



Full wwPDB X-ray Structure Validation Report ⓘ

May 28, 2020 – 07:56 pm BST

PDB ID : 1LI5
Title : Crystal Structure of Cysteinyl-tRNA Synthetase
Authors : Newberry, K.J.; Hou, Y.-M.; Perona, J.J.
Deposited on : 2002-04-17
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

<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

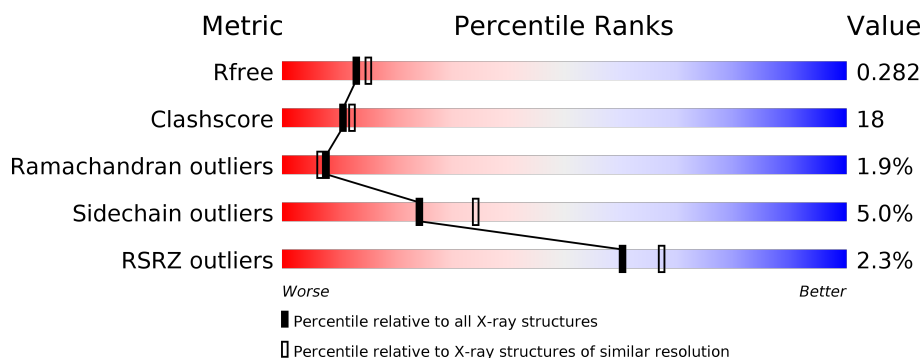
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (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 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	461	<div> <div>%</div> <div> <div></div> <div>58%</div> <div>21%</div> <div>•</div> <div>16%</div> </div> </div>
1	B	461	<div> <div>3%</div> <div> <div></div> <div>53%</div> <div>24%</div> <div>••</div> <div>20%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5778 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 CYSTEINYL-TRNA SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	386	Total	C	N	O	S	0	0	0
			2949	1869	508	547	25			
1	B	369	Total	C	N	O	S	0	0	0
			2725	1727	475	502	21			

- 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		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	73	Total	O	0	0
			73	73		
3	B	29	Total	O	0	0
			29	29		

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	119.16 Å 119.16 Å 144.30 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.89 – 2.30 45.94 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.3 (19.89-2.30) 98.4 (45.94-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 2.20 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.245 , 0.283 0.244 , 0.282	Depositor DCC
R_{free} test set	5306 reflections (10.12%)	wwPDB-VP
Wilson B-factor (Å ²)	34.0	Xtriage
Anisotropy	0.131	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5778	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.75% 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	0.47	1/3021 (0.0%)	0.87	10/4105 (0.2%)
1	B	0.53	6/2790 (0.2%)	0.82	6/3798 (0.2%)
All	All	0.50	7/5811 (0.1%)	0.85	16/7903 (0.2%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	249	GLN	N-CA	9.65	1.65	1.46
1	B	250	TYR	N-CA	7.71	1.61	1.46
1	B	248	GLY	N-CA	-5.75	1.37	1.46
1	B	247	ASP	N-CA	-5.33	1.35	1.46
1	A	265	GLU	C-N	-5.29	1.21	1.34
1	B	249	GLN	C-N	5.15	1.45	1.34
1	B	156	SER	CA-CB	5.01	1.60	1.52

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	232	PHE	C-N-CD	-25.10	65.39	120.60
1	B	232	PHE	C-N-CD	-20.22	76.11	120.60
1	B	232	PHE	C-N-CA	13.74	179.71	122.00
1	A	264	ARG	C-N-CA	10.52	148.00	121.70
1	A	232	PHE	C-N-CA	10.42	165.75	122.00
1	A	71	ASP	N-CA-C	-8.43	88.24	111.00
1	A	31	THR	N-CA-C	-8.30	88.59	111.00
1	B	246	HIS	N-CA-C	7.26	130.60	111.00
1	A	233	PRO	CA-N-CD	-6.69	102.14	111.50
1	A	265	GLU	N-CA-CB	6.60	122.48	110.60
1	B	247	ASP	CA-C-N	-6.49	103.22	116.20
1	B	233	PRO	CA-N-CD	-5.57	103.70	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	249	GLN	CA-C-N	-5.21	105.74	117.20
1	A	72	ASP	N-CA-C	5.13	124.86	111.00
1	A	248	GLY	CA-C-N	-5.04	106.11	117.20
1	B	266	LYS	N-CA-C	5.01	124.54	111.00

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	2949	0	2723	103	0
1	B	2725	0	2430	95	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	73	0	0	2	0
3	B	29	0	0	0	0
All	All	5778	0	5153	198	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 18.

