



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:31 PM UTC

PDB ID : 5X87 / pdb_00005x87
Title : Crystal structure of a bacterial Bestrophin homolog from *Klebsiella pneumoniae* with a mutation L177T
Authors : Zhang, Y.; Chen, S.; Yang, T.
Deposited on : 2017-03-01
Resolution : 3.14 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
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

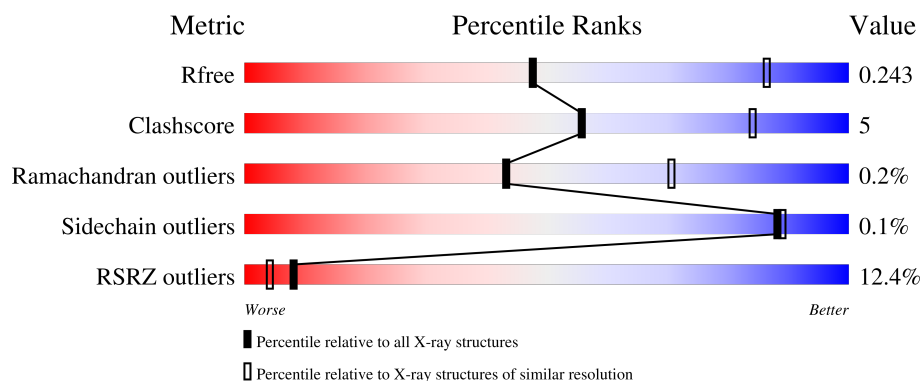
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.14 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	2351 (3.18-3.10)
Clashscore	190562	2452 (3.18-3.10)
Ramachandran outliers	187476	2324 (3.18-3.10)
Sidechain outliers	187428	2324 (3.18-3.10)
RSRZ outliers	180081	2351 (3.18-3.10)

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	297	7% 81% 8% 10%
1	B	297	8% 79% 11% 10%
1	C	297	10% 80% 10% 9%
1	D	297	18% 78% 12% 10%
1	E	297	13% 79% 11% 9%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10678 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 Bestrophin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	268	Total	C	N	O	S	0	0	0
			2119	1371	359	380	9			
1	B	268	Total	C	N	O	S	0	0	0
			2130	1378	360	383	9			
1	C	269	Total	C	N	O	S	0	0	0
			2109	1360	362	378	9			
1	D	268	Total	C	N	O	S	0	0	0
			2113	1365	359	380	9			
1	E	270	Total	C	N	O	S	0	0	0
			2151	1394	364	384	9			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP W1ELP7
A	-1	ASN	-	expression tag	UNP W1ELP7
A	0	ALA	-	expression tag	UNP W1ELP7
A	177	THR	LEU	engineered mutation	UNP W1ELP7
B	-2	SER	-	expression tag	UNP W1ELP7
B	-1	ASN	-	expression tag	UNP W1ELP7
B	0	ALA	-	expression tag	UNP W1ELP7
B	177	THR	LEU	engineered mutation	UNP W1ELP7
C	-2	SER	-	expression tag	UNP W1ELP7
C	-1	ASN	-	expression tag	UNP W1ELP7
C	0	ALA	-	expression tag	UNP W1ELP7
C	177	THR	LEU	engineered mutation	UNP W1ELP7
D	-2	SER	-	expression tag	UNP W1ELP7
D	-1	ASN	-	expression tag	UNP W1ELP7
D	0	ALA	-	expression tag	UNP W1ELP7
D	177	THR	LEU	engineered mutation	UNP W1ELP7
E	-2	SER	-	expression tag	UNP W1ELP7
E	-1	ASN	-	expression tag	UNP W1ELP7
E	0	ALA	-	expression tag	UNP W1ELP7

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Chain	Residue	Modelled	Actual	Comment	Reference
E	177	THR	LEU	engineered mutation	UNP W1ELP7

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total Zn 4 4	0	0
2	B	3	Total Zn 3 3	0	0
2	C	3	Total Zn 3 3	0	0
2	D	3	Total Zn 3 3	0	0
2	E	2	Total Zn 2 2	0	0

