



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:22 AM GMT

PDB ID : 3ED0
Title : Crystal structure of (3R)-Hydroxyacyl-Acyl Carrier Protein Dehydratase (FabZ) from Helicobacter pylori in complex with emodin
Authors : Zhang, L.; Zhang, H.; Liu, W.; Guo, Y.; Shen, X.; Jiang, H.
Deposited on : 2008-09-02
Resolution : 2.30 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

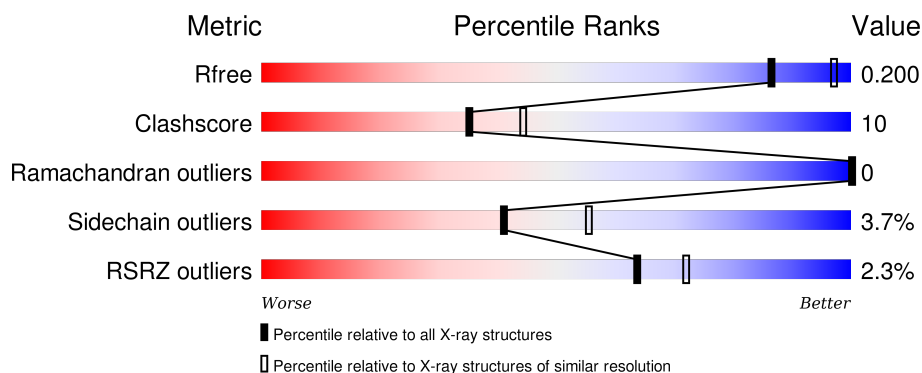
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	159	 2% 73% 21% • •
1	B	159	 3% 72% 21% • 6%
1	C	159	 2% 73% 21% • 6%
1	D	159	 4% 80% 13% • •
1	E	159	 % 76% 18% • 5%

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Mol	Chain	Length	Quality of chain
1	F	159	 78% 13% 7%

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	BEN	A	160	-	-	-	X
2	BEN	A	161	-	-	-	X
2	BEN	B	160	-	-	X	X
2	BEN	B	161	-	-	-	X
2	BEN	D	160	-	-	-	X
2	BEN	E	160	-	-	-	X
2	BEN	E	161	-	-	-	X
3	CL	F	160	-	-	-	X
4	EMO	A	163	-	-	-	X
4	EMO	C	161	-	-	X	X

2 Entry composition [i](#)

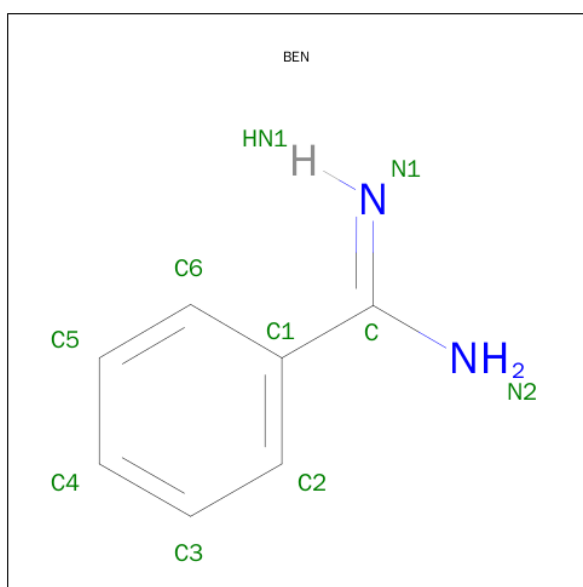
There are 5 unique types of molecules in this entry. The entry contains 7851 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 (3R)-hydroxymyristoyl-acyl carrier protein dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	152	Total	C	N	O	S	0	0	0
			1225	803	203	214	5			
1	B	150	Total	C	N	O	S	0	0	0
			1208	792	200	211	5			
1	C	150	Total	C	N	O	S	0	0	0
			1207	792	201	209	5			
1	D	152	Total	C	N	O	S	0	0	0
			1225	803	203	214	5			
1	E	151	Total	C	N	O	S	0	0	0
			1217	797	202	213	5			
1	F	148	Total	C	N	O	S	0	0	0
			1192	784	198	205	5			

- Molecule 2 is BENZAMIDINE (three-letter code: BEN) (formula: C₇H₈N₂).