All (198) 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:246:HIS:HD2	3:A:1099:HOH:O	1.39	1.04
1:B:148:THR:O	1:B:150:PRO:HD3	1.64	0.98
1:A:287:GLU:HG2	1:A:316:LEU:HD21	1.46	0.92
1:A:235:HIS:HD2	1:A:256:HIS:HE1	1.20	0.90
1:A:362:MET:HE3	1:A:384:LEU:HD13	1.56	0.86
1:A:146:VAL:HG13	1:A:147:PRO:HD3	1.56	0.85
1:A:112:PRO:HB2	1:A:212:MET:HE2	1.59	0.84
1:A:65:ARG:HG2	1:A:65:ARG:HH11	1.42	0.84
1:A:235:HIS:HD2	1:A:256:HIS:CE1	1.96	0.83
1:B:35:LEU:H	1:B:35:LEU:HD12	1.45	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:335:GLY:HA2	1:A:380:MET:HE1	1.63	0.80
1:B:149:ASP:HB3	1:B:152:TYR:HB2	1.64	0.79
1:A:146:VAL:HG11	1:A:179:MET:HB2	1.66	0.77
1:A:326:THR:HG21	1:A:385:ARG:HH12	1.49	0.77
1:B:143:MET:HE1	1:B:182:VAL:HG22	1.68	0.75
1:B:235:HIS:HD2	1:B:256:HIS:NE2	1.85	0.75
1:B:38:ILE:HD12	1:B:39:GLY:H	1.51	0.74
1:B:246:HIS:O	1:B:247:ASP:CB	2.28	0.74
1:B:223:ILE:HD13	1:B:255:MET:SD	2.27	0.74
1:B:232:PHE:CD2	1:B:233:PRO:HD3	2.23	0.73
1:A:28:CYS:SG	1:A:235:HIS:HE1	2.13	0.72
1:A:246:HIS:CD2	3:A:1099:HOH:O	2.25	0.72
1:B:37:HIS:HA	1:B:276:THR:HA	1.71	0.72
1:B:38:ILE:HD12	1:B:39:GLY:N	2.04	0.72
1:B:220:HIS:HE1	1:B:252:ASN:OD1	1.72	0.71
1:A:112:PRO:HB2	1:A:212:MET:CE	2.20	0.71
1:B:65:ARG:HG2	1:B:65:ARG:HH11	1.56	0.71
1:A:1:MET:HG3	1:A:14:GLU:HG3	1.72	0.70
1:A:69:ASP:HB3	1:A:115:THR:HG23	1.74	0.69
1:A:6:ASN:ND2	1:A:254:TRP:H	1.91	0.69
1:B:107:ARG:HG2	1:B:107:ARG:HH11	1.58	0.69
1:B:183:LEU:HD22	1:B:207:ILE:HD13	1.75	0.68
1:B:112:PRO:HG2	1:B:212:MET:HE3	1.74	0.68
1:B:35:LEU:N	1:B:35:LEU:HD12	2.07	0.68
1:A:146:VAL:HG11	1:A:179:MET:CB	2.24	0.67
1:B:146:VAL:HB	1:B:147:PRO:HD3	1.77	0.67
1:A:37:HIS:HA	1:A:276:THR:HA	1.75	0.67
1:A:65:ARG:NH1	1:A:65:ARG:HG2	2.10	0.66
1:B:177:ASN:ND2	1:B:179:MET:H	1.94	0.66
1:A:177:ASN:ND2	1:A:179:MET:H	1.93	0.65
1:A:135:TYR:CE2	1:A:145:ASP:HB3	2.32	0.65
1:A:37:HIS:HD2	1:A:39:GLY:H	1.43	0.65
1:B:287:GLU:HG2	1:B:316:LEU:HD21	1.77	0.64
1:B:132:GLY:O	1:B:148:THR:HG21	1.98	0.64
1:B:143:MET:HE2	1:B:182:VAL:HA	1.80	0.64
1:B:135:TYR:HH	1:B:176:ARG:N	1.96	0.63
1:B:366:VAL:O	1:B:370:LYS:HG2	1.98	0.63
1:B:224:HIS:HE1	1:B:238:GLU:OE1	1.82	0.63
