



Full wwPDB X-ray Structure Validation Report ⓘ

May 28, 2020 – 08:31 pm BST

PDB ID : 1T75
Title : Crystal structure of Escherichia coli beta carbonic anhydrase
Authors : Oganessian, V.; Kim, S.-H.; Kim, R.; Jancarik, J.; Berkeley Structural Genomics Center (BSGC)
Deposited on : 2004-05-07
Resolution : 2.50 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

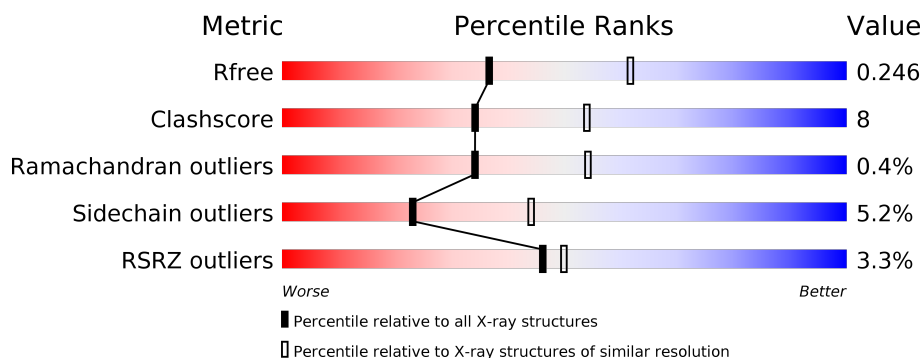
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	220	<div> <div>3%</div> <div> <div></div> <div>75%</div> <div>18%</div> <div>• •</div> </div> </div>
1	B	220	<div> <div>5%</div> <div> <div></div> <div>80%</div> <div>14%</div> <div>• • •</div> </div> </div>
1	D	220	<div> <div>%</div> <div> <div></div> <div>82%</div> <div>13%</div> <div>• •</div> </div> </div>
1	E	220	<div> <div>4%</div> <div> <div></div> <div>77%</div> <div>20%</div> <div>• •</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7058 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 Protein yadF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	0	0	0
			1715	1087	306	313	9			
1	B	214	Total	C	N	O	S	0	0	0
			1715	1087	306	313	9			
1	D	214	Total	C	N	O	S	0	0	0
			1715	1087	306	313	9			
1	E	214	Total	C	N	O	S	0	0	0
			1715	1087	306	313	9			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		
2	E	1	Total	Zn	0	0
			1	1		

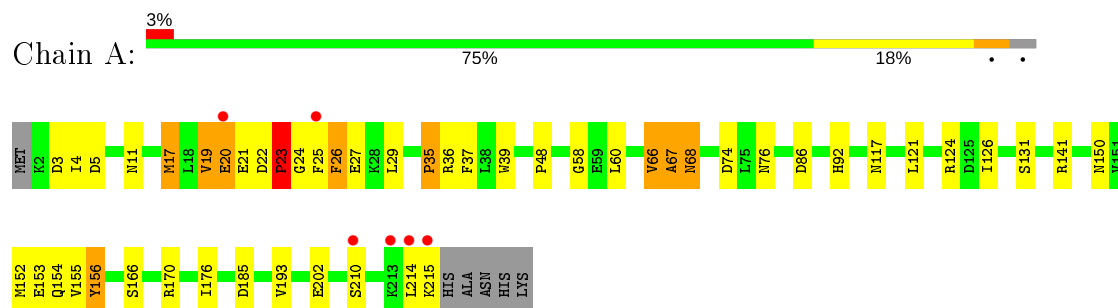
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	34	Total	O	0	0
			34	34		
3	B	66	Total	O	0	0
			66	66		
3	D	43	Total	O	0	0
			43	43		
3	E	51	Total	O	0	0
			51	51		

