1/1	0.96	0.11	-2.61	44,44,44,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.