



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 09:20 am BST

PDB ID : 6AL7
Title : Crystal structure HpiC1 F138S
Authors : Newmister, S.A.; Li, S.; Garcia-Borras, M.; Sanders, J.N.; Yang, S.; Lowell, A.N.; Yu, F.; Smith, J.L.; Williams, R.M.; Houk, K.N.; Sherman, D.H.
Deposited on : 2017-08-07
Resolution : 1.69 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

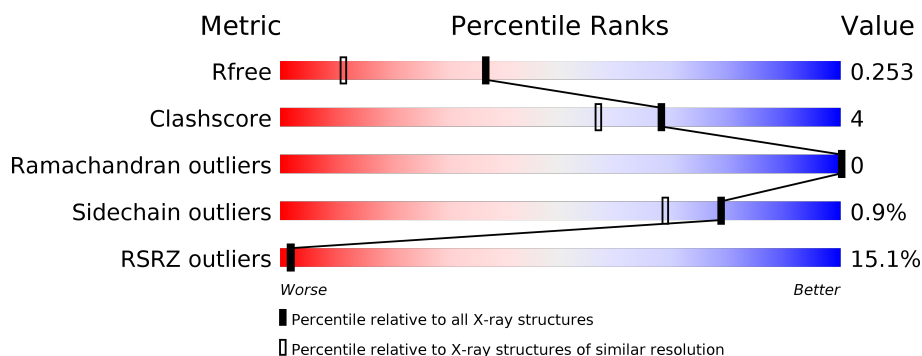
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.69 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	6780 (1.70-1.66)
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	225	<div> <div>4%</div> <div> <div></div> <div>83%</div> <div>5%</div> <div>12%</div> </div> </div>
1	B	225	<div> <div>%</div> <div> <div></div> <div>84%</div> <div>•</div> <div>11%</div> </div> </div>
1	D	225	<div> <div>23%</div> <div> <div></div> <div>74%</div> <div>13%</div> <div>12%</div> </div> </div>
1	E	225	<div> <div>24%</div> <div> <div></div> <div>69%</div> <div>10%</div> <div>•</div> <div>20%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6370 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 12-epi-hapalindole C/U synthase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	198	Total	C	N	O	0	1	0
			1529	978	247	304			
1	B	200	Total	C	N	O	0	0	0
			1538	983	249	306			
1	D	198	Total	C	N	O	0	0	0
			1524	975	247	302			
1	E	180	Total	C	N	O	0	0	0
			1366	874	225	267			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	MET	-	initiating methionine	UNP A0A076NBW8
A	4	GLY	-	expression tag	UNP A0A076NBW8
A	5	SER	-	expression tag	UNP A0A076NBW8
A	6	SER	-	expression tag	UNP A0A076NBW8
A	7	HIS	-	expression tag	UNP A0A076NBW8
A	8	HIS	-	expression tag	UNP A0A076NBW8
A	9	HIS	-	expression tag	UNP A0A076NBW8
A	10	HIS	-	expression tag	UNP A0A076NBW8
A	11	HIS	-	expression tag	UNP A0A076NBW8
A	12	HIS	-	expression tag	UNP A0A076NBW8
A	13	SER	-	expression tag	UNP A0A076NBW8
A	14	SER	-	expression tag	UNP A0A076NBW8
A	15	GLY	-	expression tag	UNP A0A076NBW8
A	16	LEU	-	expression tag	UNP A0A076NBW8
A	17	VAL	-	expression tag	UNP A0A076NBW8
A	18	PRO	-	expression tag	UNP A0A076NBW8
A	19	ARG	-	expression tag	UNP A0A076NBW8
A	20	GLY	-	expression tag	UNP A0A076NBW8
A	21	SER	-	expression tag	UNP A0A076NBW8
A	22	HIS	-	expression tag	UNP A0A076NBW8
A	23	MET	-	expression tag	UNP A0A076NBW8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	24	ALA	-	expression tag	UNP A0A076NBW8
A	25	SER	-	expression tag	UNP A0A076NBW8
A	138	SER	PHE	engineered mutation	UNP A0A076NBW8
B	3	MET	-	initiating methionine	UNP A0A076NBW8
B	4	GLY	-	expression tag	UNP A0A076NBW8
B	5	SER	-	expression tag	UNP A0A076NBW8
B	6	SER	-	expression tag	UNP A0A076NBW8
B	7	HIS	-	expression tag	UNP A0A076NBW8
B	8	HIS	-	expression tag	UNP A0A076NBW8
B	9	HIS	-	expression tag	UNP A0A076NBW8