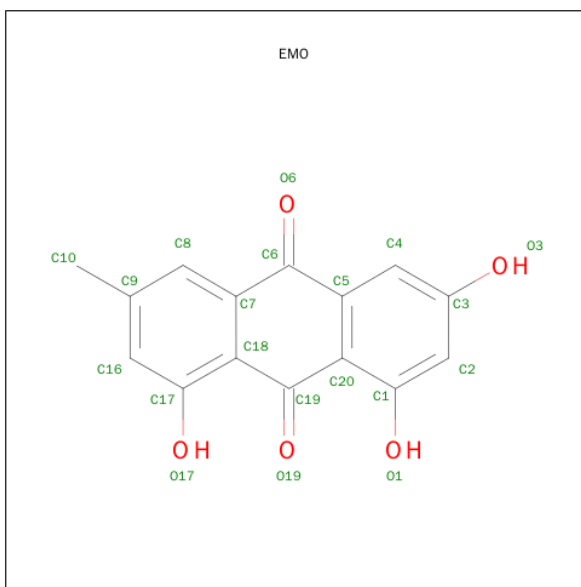


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N 9 7 2	0	0
2	A	1	Total C N 9 7 2	0	0
2	B	1	Total C N 9 7 2	0	0
2	B	1	Total C N 9 7 2	0	0
2	D	1	Total C N 9 7 2	0	0
2	E	1	Total C N 9 7 2	0	0
2	E	1	Total C N 9 7 2	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total Cl 1 1	0	0
3	E	1	Total Cl 1 1	0	0
3	B	1	Total Cl 1 1	0	0
3	C	1	Total Cl 1 1	0	0
3	A	1	Total Cl 1 1	0	0
3	F	1	Total Cl 1 1	0	0

- Molecule 4 is 3-METHYL-1,6,8-TRIHIDROXYANTHRAQUINONE (three-letter code: EMO) (formula: C₁₅H₁₀O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			20	15	5		
4	C	1	Total	C	O	0	0
			20	15	5		

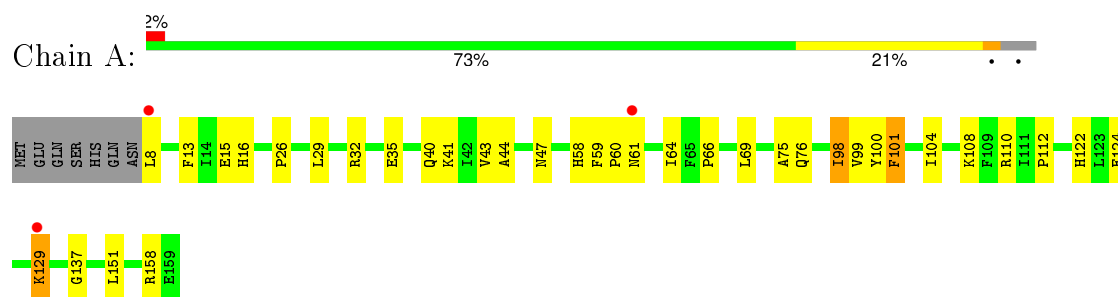
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	93	Total	O	0	0
			93	93		
5	B	82	Total	O	0	0
			82	82		
5	C	72	Total	O	0	0
			72	72		
5	D	71	Total	O	0	0
			71	71		
5	E	77	Total	O	0	0
			77	77		
5	F	73	Total	O	0	0
			73	73		

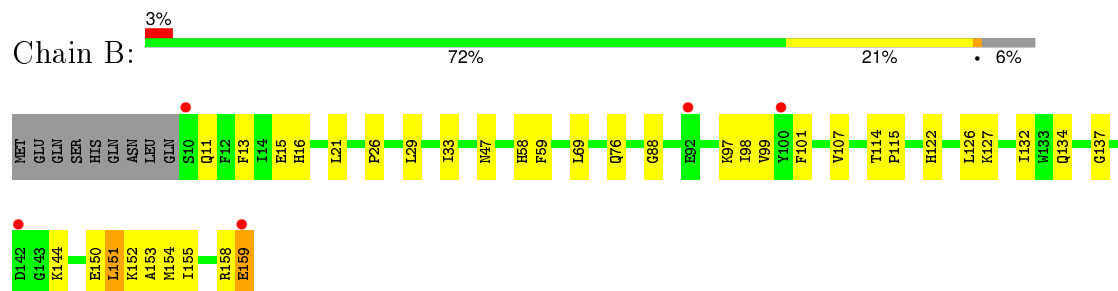
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