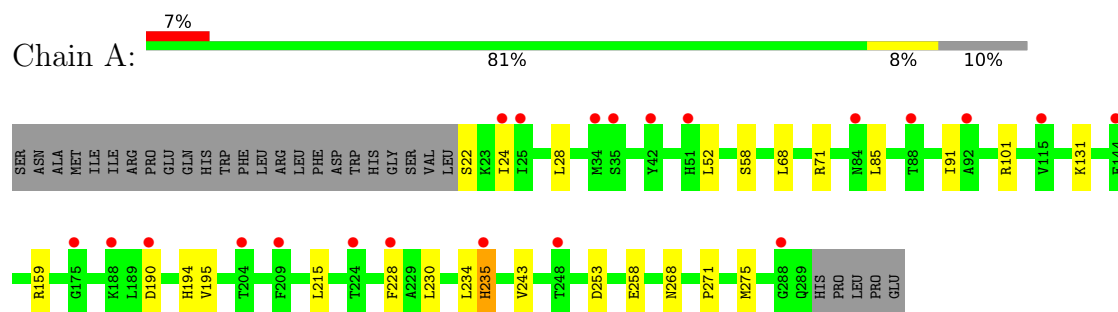
- Molecule 3 is water.

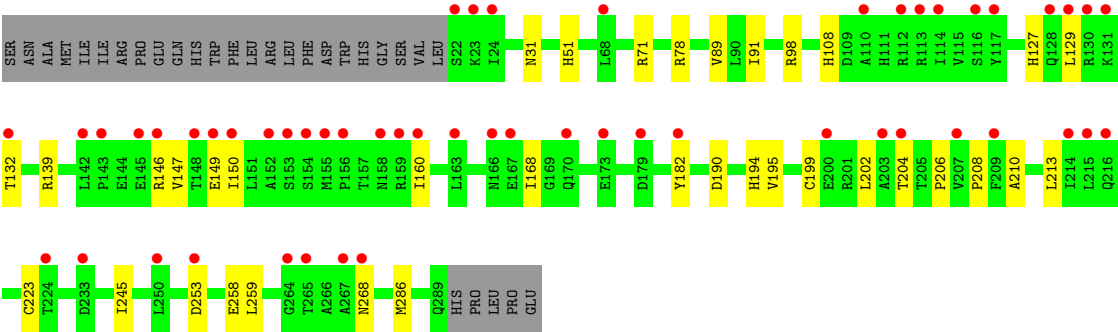
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	6	Total O 6 6	0	0
3	B	5	Total O 5 5	0	0
3	C	10	Total O 10 10	0	0
3	D	10	Total O 10 10	0	0
3	E	10	Total O 10 10	0	0

3 Residue-property plots [i](#)

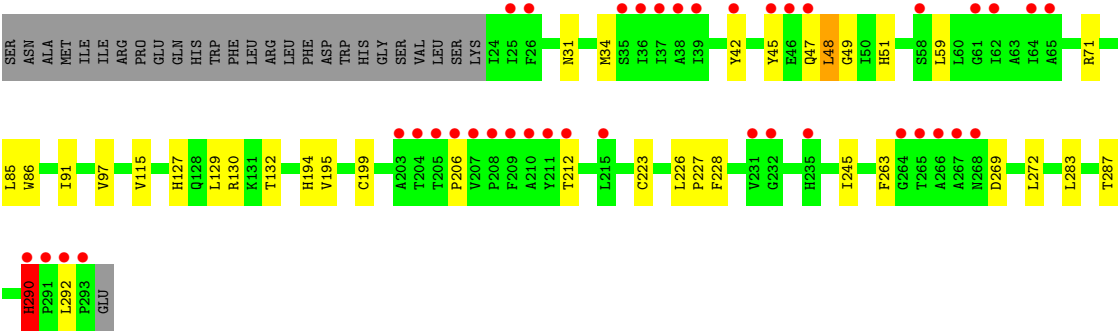
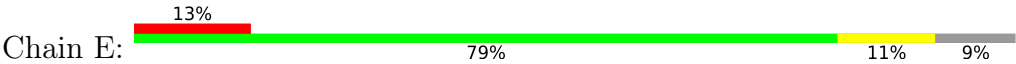
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Bestrophin