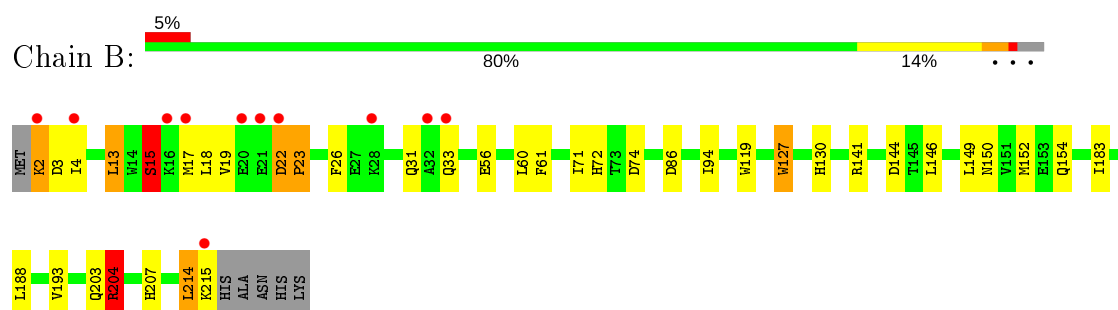
3 Residue-property plots [i](#)

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.

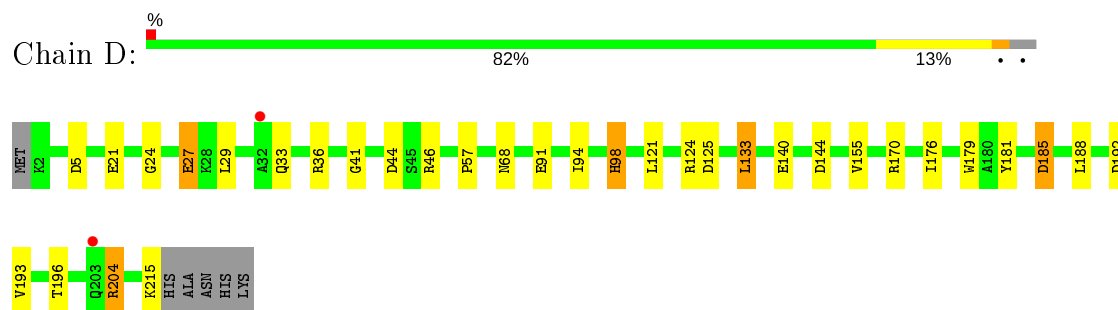
• Molecule 1: Protein yadF



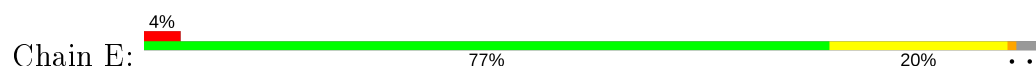
• Molecule 1: Protein yadF

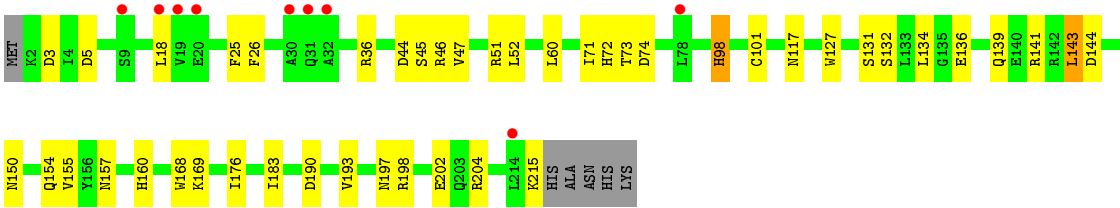


• Molecule 1: Protein yadF



• Molecule 1: Protein yadF





4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	110.45Å 110.45Å 162.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	91.29 – 2.50 48.64 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.8 (91.29-2.50) 97.9 (48.64-2.50)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.75 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.196 , 0.246 0.204 , 0.246	Depositor DCC
R_{free} test set	1750 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	43.0	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 30.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7058	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.27% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.72	2/1752 (0.1%)	1.11	11/2376 (0.5%)
1	B	0.78	1/1752 (0.1%)	1.00	8/2376 (0.3%)
1	D	0.67	0/1752	0.81	4/2376 (0.2%)
1	E	0.69	0/1752	0.85	4/2376 (0.2%)
All	All	0.72	3/7008 (0.0%)	0.95	27/9504 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	15	SER	C-N	-13.56	1.02	1.34
1	A	27	GLU	CB-CG	-9.47	1.34	1.52
1	A	26	PHE	C-N	-5.91	1.20	1.34