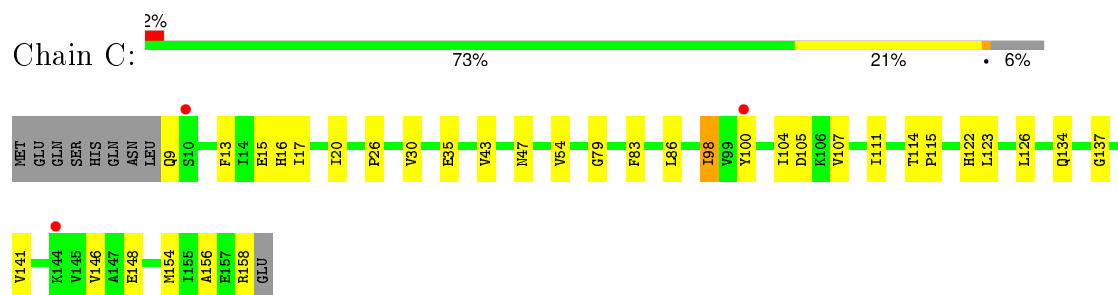
- Molecule 1: (3R)-hydroxymyristoyl-acyl carrier protein dehydratase



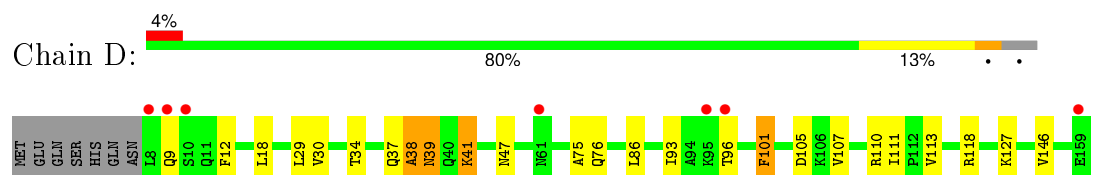
- Molecule 1: (3R)-hydroxymyristoyl-acyl carrier protein dehydratase



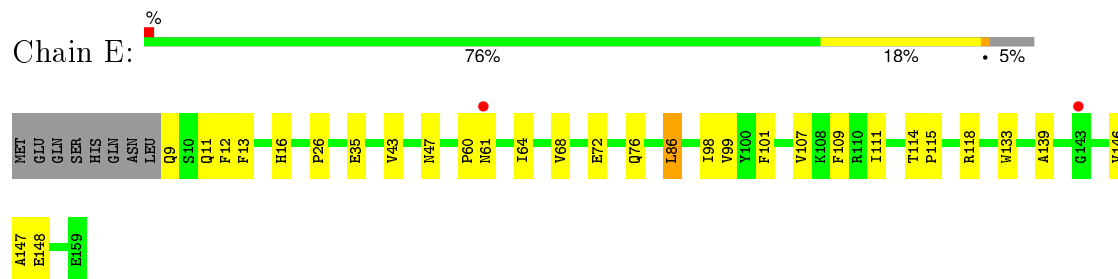
- Molecule 1: (3R)-hydroxymyristoyl-acyl carrier protein dehydratase



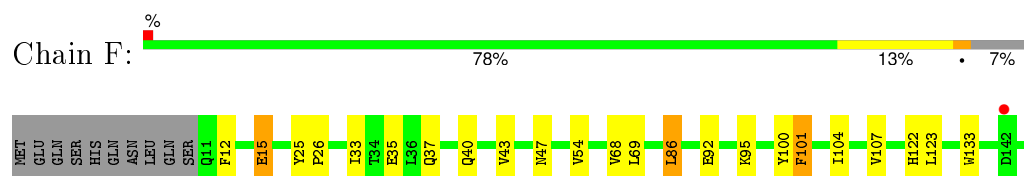
- Molecule 1: (3R)-hydroxymyristoyl-acyl carrier protein dehydratase