1:A:326:THR:CG2	1:A:385:ARG:HH12	2.12	0.63
1:A:124:LEU:HD12	1:A:211:ALA:HA	1.81	0.62
1:A:328:LYS:HA	1:A:385:ARG:NH2	2.15	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:ILE:H	1:A:30:ILE:CD1	2.12	0.62
1:A:31:THR:HA	1:A:68:THR:HB	1.83	0.61
1:B:95:GLU:CD	1:B:278:ARG:HH22	2.05	0.61
1:A:112:PRO:C	1:A:212:MET:HE1	2.21	0.60
1:A:232:PHE:CD2	1:A:233:PRO:HD3	2.36	0.60
1:B:112:PRO:CG	1:B:212:MET:HE3	2.31	0.60
1:A:323:LEU:O	1:A:326:THR:HB	2.02	0.60
1:B:261:MET:HB3	1:B:265:GLU:O	2.02	0.60
1:A:30:ILE:H	1:A:30:ILE:HD13	1.67	0.59
1:A:224:HIS:HE1	1:A:238:GLU:OE1	1.85	0.59
1:B:137:ALA:O	1:B:140:GLY:N	2.34	0.59
1:A:32:VAL:HG21	1:A:67:ILE:HG23	1.85	0.59
1:B:195:PRO:O	1:B:196:SER:CB	2.50	0.59
1:B:141:ASP:HB3	1:B:143:MET:CE	2.33	0.58
1:A:95:GLU:HG3	1:A:278:ARG:NH2	2.18	0.58
1:B:313:ARG:O	1:B:317:GLU:HG3	2.03	0.58
1:A:95:GLU:HG3	1:A:278:ARG:HH22	1.70	0.57
1:A:30:ILE:HD11	1:A:96:MET:SD	2.45	0.57
1:A:122:ILE:O	1:A:126:GLU:HG3	2.04	0.57
1:B:38:ILE:HD11	1:B:267:MET:SD	2.45	0.57
1:B:318:ARG:HH11	1:B:318:ARG:HG3	1.71	0.56
1:A:235:HIS:CD2	1:A:256:HIS:HE1	2.12	0.56
1:B:298:TYR:CE1	1:B:299:ARG:HG3	2.41	0.55
1:B:141:ASP:HB3	1:B:143:MET:HE1	1.88	0.55
1:A:262:VAL:HB	1:A:273:ASN:HB2	1.88	0.55
1:A:32:VAL:HG12	1:A:92:MET:HB2	1.88	0.55
1:B:146:VAL:HG23	1:B:180:ASP:HA	1.89	0.55
1:B:143:MET:CE	1:B:182:VAL:HG22	2.35	0.54
1:B:145:ASP:O	1:B:148:THR:OG1	2.15	0.54
1:A:135:TYR:HE2	1:A:145:ASP:HB3	1.70	0.53
1:A:220:HIS:HE1	1:A:252:ASN:OD1	1.90	0.53
1:B:110:MET:HE2	1:B:110:MET:HA	1.89	0.53
1:B:184:TRP:NE1	1:B:201:GLY:HA3	2.23	0.53
1:A:35:LEU:HD22	1:A:35:LEU:H	1.73	0.53
1:A:7:THR:OG1	1:A:256:HIS:HD2	1.92	0.53
1:B:117:HIS:O	1:B:121:ILE:HG13	2.09	0.53
1:A:1:MET:HE3	1:A:14:GLU:OE1	2.08	0.52
1:A:206:HIS:CD2	1:A:237:ASN:HD22	2.27	0.52
1:B:69:ASP:OD1	1:B:115:THR:HB	2.09	0.52
1:B:326:THR:HG21	1:B:381:ALA:CB	2.40	0.51
1:A:117:HIS:HB3	1:A:120:GLU:HG2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:TYR:HE2	1:A:145:ASP:CB	2.23	0.51
1:A:107:ARG:HH11	1:A:107:ARG:HG2	1.76	0.51
1:A:224:HIS:CE1	1:A:238:GLU:OE1	2.63	0.51
1:B:107:ARG:HG2	1:B:107:ARG:NH1	2.24	0.51