● Molecule 1: Bestrophin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	114.48Å 160.57Å 162.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	65.73 – 3.14 65.73 – 3.14	Depositor EDS
% Data completeness (in resolution range)	99.9 (65.73-3.14) 89.6 (65.73-3.14)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.67 (at 3.13Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.199 , 0.237 0.206 , 0.243	Depositor DCC
R_{free} test set	1998 reflections (3.77%)	wwPDB-VP
Wilson B-factor (Å ²)	74.6	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 56.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.017 for -h,l,k	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	10678	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% 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:
ZN

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	0.10	0/2165	0.29	1/2949 (0.0%)
1	B	0.21	0/2176	0.33	1/2963 (0.0%)
1	C	0.10	0/2154	0.27	0/2936
1	D	0.09	0/2158	0.26	0/2940
1	E	0.23	0/2200	0.47	3/2998 (0.1%)
All	All	0.16	0/10853	0.33	5/14786 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	290	HIS	CA-C-N	-10.62	109.52	120.03
1	E	290	HIS	C-N-CA	-10.62	109.52	120.03
1	E	48	LEU	N-CA-C	-9.93	101.17	113.28
1	A	235	HIS	CB-CA-C	-5.57	110.17	116.63
1	B	287	THR	CB-CA-C	-5.20	100.95	109.80

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	2119	0	2147	23	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2130	0	2166	25	0
1	C	2109	0	2130	23	0
1	D	2113	0	2140	25	0
1	E	2151	0	2191	27	1
2	A	4	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	0	0
2	E	2	0	0	0	0
3	A	6	0	0	0	0
3	B	5	0	0	0	0
3	C	10	0	0	0	0
3	D	10	0	0	1	0
3	E	10	0	0	0	0
All	All	10678	0	10774	100	1

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 5.