- Molecule 1: (3R)-hydroxymyristoyl-acyl carrier protein dehydratase



- Molecule 1: (3R)-hydroxymyristoyl-acyl carrier protein dehydratase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.20Å 100.40Å 186.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30 19.96 – 2.30	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.30) 99.7 (19.96-2.30)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 2.30Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.230 , 0.265 0.202 , 0.200	Depositor DCC
R_{free} test set	3166 reflections (5.07%)	DCC
Wilson B-factor (Å ²)	25.3	Xtriage
Anisotropy	0.384	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 46.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 62424 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7851	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 29.05 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.6572e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: EMO, BEN, 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	0.42	0/1256	0.63	0/1698
1	B	0.43	0/1239	0.60	0/1675
1	C	0.40	0/1238	0.64	0/1675
1	D	0.44	0/1256	0.69	2/1698 (0.1%)
1	E	0.52	2/1248 (0.2%)	0.71	1/1687 (0.1%)
1	F	0.40	0/1223	0.63	0/1655
All	All	0.44	2/7460 (0.0%)	0.65	3/10088 (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	D	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	60	PRO	N-CD	7.96	1.58	1.47
1	E	61	ASN	CB-CG	-7.64	1.33	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	60	PRO	N-CA-CB	6.92	111.60	103.30
1	D	38	ALA	N-CA-CB	6.87	119.72	110.10
1	D	39	ASN	CB-CG-OD1	5.07	131.74	121.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	38	ALA	Mainchain

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	1225	0	1243	34	0
1	B	1208	0	1224	35	0
1	C	1207	0	1226	30	0
1	D	1225	0	1243	18	0
1	E	1217	0	1232	17	0
1	F	1192	0	1213	19	0
2	A	18	0	14	1	0
2	B	18	0	14	9	0
2	D	9	0	7	0	0
2	E	18	0	14	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	20	0	7	5	0
4	C	20	0	7	10	0
5	A	93	0	0	2	0
5	B	82	0	0	5	0
5	C	72	0	0	2	0
5	D	71	0	0	5	0
5	E	77	0	0	1	0
5	F	73	0	0	1	0
All	All	7851	0	7444	145	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 10.