B	10	HIS	-	expression tag	UNP A0A076NBW8
B	11	HIS	-	expression tag	UNP A0A076NBW8
B	12	HIS	-	expression tag	UNP A0A076NBW8
B	13	SER	-	expression tag	UNP A0A076NBW8
B	14	SER	-	expression tag	UNP A0A076NBW8
B	15	GLY	-	expression tag	UNP A0A076NBW8
B	16	LEU	-	expression tag	UNP A0A076NBW8
B	17	VAL	-	expression tag	UNP A0A076NBW8
B	18	PRO	-	expression tag	UNP A0A076NBW8
B	19	ARG	-	expression tag	UNP A0A076NBW8
B	20	GLY	-	expression tag	UNP A0A076NBW8
B	21	SER	-	expression tag	UNP A0A076NBW8
B	22	HIS	-	expression tag	UNP A0A076NBW8
B	23	MET	-	expression tag	UNP A0A076NBW8
B	24	ALA	-	expression tag	UNP A0A076NBW8
B	25	SER	-	expression tag	UNP A0A076NBW8
B	138	SER	PHE	engineered mutation	UNP A0A076NBW8
D	3	MET	-	initiating methionine	UNP A0A076NBW8
D	4	GLY	-	expression tag	UNP A0A076NBW8
D	5	SER	-	expression tag	UNP A0A076NBW8
D	6	SER	-	expression tag	UNP A0A076NBW8
D	7	HIS	-	expression tag	UNP A0A076NBW8
D	8	HIS	-	expression tag	UNP A0A076NBW8
D	9	HIS	-	expression tag	UNP A0A076NBW8
D	10	HIS	-	expression tag	UNP A0A076NBW8
D	11	HIS	-	expression tag	UNP A0A076NBW8
D	12	HIS	-	expression tag	UNP A0A076NBW8
D	13	SER	-	expression tag	UNP A0A076NBW8
D	14	SER	-	expression tag	UNP A0A076NBW8
D	15	GLY	-	expression tag	UNP A0A076NBW8
D	16	LEU	-	expression tag	UNP A0A076NBW8
D	17	VAL	-	expression tag	UNP A0A076NBW8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	18	PRO	-	expression tag	UNP A0A076NBW8
D	19	ARG	-	expression tag	UNP A0A076NBW8
D	20	GLY	-	expression tag	UNP A0A076NBW8
D	21	SER	-	expression tag	UNP A0A076NBW8
D	22	HIS	-	expression tag	UNP A0A076NBW8
D	23	MET	-	expression tag	UNP A0A076NBW8
D	24	ALA	-	expression tag	UNP A0A076NBW8
D	25	SER	-	expression tag	UNP A0A076NBW8
D	138	SER	PHE	engineered mutation	UNP A0A076NBW8
E	3	MET	-	initiating methionine	UNP A0A076NBW8
E	4	GLY	-	expression tag	UNP A0A076NBW8
E	5	SER	-	expression tag	UNP A0A076NBW8
E	6	SER	-	expression tag	UNP A0A076NBW8
E	7	HIS	-	expression tag	UNP A0A076NBW8
E	8	HIS	-	expression tag	UNP A0A076NBW8
E	9	HIS	-	expression tag	UNP A0A076NBW8
E	10	HIS	-	expression tag	UNP A0A076NBW8
E	11	HIS	-	expression tag	UNP A0A076NBW8
E	12	HIS	-	expression tag	UNP A0A076NBW8
E	13	SER	-	expression tag	UNP A0A076NBW8
E	14	SER	-	expression tag	UNP A0A076NBW8
E	15	GLY	-	expression tag	UNP A0A076NBW8
E	16	LEU	-	expression tag	UNP A0A076NBW8
E	17	VAL	-	expression tag	UNP A0A076NBW8
E	18	PRO	-	expression tag	UNP A0A076NBW8
E	19	ARG	-	expression tag	UNP A0A076NBW8
E	20	GLY	-	expression tag	UNP A0A076NBW8
E	21	SER	-	expression tag	UNP A0A076NBW8
E	22	HIS	-	expression tag	UNP A0A076NBW8
E	23	MET	-	expression tag	UNP A0A076NBW8
E	24	ALA	-	expression tag	UNP A0A076NBW8
E	25	SER	-	expression tag	UNP A0A076NBW8
E	138	SER	PHE	engineered mutation	UNP A0A076NBW8