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	35	PRO	CA-N-CD	-20.17	83.26	111.50
1	B	23	PRO	CA-N-CD	-15.35	90.01	111.50
1	A	48	PRO	CA-N-CD	-14.71	90.91	111.50
1	A	23	PRO	CA-N-CD	-10.36	97.00	111.50
1	A	27	GLU	CA-CB-CG	9.92	135.23	113.40
1	E	74	ASP	CB-CG-OD2	8.93	126.33	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	74	ASP	CB-CG-OD2	8.35	125.81	118.30
1	B	22	ASP	C-N-CD	-7.68	103.70	120.60
1	A	86	ASP	CB-CG-OD2	7.62	125.16	118.30
1	B	31	GLN	CB-CA-C	7.33	125.06	110.40
1	D	125	ASP	CB-CG-OD2	7.24	124.82	118.30
1	A	5	ASP	CB-CG-OD2	7.09	124.69	118.30
1	B	74	ASP	CB-CG-OD2	7.09	124.69	118.30
1	E	190	ASP	CB-CG-OD1	6.87	124.49	118.30
1	B	15	SER	C-N-CA	-6.79	104.72	121.70
1	B	86	ASP	CB-CG-OD2	6.63	124.27	118.30
1	B	204	ARG	NE-CZ-NH1	6.44	123.52	120.30
1	E	144	ASP	CB-CG-OD2	6.43	124.08	118.30
1	D	144	ASP	CB-CG-OD2	6.18	123.86	118.30
1	A	19	VAL	CB-CA-C	-6.16	99.69	111.40
1	A	3	ASP	CB-CG-OD2	6.06	123.76	118.30
1	A	20	GLU	CA-CB-CG	5.89	126.37	113.40
1	D	44	ASP	CB-CG-OD2	5.68	123.41	118.30
1	E	5	ASP	CB-CG-OD2	5.57	123.31	118.30
1	D	5	ASP	CB-CG-OD2	5.31	123.08	118.30
1	B	144	ASP	CB-CG-OD2	5.26	123.03	118.30
1	A	124	ARG	NE-CZ-NH1	5.12	122.86	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	15	SER	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	1715	0	1699	41	0
1	B	1715	0	1698	49	1
1	D	1715	0	1699	20	0
1	E	1715	0	1699	22	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
3	A	34	0	0	0	0
3	B	66	0	0	6	0
3	D	43	0	0	1	0
3	E	51	0	0	0	0
All	All	7058	0	6795	114	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 8.