All (145) 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:29:LEU:H	1:D:76:GLN:HE22	1.09	1.00
1:B:98:ILE:HD12	2:B:160:BEN:HN21	1.30	0.94
1:C:98:ILE:HA	4:C:161:EMO:O17	1.70	0.92
1:B:13:PHE:H	1:B:16:HIS:HD2	1.21	0.87
1:C:13:PHE:H	1:C:16:HIS:HD2	1.20	0.85
1:A:13:PHE:H	1:A:16:HIS:HD2	1.27	0.82
1:A:40:GLN:HE21	2:A:160:BEN:HN22	1.28	0.81
1:C:83:PHE:CB	4:C:161:EMO:H102	2.11	0.80
1:C:83:PHE:CG	4:C:161:EMO:H102	2.15	0.80
1:C:98:ILE:HD11	1:C:156:ALA:HB3	1.64	0.79
1:B:132:ILE:HD13	1:B:154:MET:HG3	1.67	0.76
1:C:47:ASN:HB3	1:E:47:ASN:HB3	1.67	0.76
1:C:15:GLU:HB3	5:C:180:HOH:O	1.86	0.75
1:A:29:LEU:H	1:A:76:GLN:HE22	1.36	0.74
1:D:93:ILE:O	1:D:96:THR:HG22	1.88	0.73
1:C:83:PHE:HB2	4:C:161:EMO:H102	1.71	0.73
1:B:29:LEU:H	1:B:76:GLN:HE22	1.36	0.72
1:A:47:ASN:HB3	1:D:47:ASN:HB3	1.76	0.68
1:A:58:HIS:HD2	1:A:64:ILE:O	1.77	0.67
1:A:108:LYS:NZ	1:A:110:ARG:HH22	1.92	0.67
1:C:111:ILE:O	1:C:146:VAL:HG13	1.95	0.67
1:B:47:ASN:HB3	1:F:47:ASN:HB3	1.78	0.66
1:A:108:LYS:HZ1	1:A:110:ARG:HH22	1.43	0.65
1:A:158:ARG:HD3	5:B:236:HOH:O	1.96	0.64
1:A:98:ILE:HD13	1:A:99:VAL:N	2.12	0.64
1:C:20:ILE:HG22	4:C:161:EMO:H103	1.79	0.64
1:A:15:GLU:HB3	5:D:214:HOH:O	1.97	0.64
1:B:98:ILE:CD1	2:B:160:BEN:HN21	2.09	0.63
1:F:37:GLN:HE21	1:F:40:GLN:HE21	1.45	0.63
1:C:83:PHE:CG	4:C:161:EMO:C10	2.82	0.63
1:A:108:LYS:NZ	1:A:110:ARG:NH2	2.47	0.62
1:F:54:VAL:HG23	5:F:195:HOH:O	1.98	0.62
1:C:98:ILE:HG13	1:C:100:TYR:CE1	2.35	0.61
1:C:126:LEU:HB2	1:C:134:GLN:HG2	1.83	0.61
1:E:35:GLU:HG2	1:E:43:VAL:HB	1.82	0.60
1:A:110:ARG:O	4:A:163:EMO:H101	2.01	0.60
1:B:159:GLU:CD	1:B:159:GLU:H	2.05	0.59
1:D:111:ILE:HB	1:D:146:VAL:HG22	1.85	0.59
1:C:98:ILE:CD1	1:C:156:ALA:HB3	2.34	0.58
1:A:35:GLU:CG	1:A:43:VAL:HB	2.35	0.57
1:B:98:ILE:HD12	2:B:160:BEN:N2	2.11	0.56
1:D:29:LEU:H	1:D:76:GLN:NE2	1.92	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:118:ARG:HD2	5:E:212:HOH:O	2.06	0.56
1:B:15:GLU:HB3	5:B:232:HOH:O	2.06	0.55
1:B:99:VAL:HB	2:B:160:BEN:C	2.36	0.55
1:D:127:LYS:NZ	5:D:179:HOH:O	2.40	0.55
1:F:122:HIS:C	1:F:123:LEU:HD22	2.28	0.54
1:B:144:LYS:N	1:B:144:LYS:HD2	2.23	0.54
1:B:132:ILE:CD1	1:B:154:MET:HG3	2.36	0.53
1:B:98:ILE:HD12	1:B:99:VAL:H	1.73	0.53
1:C:13:PHE:H	1:C:16:HIS:CD2	2.12	0.52
1:B:101:PHE:CE2	1:B:153:ALA:HB2	2.45	0.52
4:A:163:EMO:O3	1:B:98:ILE:HG12	2.10	0.52
1:E:98:ILE:HG22	1:E:99:VAL:N	2.25	0.52
1:C:35:GLU:HB2	1:C:43:VAL:HB	1.91	0.51
1:F:37:GLN:HE21	1:F:40:GLN:NE2	2.09	0.51
1:E:9:GLN:O	1:E:9:GLN:HG3	2.10	0.51
1:A:35:GLU:HG2	1:A:43:VAL:HB	1.93	0.51
1:B:159:GLU:OXT	1:B:159:GLU:HG2	2.11	0.50
1:C:79:GLY:HA3	4:C:161:EMO:O6	2.11	0.50
1:E:64:ILE:HD13	1:F:100:TYR:CE2	2.46	0.50
1:A:66:PRO:HB2	1:A:69:LEU:HG	1.94	0.49
1:D:113:VAL:CG2	1:D:146:VAL:HG11	2.42	0.49
1:E:86:LEU:HD13	1:E:133:TRP:HZ2	1.77	0.49
1:F:92:GLU:OE1	1:F:95:LYS:HE3	2.13	0.48
1:A:122:HIS:O	1:A:137:GLY:HA3	2.13	0.48
1:D:75:ALA:HB2	1:D:101:PHE:CZ	2.48	0.48
1:C:83:PHE:CD1	4:C:161:EMO:C10	2.97	0.48
1:A:58:HIS:HE1	5:B:178:HOH:O	1.97	0.48
1:D:37:GLN:NE2	1:D:41:LYS:HD2	2.28	0.48
1:A:35:GLU:HG3	1:A:43:VAL:HB	1.94	0.48
1:F:37:GLN:NE2	1:F:40:GLN:NE2	2.61	0.47
1:B:122:HIS:O	1:B:137:GLY:HA3	2.15	0.47
1:C:141:VAL:HG23	1:C:146:VAL:HG21	1.96	0.47
1:B:151:LEU:N	1:B:151:LEU:HD12	2.29	0.47
1:A:112:PRO:HD3	4:A:163:EMO:C9	2.45	0.47
1:A:58:HIS:CD2	1:A:64:ILE:O	2.64	0.47
1:E:11:GLN:OE1	1:E:13:PHE:CE1	2.68	0.46
1:B:97:LYS:O	2:B:160:BEN:H3	2.16	0.46
1:C:98:ILE:CG2	1:C:158:ARG:HA	2.45	0.46
1:B:99:VAL:HG22	1:B:155:ILE:HG12	1.96	0.46