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Ca 2 2	0	0
2	A	3	Total Ca 3 3	0	0
2	D	2	Total Ca 2 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	E	2	Total	Ca	0	0
			2	2		

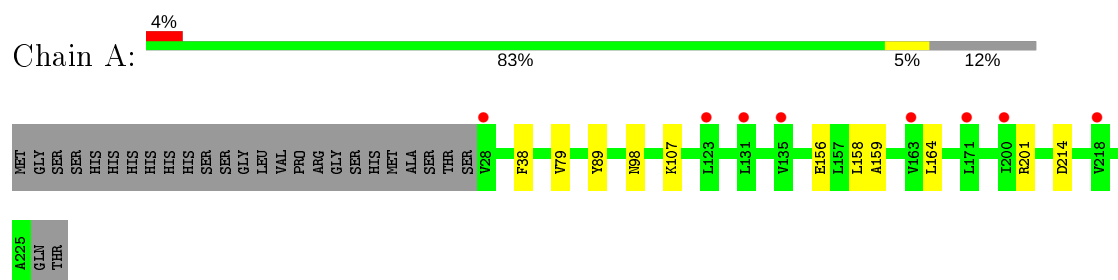
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	195	Total	O	0	0
			195	195		
3	B	152	Total	O	0	0
			152	152		
3	D	22	Total	O	0	0
			22	22		
3	E	35	Total	O	0	0
			35	35		

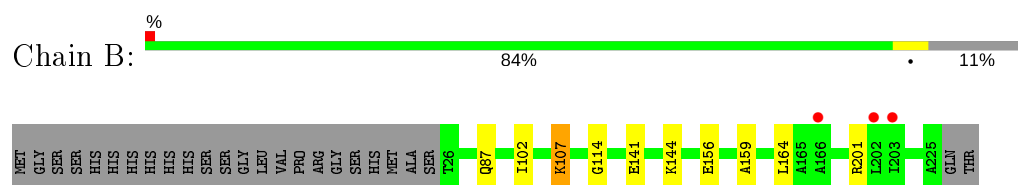
3 Residue-property plots [i](#)

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

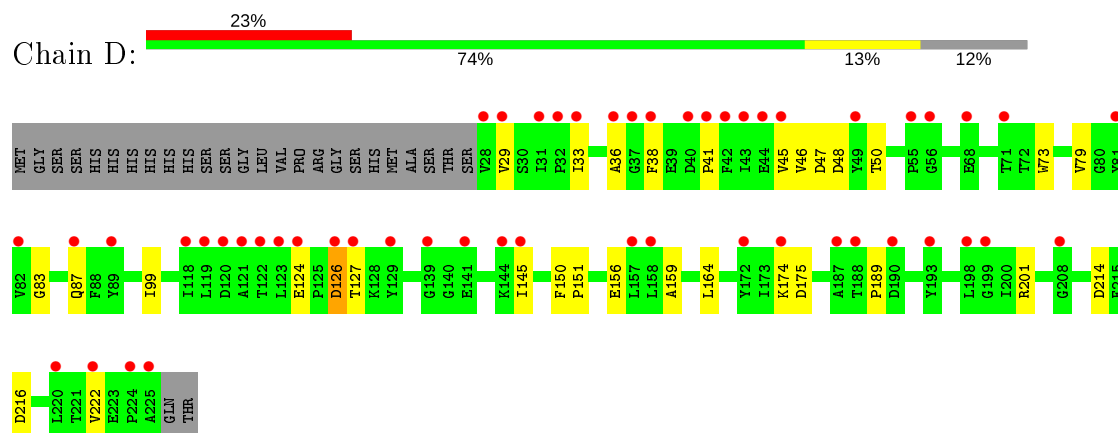
- Molecule 1: 12-epi-hapalindole C/U synthase