All (100) 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:A:235:HIS:ND1	1:E:51:HIS:HD2	1.03	1.49
1:A:235:HIS:ND1	1:E:51:HIS:CD2	1.90	1.37
1:A:235:HIS:CE1	1:E:51:HIS:CD2	2.36	1.12
1:A:235:HIS:CE1	1:E:51:HIS:HD2	1.72	1.06
1:B:127:HIS:HD1	1:B:132:THR:HG1	1.13	0.92
1:B:71:ARG:NH1	1:B:260:GLU:OE2	2.12	0.81
1:A:258:GLU:OE1	1:A:268:ASN:ND2	2.21	0.72
1:A:235:HIS:CG	1:E:51:HIS:CD2	2.77	0.71
1:E:47:GLN:O	1:E:47:GLN:HG2	1.90	0.71
1:D:78:ARG:NH2	1:D:202:LEU:O	2.26	0.68
1:B:41:SER:HA	1:B:44:TRP:HD1	1.59	0.66
1:A:230:LEU:HB3	1:A:234:LEU:HD12	1.78	0.65
1:B:71:ARG:HH22	1:B:212:THR:HG22	1.62	0.65
1:D:258:GLU:OE1	1:D:268:ASN:ND2	2.30	0.64
1:E:48:LEU:HD23	1:E:48:LEU:N	2.13	0.63
1:A:68:LEU:HD23	1:A:215:LEU:HD13	1.81	0.61
1:A:91:ILE:HD13	1:E:194:HIS:HA	1.82	0.61
1:C:91:ILE:HD13	1:D:194:HIS:HA	1.82	0.61
1:C:194:HIS:HA	1:E:91:ILE:HD13	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:103:ILE:HD13	1:B:181:THR:HB	1.83	0.59
1:B:24:ILE:HG22	1:B:28:LEU:HG	1.84	0.58
1:B:78:ARG:NH2	1:B:202:LEU:O	2.36	0.58
1:B:190:ASP:OD1	1:D:98:ARG:NH2	2.38	0.57
1:C:208:PRO:O	1:C:210:ALA:N	2.38	0.57
1:B:194:HIS:HA	1:D:91:ILE:HD13	1.85	0.56
1:A:194:HIS:HA	1:B:91:ILE:HD13	1.86	0.56
1:D:71:ARG:NH2	1:D:253:ASP:OD1	2.32	0.55
1:C:98:ARG:NH2	1:D:190:ASP:OD1	2.41	0.54
1:E:31:ASN:ND2	1:E:223:CYS:O	2.33	0.54
1:C:115:VAL:HG21	1:C:287:THR:HG21	1.91	0.52
1:C:68:LEU:HD23	1:C:215:LEU:HD13	1.91	0.52
1:B:24:ILE:HD12	1:B:250:LEU:HB3	1.90	0.52
1:B:211:TYR:O	1:B:215:LEU:HB2	2.10	0.52
1:C:42:TYR:HA	1:C:45:TYR:CD1	2.45	0.52
1:C:71:ARG:NH1	1:C:260:GLU:OE2	2.42	0.52
1:D:31:ASN:ND2	1:D:223:CYS:O	2.43	0.51
1:B:208:PRO:HG2	1:D:259:LEU:HD21	1.92	0.51
1:E:42:TYR:HA	1:E:45:TYR:CD1	2.46	0.50
1:C:208:PRO:C	1:C:210:ALA:H	2.20	0.50
1:A:28:LEU:HD22	1:A:243:VAL:HG13	1.94	0.50
1:C:71:ARG:NH2	1:C:253:ASP:OD1	2.43	0.50
1:B:60:LEU:HD13	1:D:245:ILE:HG12	1.94	0.49
1:A:22:SER:HB2	1:A:24:ILE:HG22	1.94	0.49
1:D:146:ARG:NH1	1:D:149:GLU:OE1	2.42	0.49
1:C:96:LEU:HD23	1:C:118:LEU:HD11	1.94	0.48
1:D:108:HIS:ND1	3:D:402:HOH:O	2.35	0.48
1:C:150:ILE:HA	1:C:159:ARG:HG2	1.95	0.48
1:D:139:ARG:HG3	1:D:147:VAL:HG11	1.96	0.48
1:A:159:ARG:NH2	1:B:289:GLN:O	2.46	0.48
1:A:52:LEU:HD12	1:A:228:PHE:HB3	1.96	0.48
1:E:115:VAL:HG21	1:E:287:THR:HG21	1.97	0.47