1:B:29:LEU:N	1:B:76:GLN:HE22	2.11	0.46
1:D:110:ARG:HH11	1:D:110:ARG:HG2	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:100:TYR:HD2	1:C:154:MET:HE3	1.81	0.45
1:B:152:LYS:NZ	5:B:223:HOH:O	2.46	0.45
1:C:122:HIS:O	1:C:137:GLY:HA3	2.17	0.45
1:E:109:PHE:CD1	1:F:101:PHE:HB3	2.52	0.45
1:C:83:PHE:CD1	4:C:161:EMO:H102	2.51	0.45
1:B:13:PHE:H	1:B:16:HIS:CD2	2.14	0.45
1:B:134:GLN:NE2	5:B:200:HOH:O	2.49	0.45
1:F:86:LEU:HD13	1:F:133:TRP:HZ2	1.81	0.45
1:A:59:PHE:CE2	4:A:163:EMO:H2	2.53	0.44
1:C:98:ILE:HG23	1:C:158:ARG:HA	1.97	0.44
1:A:104:ILE:HB	1:B:107:VAL:HB	1.99	0.44
1:D:93:ILE:O	1:D:96:THR:CG2	2.62	0.44
1:A:75:ALA:HB2	1:A:101:PHE:CZ	2.53	0.44
1:A:41:LYS:HE2	5:A:237:HOH:O	2.18	0.44
1:A:108:LYS:HZ2	1:A:110:ARG:NH2	2.15	0.44
1:A:124:GLU:HG3	5:A:211:HOH:O	2.16	0.44
1:F:86:LEU:HD13	1:F:133:TRP:CZ2	2.52	0.43
1:A:108:LYS:HZ1	1:A:110:ARG:NH2	2.07	0.43
1:F:107:VAL:HA	1:F:148:GLU:O	2.18	0.43
1:A:108:LYS:HZ2	1:A:110:ARG:NH1	2.17	0.43
1:E:111:ILE:HB	1:E:146:VAL:HG12	2.01	0.43
1:A:60:PRO:O	1:A:61:ASN:HB2	2.18	0.43
1:E:107:VAL:HA	1:E:148:GLU:O	2.19	0.43
1:D:29:LEU:N	1:D:76:GLN:HE22	1.93	0.43
1:D:41:LYS:NZ	5:D:211:HOH:O	2.49	0.43
1:C:54:VAL:HG13	5:C:170:HOH:O	2.19	0.43
1:D:118:ARG:HD2	5:D:175:HOH:O	2.19	0.42
1:E:98:ILE:CG2	1:E:99:VAL:N	2.82	0.42
1:B:98:ILE:HA	2:B:160:BEN:H2	2.01	0.42
1:B:99:VAL:H	2:B:160:BEN:HN21	1.66	0.42
1:E:114:THR:HB	1:E:115:PRO:HD2	2.02	0.42
1:B:98:ILE:HD12	1:B:99:VAL:N	2.34	0.42
1:F:12:PHE:HB2	1:F:33:ILE:HB	2.01	0.42
1:D:9:GLN:HG2	1:D:12:PHE:CZ	2.55	0.42
1:B:114:THR:HB	1:B:115:PRO:HD2	2.02	0.42
1:A:98:ILE:HD12	1:A:100:TYR:CE2	2.55	0.41
1:E:12:PHE:HB3	1:E:16:HIS:HB2	2.02	0.41
1:B:11:GLN:HG3	1:B:33:ILE:O	2.19	0.41
1:C:114:THR:HB	1:C:115:PRO:HD2	2.02	0.41
1:B:21:LEU:HD23	2:B:160:BEN:H6	2.02	0.41
1:A:32:ARG:O	1:A:44:ALA:HB1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:107:VAL:HA	1:C:148:GLU:O	2.20	0.41
1:B:88:GLY:HA3	2:B:161:BEN:C6	2.51	0.41
1:C:83:PHE:CD1	4:C:161:EMO:H101	2.56	0.41
1:F:35:GLU:HB2	1:F:43:VAL:HB	2.03	0.41
1:A:13:PHE:H	1:A:16:HIS:CD2	2.19	0.41
1:F:69:LEU:HA	1:F:69:LEU:HD23	1.90	0.41
1:F:25:TYR:HA	1:F:26:PRO:HA	1.90	0.41
1:B:58:HIS:N	1:B:59:PHE:HA	2.36	0.41
1:D:30:VAL:HG23	1:D:76:GLN:HE21	1.86	0.41
1:B:69:LEU:HA	1:B:69:LEU:HD23	1.93	0.40
1:E:68:VAL:HB	1:F:68:VAL:HB	2.03	0.40
1:E:139:ALA:HB3	1:E:147:ALA:HB3	2.03	0.40
1:A:110:ARG:C	4:A:163:EMO:H101	2.41	0.40
1:E:72:GLU:HG3	1:E:76:GLN:HE21	1.86	0.40
1:C:17:ILE:HD13	1:C:30:VAL:HG12	2.03	0.40
1:F:15:GLU:HG3	1:F:15:GLU:H	1.57	0.40
1:D:34:THR:HG21	5:D:187:HOH:O	2.22	0.40
1:C:104:ILE:HB	1:D:107:VAL:HB	2.02	0.40
1:F:101:PHE:CE2	1:F:104:ILE:HG12	2.56	0.40
1:B:126:LEU:HD11	1:B:150:GLU:HG2	2.03	0.40
1:A:129:LYS:C	1:A:129:LYS:HE2	2.41	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	150/159 (94%)	147 (98%)	3 (2%)	0	100	100
1	B	148/159 (93%)	144 (97%)	4 (3%)	0	100	100
1	C	148/159 (93%)	144 (97%)	4 (3%)	0	100	100
1	D	150/159 (94%)	144 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	149/159 (94%)	144 (97%)	5 (3%)	0	100	100
1	F	146/159 (92%)	141 (97%)	5 (3%)	0	100	100
All	All	891/954 (93%)	864 (97%)	27 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	131/138 (95%)	125 (95%)	6 (5%)	33	44
1	B	129/138 (94%)	124 (96%)	5 (4%)	39	53
1	C	129/138 (94%)	123 (95%)	6 (5%)	32	43
1	D	131/138 (95%)	125 (95%)	6 (5%)	33	44
1	E	130/138 (94%)	127 (98%)	3 (2%)	58	75
1	F	127/138 (92%)	124 (98%)	3 (2%)	57	74
All	All	777/828 (94%)	748 (96%)	29 (4%)	41	55