1:B:35:LEU:CD1	1:B:35:LEU:H	2.19	0.51
1:B:235:HIS:CD2	1:B:256:HIS:NE2	2.72	0.51
1:A:177:ASN:HD22	1:A:179:MET:H	1.58	0.51
1:A:362:MET:HE3	1:A:384:LEU:CD1	2.35	0.51
1:B:154:VAL:HG13	1:B:155:LEU:N	2.25	0.50
1:B:297:HIS:HD2	1:B:299:ARG:HB2	1.76	0.50
1:A:335:GLY:H	1:A:383:HIS:CD2	2.29	0.50
1:B:318:ARG:HG3	1:B:318:ARG:NH1	2.26	0.50
1:A:339:GLU:OE1	1:A:383:HIS:HE1	1.95	0.50
1:A:334:GLY:C	1:A:380:MET:HE2	2.32	0.49
1:A:153:GLY:HA2	1:A:236:GLU:CD	2.33	0.49
1:B:6:ASN:ND2	1:B:254:TRP:H	2.10	0.49
1:B:367:ASN:HA	1:B:370:LYS:HG3	1.95	0.49
1:A:214:CYS:HB2	1:A:219:ASN:HD22	1.77	0.49
1:A:145:ASP:HA	1:A:180:ASP:OD1	2.12	0.49
1:A:320:TYR:CZ	1:A:394:LEU:HA	2.48	0.49
1:B:145:ASP:HB3	1:B:148:THR:OG1	2.12	0.49
1:B:135:TYR:C	1:B:135:TYR:CD1	2.86	0.48
1:B:65:ARG:NH1	1:B:65:ARG:HG2	2.25	0.48
1:B:86:VAL:O	1:B:89:VAL:HG22	2.12	0.48
1:A:1:MET:HE2	1:A:14:GLU:HB2	1.96	0.48
1:A:30:ILE:N	1:A:30:ILE:HD13	2.28	0.48
1:B:25:MET:HG3	1:B:223:ILE:HG13	1.95	0.48
1:A:101:ASP:OD1	1:A:107:ARG:NH1	2.47	0.47
1:B:262:VAL:N	1:B:265:GLU:O	2.47	0.47
1:A:32:VAL:HG12	1:A:92:MET:CB	2.43	0.47
1:A:237:ASN:O	1:A:241:GLN:HG3	2.15	0.47
1:B:110:MET:HA	1:B:110:MET:CE	2.45	0.47
1:B:177:ASN:HD22	1:B:179:MET:H	1.60	0.47
1:B:297:HIS:CD2	1:B:299:ARG:HB2	2.50	0.47
1:A:362:MET:HE1	1:A:384:LEU:HA	1.97	0.46
1:B:112:PRO:HB2	1:B:212:MET:HE3	1.97	0.46
1:A:235:HIS:CD2	1:A:256:HIS:CE1	2.88	0.46
1:B:97:HIS:HE1	1:B:111:GLU:OE1	1.98	0.46
1:B:214:CYS:HB2	1:B:219:ASN:HD22	1.80	0.46
1:B:219:ASN:O	1:B:250:TYR:HA	2.15	0.46
1:A:188:LYS:O	1:A:191:GLU:HG2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:220:HIS:CE1	1:A:249:GLN:HB3	2.50	0.46
1:A:70:ILE:HD12	1:A:70:ILE:N	2.31	0.46
1:B:194:TRP:O	1:B:195:PRO:O	2.34	0.46
1:B:26:TYR:HA	1:B:64:VAL:O	2.15	0.46
1:B:353:PRO:O	1:B:356:TYR:HB2	2.16	0.46
1:A:35:LEU:HD11	1:A:95:GLU:HG2	1.96	0.46
1:B:262:VAL:O	1:B:263:ASP:CB	2.64	0.46
1:B:220:HIS:CE1	1:B:252:ASN:OD1	2.60	0.45
1:B:333:ALA:HB3	1:B:379:ALA:HB1	1.97	0.45
1:B:223:ILE:HD12	1:B:224:HIS:N	2.31	0.45
1:B:29:GLY:HA3	1:B:66:ASN:O	2.17	0.45
1:B:135:TYR:HE1	1:B:137:ALA:HB2	1.82	0.45
1:A:26:TYR:HA	1:A:64:VAL:O	2.17	0.45