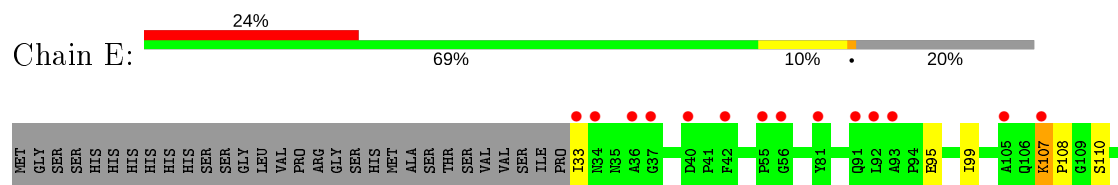
- Molecule 1: 12-epi-hapalindole C/U synthase

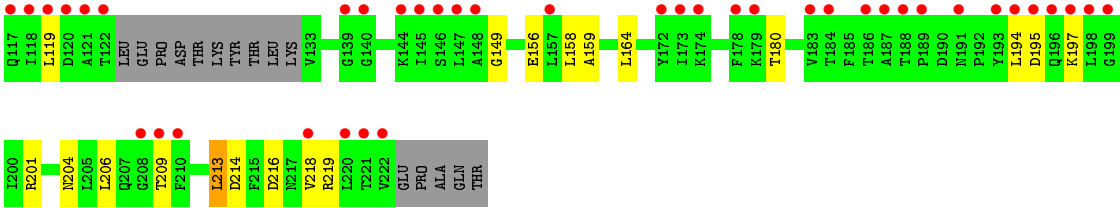


- Molecule 1: 12-epi-hapalindole C/U synthase



- Molecule 1: 12-epi-hapalindole C/U synthase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	62.05Å 47.94Å 174.26Å 90.00° 97.19° 90.00°	Depositor
Resolution (Å)	46.20 – 1.69 46.20 – 1.69	Depositor EDS
% Data completeness (in resolution range)	97.7 (46.20-1.69) 97.9 (46.20-1.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.32 (at 1.69Å)	Xtriage
Refinement program	PHENIX 1.11.1 _2575	Depositor
R, R_{free}	0.223 , 0.253 0.223 , 0.253	Depositor DCC
R_{free} test set	5663 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	32.0	Xtriage
Anisotropy	0.421	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 46.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6370	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.33% 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: CA

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	0/1570	0.61	0/2149
1	B	0.39	0/1576	0.60	0/2157
1	D	0.28	0/1562	0.51	0/2138
1	E	0.30	0/1399	0.53	0/1914
All	All	0.36	0/6107	0.57	0/8358