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	LEU
1	A	26	PRO
1	A	98	ILE
1	A	101	PHE
1	A	129	LYS
1	A	151	LEU
1	B	26	PRO
1	B	127	LYS
1	B	151	LEU
1	B	158	ARG
1	B	159	GLU
1	C	9	GLN

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Mol	Chain	Res	Type
1	C	26	PRO
1	C	86	LEU
1	C	98	ILE
1	C	105	ASP
1	C	123	LEU
1	D	18	LEU
1	D	39	ASN
1	D	41	LYS
1	D	86	LEU
1	D	101	PHE
1	D	105	ASP
1	E	26	PRO
1	E	86	LEU
1	E	101	PHE
1	F	15	GLU
1	F	86	LEU
1	F	101	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	HIS
1	A	39	ASN
1	A	40	GLN
1	A	51	ASN
1	A	58	HIS
1	A	61	ASN
1	A	76	GLN
1	B	11	GLN
1	B	16	HIS
1	B	37	GLN
1	B	51	ASN
1	B	76	GLN
1	B	134	GLN
1	C	9	GLN
1	C	11	GLN
1	C	16	HIS
1	C	37	GLN
1	C	51	ASN
1	D	37	GLN
1	D	39	ASN
1	D	76	GLN

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Mol	Chain	Res	Type
1	D	134	GLN
1	E	11	GLN
1	E	37	GLN
1	E	40	GLN
1	F	37	GLN
1	F	39	ASN
1	F	40	GLN
1	F	51	ASN

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 15 ligands modelled in this entry, 6 are monoatomic - leaving 9 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	BEN	A	160	-	9,9,9	1.68	1 (11%)	9,11,11	0.54	0
2	BEN	A	161	-	9,9,9	1.69	1 (11%)	9,11,11	0.57	0
4	EMO	A	163	-	22,22,22	1.78	4 (18%)	34,34,34	0.98	1 (2%)
2	BEN	B	160	-	9,9,9	1.67	1 (11%)	9,11,11	0.59	0
2	BEN	B	161	-	9,9,9	1.70	1 (11%)	9,11,11	0.55	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EMO	C	161	-	22,22,22	1.85	4 (18%)	34,34,34	0.82	2 (5%)
2	BEN	D	160	-	9,9,9	1.69	1 (11%)	9,11,11	0.62	0
2	BEN	E	160	-	9,9,9	1.70	1 (11%)	9,11,11	0.62	0
2	BEN	E	161	-	9,9,9	1.69	1 (11%)	9,11,11	0.58	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BEN	A	160	-	-	0/4/4/4	0/1/1/1
2	BEN	A	161	-	-	0/4/4/4	0/1/1/1
4	EMO	A	163	-	-	0/0/16/16	0/3/3/3
2	BEN	B	160	-	-	0/4/4/4	0/1/1/1
2	BEN	B	161	-	-	0/4/4/4	0/1/1/1
4	EMO	C	161	-	-	0/0/16/16	0/3/3/3
2	BEN	D	160	-	-	0/4/4/4	0/1/1/1
2	BEN	E	160	-	-	0/4/4/4	0/1/1/1
2	BEN	E	161	-	-	0/4/4/4	0/1/1/1