1:B:150:ILE:HD13	1:B:160:ILE:HG12	1.96	0.47
1:C:146:ARG:HH11	1:C:146:ARG:HA	1.80	0.47
1:D:150:ILE:HD13	1:D:160:ILE:HG12	1.97	0.47
1:E:130:ARG:NH1	1:E:269:ASP:OD2	2.47	0.47
1:E:42:TYR:HA	1:E:45:TYR:CE1	2.50	0.46
1:E:97:VAL:HG21	1:E:283:LEU:HD22	1.97	0.46
1:A:85:LEU:HD22	1:A:195:VAL:HA	1.97	0.46
1:C:188:LYS:HA	1:C:188:LYS:HD3	1.78	0.46
1:A:190:ASP:OD1	1:B:98:ARG:NH2	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:208:PRO:O	1:B:211:TYR:HB2	2.15	0.46
1:C:100:LEU:HD11	1:C:114:ILE:HD12	1.97	0.46
1:E:85:LEU:HD22	1:E:195:VAL:HA	1.98	0.46
1:E:129:LEU:HD21	1:E:199:CYS:HB3	1.98	0.45
1:D:204:THR:O	1:D:206:PRO:HD3	2.16	0.45
1:E:71:ARG:NH1	1:E:212:THR:OG1	2.39	0.45
1:A:71:ARG:NH2	1:A:253:ASP:OD1	2.42	0.45
1:D:129:LEU:HD21	1:D:199:CYS:HB3	1.98	0.45
1:B:85:LEU:HD22	1:B:195:VAL:HA	1.98	0.45
1:E:127:HIS:ND1	1:E:132:THR:OG1	2.44	0.45
1:B:127:HIS:ND1	1:B:132:THR:OG1	2.24	0.44
1:A:58:SER:HA	1:E:59:LEU:HD13	1.99	0.44
1:C:135:THR:HG23	1:C:151:LEU:HD11	2.00	0.44
1:C:60:LEU:HD13	1:E:245:ILE:HG12	2.00	0.43
1:E:86:TRP:CE2	1:E:272:LEU:HD11	2.54	0.43
1:C:150:ILE:HD13	1:C:160:ILE:HG12	2.00	0.43
1:A:52:LEU:HA	1:B:234:LEU:HD22	2.00	0.43
1:D:127:HIS:ND1	1:D:132:THR:OG1	2.43	0.43
1:D:168:ILE:HG22	1:D:182:TYR:HD1	1.84	0.43
1:D:210:ALA:HA	1:D:213:LEU:HB3	2.00	0.43
1:C:255:LEU:HD13	1:D:210:ALA:HB3	2.01	0.43
1:A:271:PRO:HD2	1:A:275:MET:HE3	2.00	0.43
1:B:234:LEU:O	1:B:238:THR:OG1	2.37	0.43
1:B:285:ASP:HB3	1:B:289:GLN:O	2.19	0.43
1:C:95:THR:OG1	1:C:188:LYS:HD2	2.20	0.42
1:D:98:ARG:HB2	1:D:286:MET:HE1	2.01	0.42
1:A:235:HIS:HB2	1:E:49:GLY:O	2.20	0.42
1:D:89:VAL:HG23	1:D:195:VAL:HG11	2.01	0.42
1:C:76:TYR:HE1	1:D:208:PRO:HD2	1.85	0.42
1:B:81:GLU:OE2	1:B:201:ARG:NH2	2.49	0.41
1:E:129:LEU:HB3	1:E:263:PHE:HB3	2.02	0.41
1:C:234:LEU:HB3	1:C:237:MET:HB2	2.02	0.41
1:A:101:ARG:HE	1:A:101:ARG:HB3	1.60	0.41
1:E:34:MET:HE3	1:E:228:PHE:CE1	2.55	0.41
1:A:234:LEU:O	1:A:235:HIS:HB2	2.21	0.41
1:D:168:ILE:HG22	1:D:182:TYR:CD1	2.56	0.41
1:E:226:LEU:N	1:E:227:PRO:HD2	2.36	0.41
1:E:292:LEU:HD23	1:E:292:LEU:HA	1.92	0.41
1:C:234:LEU:HA	1:D:51:HIS:HB2	2.03	0.40
1:B:287:THR:O	1:B:287:THR:OG1	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:LYS:CB	1:E:290:HIS:O[4_545]	2.17	0.03