All (114) 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:B:19:VAL:O	1:B:23:PRO:HG3	1.32	1.26
1:D:185:ASP:O	1:E:26:PHE:CZ	1.89	1.26
1:B:19:VAL:O	1:B:23:PRO:CG	1.88	1.22
1:B:13:LEU:O	1:B:17:MET:HG3	1.49	1.07
1:B:19:VAL:O	1:B:23:PRO:CD	2.03	1.06
1:A:66:VAL:HG23	3:B:260:HOH:O	1.63	0.98
1:B:13:LEU:O	1:B:17:MET:CG	2.17	0.92
1:B:2:LYS:NZ	3:B:278:HOH:O	2.04	0.91
1:A:39:TRP:HB2	1:A:60:LEU:HD11	1.52	0.90
1:A:156:TYR:OH	1:A:202:GLU:OE2	1.88	0.90
1:D:185:ASP:O	1:E:26:PHE:CE1	2.28	0.86
1:B:141:ARG:HD3	3:B:248:HOH:O	1.77	0.84
1:A:25:PHE:CD2	1:A:26:PHE:CD2	2.68	0.81
1:A:22:ASP:O	1:A:24:GLY:N	2.14	0.80
1:B:3:ASP:OD1	1:B:4:ILE:N	2.14	0.80
1:D:185:ASP:O	1:E:26:PHE:HZ	1.59	0.80
1:D:185:ASP:OD1	1:D:185:ASP:N	2.16	0.79
1:A:66:VAL:O	1:A:67:ALA:HB3	1.83	0.78
1:A:25:PHE:HD2	1:A:26:PHE:CD2	2.03	0.76
1:A:152:MET:HG2	1:A:193:VAL:HG11	1.67	0.76
1:A:17:MET:O	1:A:21:GLU:HB2	1.87	0.75
1:A:25:PHE:CE2	1:A:26:PHE:CE2	2.74	0.75
1:A:37:PHE:HE2	1:B:4:ILE:HD13	1.50	0.75
1:B:141:ARG:CD	3:B:248:HOH:O	2.34	0.75
1:A:166:SER:O	1:A:170:ARG:HG2	1.88	0.72
1:D:185:ASP:C	1:E:26:PHE:CZ	2.67	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:ASN:HD21	1:B:188:LEU:H	1.43	0.66
1:A:37:PHE:HE2	1:B:4:ILE:CD1	2.09	0.65
1:D:29:LEU:HD21	1:D:57:PRO:HB2	1.79	0.65
1:A:22:ASP:C	1:A:24:GLY:H	2.00	0.64
1:A:25:PHE:CD2	1:A:26:PHE:CE2	2.86	0.63
1:A:37:PHE:CZ	1:B:2:LYS:O	2.54	0.60
1:A:37:PHE:HZ	1:B:2:LYS:O	1.84	0.59
1:A:29:LEU:HB3	1:B:183:ILE:HG23	1.85	0.59
1:A:66:VAL:O	1:A:67:ALA:CB	2.51	0.58
1:B:150:ASN:O	1:B:154:GLN:HG2	2.02	0.58
1:B:22:ASP:N	1:B:23:PRO:HD2	2.19	0.58
1:B:19:VAL:HG22	1:B:26:PHE:CE1	2.38	0.58
1:B:19:VAL:CG2	1:B:26:PHE:CE1	2.88	0.57
1:B:13:LEU:O	1:B:17:MET:CB	2.53	0.56
1:B:19:VAL:O	1:B:23:PRO:HD3	1.99	0.56
1:A:37:PHE:CE2	1:B:4:ILE:HD13	2.37	0.56
1:D:94:ILE:HD13	1:D:179:TRP:CZ3	2.41	0.56
1:B:19:VAL:HA	1:B:23:PRO:HD3	1.87	0.55
1:A:141:ARG:NH1	1:A:215:LYS:NZ	2.55	0.55
1:B:19:VAL:CG2	1:B:26:PHE:HE1	2.20	0.55
1:B:19:VAL:CA	1:B:23:PRO:HD3	2.38	0.54
1:D:193:VAL:HA	1:D:204:ARG:HB3	1.90	0.54
1:A:22:ASP:C	1:A:24:GLY:N	2.60	0.54
1:E:160:HIS:NE2	1:E:202:GLU:OE2	2.41	0.53
1:E:18:LEU:HD23	1:E:26:PHE:CE1	2.45	0.52
1:A:35:PRO:HD3	1:A:58:GLY:O	2.08	0.52
1:E:18:LEU:HD21	1:E:25:PHE:CD2	2.45	0.51
1:E:46:ARG:HB3	1:E:183:ILE:HD11	1.92	0.51
1:B:141:ARG:CG	3:B:248:HOH:O	2.59	0.51
1:A:19:VAL:CG1	1:A:19:VAL:O	2.56	0.51
1:B:19:VAL:HG23	1:B:26:PHE:HE1	1.76	0.51
1:E:71:ILE:HG22	1:E:73:THR:H	1.75	0.51
1:A:25:PHE:CE2	1:A:26:PHE:CD2	2.97	0.50