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	1529	0	1473	6	0
1	B	1538	0	1483	6	0
1	D	1524	0	1469	19	0
1	E	1366	0	1296	13	0
2	A	3	0	0	0	0
2	B	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
3	A	195	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	152	0	0	2	0
3	D	22	0	0	0	0
3	E	35	0	0	0	0
All	All	6370	0	5721	44	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 (44) 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:174:LYS:HZ2	1:D:175:ASP:H	1.41	0.69
1:D:45:VAL:HG23	1:D:48:ASP:CB	2.24	0.67
1:B:87:GLN:NE2	3:B:401:HOH:O	2.19	0.65
1:D:45:VAL:HG23	1:D:48:ASP:HB2	1.79	0.65
1:E:156:GLU:HB2	1:E:201:ARG:HB2	1.79	0.65
1:B:107:LYS:NZ	3:B:403:HOH:O	2.34	0.60
1:D:46:VAL:HG23	1:D:83:GLY:H	1.67	0.59
1:D:174:LYS:NZ	1:D:175:ASP:H	2.00	0.58
1:E:119:LEU:O	1:E:197:LYS:NZ	2.39	0.56
1:E:159:ALA:HB2	1:E:164:LEU:HD11	1.88	0.54
1:E:149:GLY:HA3	1:E:209:THR:O	2.06	0.54
1:E:158:LEU:HD11	1:E:201:ARG:HG3	1.89	0.53
1:D:156:GLU:HB2	1:D:201:ARG:HB2	1.90	0.53
1:A:158:LEU:HD11	1:A:201:ARG:HG3	1.91	0.52
1:E:108:PRO:HA	1:E:206:LEU:HG	1.94	0.50
1:D:99:ILE:HG22	1:D:216:ASP:HB2	1.95	0.49
1:E:99:ILE:HG22	1:E:216:ASP:HB2	1.94	0.49
1:D:99:ILE:HD13	1:D:214:ASP:HB3	1.96	0.47
1:E:33:ILE:HD13	1:E:218:VAL:HG13	1.97	0.47
1:E:99:ILE:HD13	1:E:214:ASP:HB3	1.97	0.46
1:A:89:TYR:OH	1:A:214:ASP:OD2	2.20	0.46
1:D:38:PHE:HB3	1:D:79:VAL:HG22	1.97	0.46
1:E:107:LYS:O	1:E:110:SER:OG	2.24	0.46
1:E:204:ASN:HB2	1:E:213:LEU:HD11	1.98	0.46
1:B:156:GLU:HB2	1:B:201:ARG:HB2	1.98	0.45
1:E:194:LEU:O	1:E:195:ASP:HB2	2.17	0.44
1:D:33:ILE:HB	1:D:36:ALA:HB2	2.00	0.44
1:D:150:PHE:CD1	1:D:151:PRO:HD2	2.54	0.42
1:D:29:VAL:O	1:D:222:VAL:HG12	2.19	0.42
1:B:141:GLU:OE2	1:B:144:LYS:HA	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:159:ALA:HB2	1:D:164:LEU:HD11	2.00	0.42
1:E:180:THR:HG23	1:E:219:ARG:HH22	1.83	0.42
1:A:156:GLU:HB2	1:A:201:ARG:HB2	2.02	0.42
1:D:126:ASP:OD1	1:D:189:PRO:HD3	2.20	0.42
1:D:45:VAL:HG23	1:D:48:ASP:HB3	2.02	0.42
1:D:124:GLU:O	1:D:127:THR:HG22	2.19	0.42
1:D:41:PRO:HG2	1:D:50:THR:HG21	2.01	0.42
1:B:102:ILE:HG12	1:B:114:GLY:HA2	2.02	0.41
1:A:159:ALA:HB2	1:A:164:LEU:HD11	2.03	0.41
1:A:38:PHE:HB3	1:A:79:VAL:HG22	2.02	0.41
1:A:79:VAL:HG13	1:A:98:ASN:HB3	2.02	0.41
1:D:73:TRP:CH2	1:D:145:ILE:HD12	2.56	0.41
1:B:159:ALA:HB2	1:B:164:LEU:HD11	2.02	0.40
1:D:47:ASP:OD2	1:D:87:GLN:NE2	2.54	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	197/225 (88%)	195 (99%)	2 (1%)	0	100	100
1	B	198/225 (88%)	195 (98%)	3 (2%)	0	100	100
1	D	196/225 (87%)	191 (97%)	5 (3%)	0	100	100
1	E	176/225 (78%)	171 (97%)	5 (3%)	0	100	100
All	All	767/900 (85%)	752 (98%)	15 (2%)	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	166/189 (88%)	165 (99%)	1 (1%)	86	79
1	B	167/189 (88%)	166 (99%)	1 (1%)	86	79
1	D	165/189 (87%)	164 (99%)	1 (1%)	86	79
1	E	143/189 (76%)	140 (98%)	3 (2%)	53	33
All	All	641/756 (85%)	635 (99%)	6 (1%)	78	69

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	107	LYS
1	B	107	LYS
1	D	126	ASP
1	E	95	GLU
1	E	107	LYS
1	E	213	LEU

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

Mol	Chain	Res	Type
1	D	87	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 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

5.7 Other polymers

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	198/225 (88%)	0.51	8 (4%) 38 41	26, 34, 47, 79	0
1	B	200/225 (88%)	0.48	3 (1%) 73 77	27, 36, 54, 70	0
1	D	198/225 (88%)	1.45	52 (26%) 0 0	42, 65, 86, 100	0
1	E	180/225 (80%)	1.44	54 (30%) 0 0	39, 58, 84, 98	0
All	All	776/900 (86%)	0.96	117 (15%) 2 2	26, 46, 80, 100	0

All (117) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	38	PHE	7.0
1	E	208	GLY	6.7
1	D	224	PRO	6.7
1	D	32	PRO	6.1
1	E	198	LEU	6.1
1	D	56	GLY	6.1
1	D	123	LEU	5.9
1	D	187	ALA	5.9
1	E	33	ILE	5.9
1	D	81	TYR	5.8
1	E	145	ILE	5.7
1	E	222	VAL	5.7
1	E	121	ALA	5.1
1	D	45	VAL	5.1
1	D	43	ILE	5.0
1	D	42	PHE	4.6
1	D	127	THR	4.5
1	E	120	ASP	4.5
1	D	124	GLU	4.5
1	E	139	GLY	4.5
1	D	28	VAL	4.4