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	266/297 (90%)	264 (99%)	2 (1%)	0	100	100
1	B	266/297 (90%)	258 (97%)	8 (3%)	0	100	100
1	C	267/297 (90%)	259 (97%)	6 (2%)	2 (1%)	18	47
1	D	266/297 (90%)	263 (99%)	3 (1%)	0	100	100
1	E	268/297 (90%)	262 (98%)	5 (2%)	1 (0%)	30	59
All	All	1333/1485 (90%)	1306 (98%)	24 (2%)	3 (0%)	43	70

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	209	PHE
1	C	208	PRO
1	E	206	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	229/260 (88%)	229 (100%)	0	100	100
1	B	232/260 (89%)	232 (100%)	0	100	100
1	C	226/260 (87%)	226 (100%)	0	100	100
1	D	228/260 (88%)	228 (100%)	0	100	100
1	E	235/260 (90%)	234 (100%)	1 (0%)	84	84
All	All	1150/1300 (88%)	1149 (100%)	1 (0%)	88	89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	290	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	102	ASN
1	A	289	GLN
1	B	31	ASN
1	B	72	ASN
1	B	102	ASN
1	B	289	GLN
1	C	102	ASN
1	C	216	GLN
1	D	31	ASN
1	D	43	GLN
1	D	268	ASN
1	E	51	HIS
1	E	235	HIS
1	E	282	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 15 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 [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	268/297 (90%)	0.36	21 (7%) 19 9	47, 82, 147, 188	0
1	B	268/297 (90%)	0.51	25 (9%) 14 7	50, 90, 140, 157	0
1	C	269/297 (90%)	0.55	29 (10%) 11 5	50, 83, 158, 189	0
1	D	268/297 (90%)	1.15	53 (19%) 3 1	55, 94, 141, 160	0
1	E	270/297 (90%)	0.63	39 (14%) 6 3	47, 82, 140, 186	0
All	All	1343/1485 (90%)	0.64	167 (12%) 8 4	47, 85, 145, 189	0

All (167) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	145	GLU	14.7
1	C	47	GLN	10.1
1	D	154	SER	9.8
1	D	265	THR	8.5
1	D	153	SER	8.5
1	D	131	LYS	8.1
1	D	146	ARG	7.8
1	D	149	GLU	7.8
1	C	44	TRP	7.5
1	C	285	ASP	6.7
1	B	220	TYR	6.4
1	D	130	ARG	6.3
1	E	47	GLN	6.1
1	D	233	ASP	6.0
1	B	46	GLU	5.9
1	E	266	ALA	5.9
1	D	163	LEU	5.8
1	E	265	THR	5.4
1	C	51	HIS	5.4
1	C	206	PRO	5.0