1:B:19:VAL:C	1:B:23:PRO:CD	2.78	0.50
1:A:150:ASN:O	1:A:154:GLN:HG2	2.12	0.49
1:B:19:VAL:C	1:B:23:PRO:HD3	2.33	0.49
1:E:18:LEU:HD21	1:E:25:PHE:CG	2.48	0.48
1:D:204:ARG:NE	3:D:264:HOH:O	2.46	0.48
1:D:36:ARG:NH1	1:D:91:GLU:OE1	2.46	0.48
1:D:192:ASP:CG	1:D:192:ASP:O	2.50	0.48
1:A:155:VAL:HG13	1:A:176:ILE:HG21	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:SER:O	1:A:214:LEU:HG	2.15	0.47
1:D:133:LEU:C	1:D:133:LEU:HD23	2.35	0.47
1:A:37:PHE:CE2	1:B:4:ILE:CD1	2.95	0.47
1:A:141:ARG:NH1	1:A:215:LYS:HZ1	2.13	0.46
1:E:132:SER:O	1:E:136:GLU:HG3	2.15	0.46
1:B:13:LEU:O	1:B:17:MET:HB2	2.15	0.46
1:D:24:GLY:HA2	1:D:27:GLU:HB2	1.97	0.46
1:E:47:VAL:HG12	1:E:52:LEU:HG	1.98	0.46
1:D:155:VAL:HG13	1:D:176:ILE:HG21	1.97	0.46
1:A:19:VAL:O	1:A:19:VAL:HG12	2.10	0.46
1:A:29:LEU:HB3	1:B:183:ILE:CG2	2.45	0.46
1:A:11:ASN:ND2	1:B:188:LEU:H	2.10	0.46
1:D:121:LEU:HD23	1:D:124:ARG:HD3	1.98	0.45
1:E:98:HIS:CD2	1:E:101:CYS:HB2	2.52	0.45
1:B:193:VAL:HA	1:B:204:ARG:HB3	2.00	0.44
1:E:127:TRP:CE3	1:E:134:LEU:HD13	2.52	0.44
1:A:4:ILE:HD11	1:B:94:ILE:HD11	1.99	0.44
1:D:46:ARG:HG2	1:D:98:HIS:CE1	2.53	0.44
1:A:126:ILE:HG12	1:A:153:GLU:HG3	2.00	0.44
1:B:203:GLN:O	1:B:207:HIS:HD2	2.01	0.44
1:B:19:VAL:O	1:B:23:PRO:HD2	2.04	0.43
1:A:92:HIS:CG	1:B:4:ILE:HD11	2.53	0.43
1:E:44:ASP:O	1:E:45:SER:C	2.56	0.43
1:E:150:ASN:O	1:E:154:GLN:HG2	2.19	0.43
1:E:155:VAL:HG13	1:E:176:ILE:HG21	1.99	0.43
1:B:18:LEU:O	1:B:23:PRO:HD3	2.19	0.43
1:A:36:ARG:O	1:A:36:ARG:HG2	2.19	0.43
1:E:60:LEU:H	1:E:60:LEU:HD23	1.83	0.43
1:A:117:ASN:O	1:A:121:LEU:HG	2.18	0.42
1:B:214:LEU:O	1:B:215:LYS:C	2.58	0.42
1:E:72:HIS:CE1	1:E:157:ASN:OD1	2.72	0.42
1:A:185:ASP:O	1:B:15:SER:OG	2.24	0.42
1:B:127:TRP:CD1	1:B:146:LEU:HD22	2.54	0.42
1:D:155:VAL:HG13	1:D:176:ILE:CG2	2.50	0.41
1:E:127:TRP:CZ3	1:E:134:LEU:HD13	2.55	0.41
1:D:181:TYR:HB3	1:D:188:LEU:HD23	2.02	0.41
1:A:76:ASN:HA	1:B:119:TRP:CZ3	2.56	0.41
1:B:130:HIS:CD2	1:B:149:LEU:HD22	2.55	0.41
1:B:152:MET:HG2	1:B:193:VAL:HG11	2.02	0.41
1:E:143:LEU:HD12	1:E:143:LEU:HA	1.91	0.41
1:D:33:GLN:HA	1:D:33:GLN:OE1	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:41:GLY:C	1:D:68:ASN:HB3	2.42	0.40
1:B:13:LEU:HD13	1:B:17:MET:SD	2.61	0.40
1:B:71:ILE:O	1:B:72:HIS:C	2.58	0.40
1:B:60:LEU:HD23	1:B:60:LEU:H	1.85	0.40
1:E:168:TRP:CD2	1:E:197:ASN:HA	2.56	0.40
1:B:141:ARG:HG2	3:B:248:HOH:O	2.19	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:18:LEU:CD2	1:B:22:ASP:OD2[8_666]	1.92	0.28