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	161	BEN	C1-C	-4.82	1.39	1.47
2	E	160	BEN	C1-C	-4.80	1.39	1.47
2	A	161	BEN	C1-C	-4.80	1.39	1.47
2	E	161	BEN	C1-C	-4.78	1.39	1.47
2	D	160	BEN	C1-C	-4.78	1.39	1.47
2	A	160	BEN	C1-C	-4.76	1.39	1.47
2	B	160	BEN	C1-C	-4.74	1.39	1.47
4	C	161	EMO	C5-C6	-4.59	1.38	1.48
4	C	161	EMO	C7-C6	-4.47	1.38	1.48
4	A	163	EMO	C5-C6	-4.22	1.39	1.48
4	A	163	EMO	C7-C6	-4.16	1.39	1.48
4	A	163	EMO	C20-C19	-3.61	1.38	1.47
4	A	163	EMO	C18-C19	-3.47	1.39	1.47
4	C	161	EMO	C18-C19	-3.36	1.39	1.47
4	C	161	EMO	C20-C19	-3.35	1.39	1.47

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	A	163	EMO	C17-C16-C9	-2.59	118.82	121.05
4	C	161	EMO	C17-C16-C9	-2.11	119.23	121.05
4	C	161	EMO	C16-C9-C8	2.01	120.64	118.08

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	160	BEN	1	0
4	A	163	EMO	5	0
2	B	160	BEN	8	0
2	B	161	BEN	1	0
4	C	161	EMO	10	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	152/159 (95%)	-0.32	3 (1%) 68 75	12, 20, 36, 47	0
1	B	150/159 (94%)	-0.11	5 (3%) 50 59	13, 21, 35, 64	0
1	C	150/159 (94%)	-0.14	3 (2%) 68 75	14, 22, 34, 56	0
1	D	152/159 (95%)	-0.07	7 (4%) 36 45	13, 23, 41, 65	0
1	E	151/159 (94%)	-0.28	2 (1%) 79 84	14, 22, 36, 45	0
1	F	148/159 (93%)	-0.18	1 (0%) 89 92	14, 22, 36, 49	0
All	All	903/954 (94%)	-0.18	21 (2%) 64 72	12, 22, 37, 65	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	159	GLU	4.6
1	B	10	SER	4.5
1	B	159	GLU	4.4
1	D	8	LEU	3.8
1	D	9	GLN	3.7
1	C	10	SER	3.2
1	D	96	THR	2.8
1	B	142	ASP	2.7
1	F	142	ASP	2.7
1	A	8	LEU	2.6
1	D	61	ASN	2.6
1	C	100	TYR	2.5
1	C	144	LYS	2.4
1	B	92	GLU	2.4
1	D	10	SER	2.4
1	A	61	ASN	2.3
1	E	143	GLY	2.3
1	E	61	ASN	2.2
1	B	100	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	129	LYS	2.1
1	D	95	LYS	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	BEN	E	160	9/9	0.80	0.24	8.24	40,42,46,46	0
2	BEN	B	161	9/9	0.71	0.30	6.57	36,37,39,40	0
2	BEN	B	160	9/9	0.73	0.41	6.05	37,39,44,46	0
2	BEN	A	161	9/9	0.80	0.27	5.48	42,44,47,48	0
2	BEN	D	160	9/9	0.84	0.28	5.40	29,32,40,40	0
4	EMO	C	161	20/20	0.64	0.38	5.09	35,39,42,43	20
2	BEN	E	161	9/9	0.80	0.26	4.27	41,42,43,44	0
4	EMO	A	163	20/20	0.58	0.44	2.55	42,45,46,47	20
3	CL	F	160	1/1	0.93	0.13	2.46	39,39,39,39	0
2	BEN	A	160	9/9	0.91	0.14	2.22	21,23,25,26	0
3	CL	C	160	1/1	0.98	0.11	1.52	39,39,39,39	0
3	CL	E	162	1/1	0.99	0.08	-0.81	38,38,38,38	0
3	CL	A	162	1/1	0.97	0.06	-	33,33,33,33	0
3	CL	B	162	1/1	0.95	0.07	-	47,47,47,47	0
3	CL	D	161	1/1	0.98	0.09	-	47,47,47,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.