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Mol	Chain	Res	Type	RSRZ
1	A	51	HIS	4.9
1	D	117	TYR	4.9
1	B	210	ALA	4.8
1	C	43	GLN	4.7
1	E	61	GLY	4.6
1	E	26	PHE	4.6
1	D	166	ASN	4.6
1	B	288	GLY	4.4
1	D	159	ARG	4.4
1	E	235	HIS	4.4
1	C	204	THR	4.4
1	E	25	ILE	4.3
1	E	264	GLY	4.1
1	D	129	LEU	4.1
1	E	64	ILE	4.1
1	E	42	TYR	4.0
1	D	170	GLN	3.9
1	D	128	GLN	3.8
1	C	106	ALA	3.8
1	D	23	LYS	3.8
1	D	204	THR	3.8
1	D	152	ALA	3.7
1	D	264	GLY	3.5
1	B	24	ILE	3.5
1	A	204	THR	3.5
1	C	40	ILE	3.5
1	D	224	THR	3.4
1	C	184	LEU	3.4
1	D	24	ILE	3.4
1	B	73	SER	3.4
1	B	26	PHE	3.3
1	E	208	PRO	3.3
1	E	290	HIS	3.3
1	E	39	ILE	3.3
1	E	65	ALA	3.3
1	C	288	GLY	3.2
1	C	208	PRO	3.2
1	E	291	PRO	3.2
1	C	207	VAL	3.2
1	E	45	TYR	3.2
1	C	291	PRO	3.2
1	D	143	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
1	C	41	SER	3.2
1	A	175	GLY	3.1
1	A	84	ASN	3.1
1	A	235	HIS	3.1
1	A	288	GLY	3.1
1	B	93	GLU	3.0
1	A	224	THR	3.0
1	D	110	ALA	3.0
1	D	200	GLU	3.0
1	E	204	THR	3.0
1	E	38	ALA	2.9
1	D	215	LEU	2.9
1	D	113	ARG	2.9
1	D	160	ILE	2.9
1	E	215	LEU	2.9
1	C	59	LEU	2.9
1	D	214	ILE	2.9
1	E	37	ILE	2.9
1	C	212	THR	2.8
1	D	132	THR	2.8
1	E	207	VAL	2.8
1	D	22	SER	2.8
1	D	173	GLU	2.8
1	D	150	ILE	2.8
1	D	250	LEU	2.8
1	A	34	MET	2.8
1	C	236	TYR	2.8
1	E	58	SER	2.8
1	C	46	GLU	2.8
1	D	167	GLU	2.8
1	D	158	ASN	2.8
1	C	99	GLN	2.8
1	D	148	THR	2.8
1	E	206	PRO	2.7
1	B	228	PHE	2.7
1	E	35	SER	2.7
1	D	155	MET	2.7
1	E	36	ILE	2.7
1	C	286	MET	2.7
1	E	205	THR	2.7
1	E	209	PHE	2.7
1	B	155	MET	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	248	THR	2.6
1	E	211	TYR	2.6
1	E	293	PRO	2.6
1	D	112	ARG	2.6
1	A	35	SER	2.6
1	B	154	SER	2.6
1	A	209	PHE	2.6
1	A	190	ASP	2.6
1	D	179	ASP	2.6
1	C	213	LEU	2.6
1	D	203	ALA	2.6
1	D	142	LEU	2.6
1	B	204	THR	2.6
1	A	144	GLU	2.5
1	D	156	PRO	2.5
1	A	228	PHE	2.5
1	A	188	LYS	2.5
1	B	289	GLN	2.5
1	B	205	THR	2.4
1	D	253	ASP	2.4
1	D	267	ALA	2.4
1	C	235	HIS	2.4
1	C	289	GLN	2.4
1	B	27	ARG	2.4
1	C	188	LYS	2.3
1	E	210	ALA	2.3
1	E	268	ASN	2.3
1	A	42	TYR	2.3
1	D	182	TYR	2.3
1	D	216	GLN	2.3
1	E	231	VAL	2.3
1	C	42	TYR	2.3
1	D	68	LEU	2.3
1	B	49	GLY	2.3
1	E	232	GLY	2.3
1	C	23	LYS	2.3
1	E	292	LEU	2.3
1	A	115	VAL	2.3
1	A	92	ALA	2.2
1	B	286	MET	2.2
1	B	287	THR	2.2
1	E	203	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	212	THR	2.2
1	B	207	VAL	2.2
1	D	116	SER	2.2
1	E	46	GLU	2.2
1	A	25	ILE	2.1
1	B	233	ASP	2.1
1	A	88	THR	2.1
1	C	230	LEU	2.1
1	D	209	PHE	2.1
1	B	235	HIS	2.1
1	B	22	SER	2.1
1	D	268	ASN	2.1
1	A	24	ILE	2.1
1	B	230	LEU	2.1
1	E	267	ALA	2.1
1	A	248	THR	2.0
1	D	207	VAL	2.0
1	B	192	LEU	2.0
1	E	62	ILE	2.0
1	B	213	LEU	2.0
1	D	114	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 oligosaccharides 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. 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($\text{\AA}^2$)	Q<0.9
2	ZN	D	302	1/1	0.54	0.22	113,113,113,113	0
2	ZN	E	302	1/1	0.88	0.12	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	B	301	1/1	0.95	0.16	137,137,137,137	0
2	ZN	B	303	1/1	0.96	0.12	74,74,74,74	0
2	ZN	D	303	1/1	0.97	0.11	156,156,156,156	0
2	ZN	D	301	1/1	0.98	0.06	87,87,87,87	0
2	ZN	C	301	1/1	0.98	0.11	61,61,61,61	0
2	ZN	A	304	1/1	0.99	0.08	91,91,91,91	0
2	ZN	A	302	1/1	0.99	0.03	77,77,77,77	0
2	ZN	C	302	1/1	0.99	0.07	79,79,79,79	0
2	ZN	E	301	1/1	0.99	0.10	63,63,63,63	0
2	ZN	C	303	1/1	0.99	0.04	71,71,71,71	0
2	ZN	A	301	1/1	1.00	0.04	74,74,74,74	0
2	ZN	A	303	1/1	1.00	0.09	83,83,83,83	0
2	ZN	B	302	1/1	1.00	0.03	84,84,84,84	0

6.5 Other polymers [i](#)

There are no such residues in this entry.