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	212/220 (96%)	195 (92%)	14 (7%)	3 (1%)	11	20
1	B	212/220 (96%)	198 (93%)	14 (7%)	0	100	100
1	D	212/220 (96%)	201 (95%)	11 (5%)	0	100	100
1	E	212/220 (96%)	200 (94%)	12 (6%)	0	100	100
All	All	848/880 (96%)	794 (94%)	51 (6%)	3 (0%)	34	54

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	68	ASN
1	A	23	PRO
1	A	67	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	187/192 (97%)	180 (96%)	7 (4%)	34	60
1	B	187/192 (97%)	179 (96%)	8 (4%)	29	53
1	D	187/192 (97%)	177 (95%)	10 (5%)	22	43
1	E	187/192 (97%)	173 (92%)	14 (8%)	13	26
All	All	748/768 (97%)	709 (95%)	39 (5%)	23	44

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	MET
1	A	20	GLU
1	A	23	PRO
1	A	66	VAL
1	A	68	ASN
1	A	131	SER
1	A	156	TYR
1	B	2	LYS
1	B	13	LEU
1	B	33	GLN
1	B	56	GLU
1	B	61	PHE
1	B	127	TRP
1	B	204	ARG
1	B	214	LEU
1	D	21	GLU
1	D	27	GLU
1	D	98	HIS
1	D	133	LEU
1	D	140	GLU
1	D	170	ARG
1	D	185	ASP
1	D	196	THR
1	D	204	ARG

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Mol	Chain	Res	Type
1	D	215	LYS
1	E	3	ASP
1	E	36	ARG
1	E	51	ARG
1	E	98	HIS
1	E	117	ASN
1	E	131	SER
1	E	139	GLN
1	E	141	ARG
1	E	143	LEU
1	E	169	LYS
1	E	193	VAL
1	E	198	ARG
1	E	204	ARG
1	E	215	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	11	ASN
1	A	110	ASN
1	A	160	HIS
1	B	207	HIS
1	D	10	ASN
1	D	110	ASN
1	E	33	GLN
1	E	117	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	15:SER	C	16:LYS	N	1.02

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	214/220 (97%)	0.01	6 (2%) 53 56	24, 39, 66, 77	0
1	B	214/220 (97%)	-0.15	11 (5%) 28 29	17, 29, 70, 73	0
1	D	214/220 (97%)	-0.28	2 (0%) 84 86	21, 35, 55, 69	0
1	E	214/220 (97%)	-0.12	9 (4%) 36 39	16, 28, 79, 89	0
All	All	856/880 (97%)	-0.13	28 (3%) 46 50	16, 33, 68, 89	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	19	VAL	5.4
1	B	22	ASP	5.0
1	A	215	LYS	4.1
1	E	30	ALA	4.1
1	E	20	GLU	3.4
1	B	215	LYS	3.1
1	A	25	PHE	3.0
1	E	9	SER	3.0
1	E	214	LEU	3.0
1	B	21	GLU	2.8
1	A	20	GLU	2.8
1	E	18	LEU	2.8
1	E	32	ALA	2.8
1	A	210	SER	2.6
1	E	31	GLN	2.6
1	B	20	GLU	2.5
1	B	33	GLN	2.4
1	B	2	LYS	2.4
1	B	32	ALA	2.3
1	D	32	ALA	2.3
1	A	213	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	17	MET	2.1
1	B	4	ILE	2.1
1	B	28	LYS	2.1
1	E	78	LEU	2.1
1	A	214	LEU	2.1
1	D	203	GLN	2.1
1	B	16	LYS	2.1

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. 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(\AA^2)	Q<0.9
2	ZN	D	221	1/1	0.98	0.09	39,39,39,39	0
2	ZN	A	221	1/1	0.99	0.08	40,40,40,40	0
2	ZN	E	221	1/1	0.99	0.10	32,32,32,32	0
2	ZN	B	221	1/1	1.00	0.10	34,34,34,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.