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Mol	Chain	Res	Type	RSRZ
1	E	184	THR	4.3
1	D	208	GLY	4.2
1	E	174	LYS	4.1
1	E	199	GLY	4.1
1	D	193	TYR	4.1
1	D	41	PRO	4.1
1	D	119	LEU	4.0
1	E	221	THR	4.0
1	D	36	ALA	4.0
1	E	148	ALA	3.9
1	E	55	PRO	3.8
1	D	190	ASP	3.8
1	E	220	LEU	3.8
1	D	31	ILE	3.7
1	D	37	GLY	3.7
1	A	28	VAL	3.7
1	E	91	GLN	3.6
1	D	172	TYR	3.6
1	E	118	ILE	3.6
1	E	188	THR	3.5
1	E	195	ASP	3.5
1	E	157	LEU	3.5
1	D	29	VAL	3.5
1	D	122	THR	3.5
1	E	56	GLY	3.4
1	E	173	ILE	3.4
1	E	34	ASN	3.4
1	E	209	THR	3.4
1	E	197	LYS	3.4
1	E	172	TYR	3.3
1	E	122	THR	3.3
1	E	191	ASN	3.3
1	E	147	LEU	3.3
1	D	158	LEU	3.2
1	D	129	TYR	3.2
1	E	196	GLN	3.2
1	D	157	LEU	3.2
1	A	135	VAL	3.1
1	E	81	TYR	3.1
1	D	144	LYS	3.1
1	D	222	VAL	3.1
1	D	33	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	198	LEU	3.0
1	D	199	GLY	2.9
1	D	118	ILE	2.9
1	E	189	PRO	2.9
1	D	145	ILE	2.8
1	E	187	ALA	2.8
1	D	121	ALA	2.8
1	E	193	TYR	2.7
1	B	166	ALA	2.7
1	B	202	LEU	2.7
1	E	40	ASP	2.7
1	D	49	TYR	2.6
1	D	89	TYR	2.6
1	E	119	LEU	2.6
1	E	194	LEU	2.6
1	E	93	ALA	2.5
1	E	183	VAL	2.5
1	D	40	ASP	2.5
1	D	188	THR	2.5
1	E	140	GLY	2.5
1	A	123	LEU	2.5
1	E	105	ALA	2.5
1	E	210	PHE	2.5
1	A	218	VAL	2.5
1	D	71	THR	2.4
1	D	55	PRO	2.4
1	A	200	ILE	2.4
1	E	186	THR	2.3
1	D	82	VAL	2.3
1	E	92	LEU	2.3
1	E	37	GLY	2.3
1	E	107	LYS	2.3
1	D	139	GLY	2.3
1	E	36	ALA	2.3
1	D	44	GLU	2.3
1	D	225	ALA	2.3
1	E	146	SER	2.3
1	D	68	GLU	2.2
1	E	144	LYS	2.2
1	E	42	PHE	2.2
1	E	218	VAL	2.2
1	D	220	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	126	ASP	2.2
1	E	179	LYS	2.2
1	A	163	VAL	2.1
1	D	174	LYS	2.1
1	D	87	GLN	2.1
1	E	178	PHE	2.1
1	A	131	LEU	2.1
1	E	117	GLN	2.0
1	D	141	GLU	2.0
1	D	120	ASP	2.0
1	A	171	LEU	2.0
1	B	203	ILE	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CA	A	303	1/1	0.60	0.09	73,73,73,73	0
2	CA	E	301	1/1	0.83	0.08	55,55,55,55	0
2	CA	E	302	1/1	0.86	0.06	68,68,68,68	0
2	CA	D	301	1/1	0.89	0.08	58,58,58,58	0
2	CA	D	302	1/1	0.96	0.06	54,54,54,54	0
2	CA	B	301	1/1	0.98	0.09	31,31,31,31	0
2	CA	A	302	1/1	0.98	0.10	29,29,29,29	0
2	CA	A	301	1/1	0.99	0.37	64,64,64,64	0
2	CA	B	302	1/1	1.00	0.12	29,29,29,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.