1:A:294:MET:HB2	1:A:356:TYR:OH	2.17	0.45
1:A:307:GLU:O	1:A:311:GLN:HG2	2.16	0.45
1:A:71:ASP:OD2	1:A:71:ASP:O	2.35	0.45
1:A:297:HIS:HE1	1:A:349:ASP:O	2.00	0.45
1:A:37:HIS:HD2	1:A:39:GLY:N	2.13	0.44
1:A:362:MET:CE	1:A:384:LEU:HA	2.48	0.44
1:A:70:ILE:HD12	1:A:70:ILE:H	1.82	0.44
1:B:214:CYS:HA	1:B:218:GLY:O	2.18	0.44
1:A:262:VAL:O	1:A:263:ASP:CB	2.64	0.44
1:B:309:LEU:O	1:B:312:ALA:HB3	2.17	0.44
1:B:112:PRO:CB	1:B:212:MET:HE3	2.48	0.44
1:A:366:VAL:O	1:A:370:LYS:HG2	2.18	0.43
1:A:38:ILE:HG12	1:A:275:PHE:O	2.18	0.43
1:A:146:VAL:HG12	1:A:180:ASP:OD1	2.18	0.43
1:A:263:ASP:O	1:A:264:ARG:CB	2.64	0.43
1:A:42:ARG:NH2	1:A:300:SER:O	2.50	0.43
1:A:35:LEU:HD22	1:A:35:LEU:N	2.33	0.43
1:B:5:PHE:HA	1:B:12:LYS:HA	2.00	0.43
1:B:326:THR:HG21	1:B:381:ALA:HB3	2.00	0.43
1:B:141:ASP:HB3	1:B:143:MET:HE3	2.01	0.43
1:A:72:ASP:HB2	1:A:205:TRP:CH2	2.53	0.42
1:B:214:CYS:HB2	1:B:219:ASN:ND2	2.34	0.42
1:A:86:VAL:HG23	1:A:87:ALA:N	2.34	0.42
1:B:196:SER:O	1:B:199:GLY:N	2.43	0.42
1:B:314:ALA:O	1:B:317:GLU:HB2	2.20	0.42
1:A:26:TYR:CD1	1:A:213:ASN:HB3	2.55	0.42
1:A:118:ILE:HD12	1:A:118:ILE:N	2.35	0.42
1:B:112:PRO:O	1:B:212:MET:HE1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:330:VAL:HG21	1:B:378:ASN:HB3	2.00	0.42
1:A:327:ASP:CG	1:A:329:THR:HG22	2.40	0.42
1:B:187:SER:N	1:B:201:GLY:HA2	2.35	0.42
1:B:92:MET:CE	1:B:92:MET:HA	2.49	0.42
1:A:232:PHE:CG	1:A:233:PRO:HD3	2.54	0.41
1:A:154:VAL:HG13	1:A:155:LEU:N	2.34	0.41
1:A:208:GLU:O	1:A:212:MET:HG3	2.20	0.41
1:A:39:GLY:HA2	1:A:260:VAL:CG2	2.50	0.41
1:A:31:THR:HG21	1:A:71:ASP:OD1	2.20	0.41
1:B:185:LYS:O	1:B:186:MET:C	2.58	0.41
1:B:72:ASP:OD1	1:B:202:ARG:NH2	2.53	0.41
1:A:135:TYR:CD2	1:A:145:ASP:HB3	2.56	0.41
1:A:5:PHE:HA	1:A:12:LYS:HA	2.02	0.41
1:B:284:TYR:CG	1:B:309:LEU:HD23	2.55	0.41
1:B:320:TYR:CZ	1:B:394:LEU:HA	2.55	0.41
1:A:29:GLY:HA3	1:A:66:ASN:O	2.21	0.41
1:A:297:HIS:CD2	1:A:299:ARG:H	2.39	0.41
1:A:92:MET:CE	1:A:92:MET:HA	2.51	0.41
1:B:246:HIS:C	1:B:247:ASP:O	2.59	0.41
1:A:30:ILE:HG12	1:A:31:THR:O	2.21	0.40
1:B:297:HIS:CD2	1:B:299:ARG:H	2.39	0.40
1:B:37:HIS:HD2	1:B:39:GLY:H	1.69	0.40
1:A:95:GLU:CG	1:A:278:ARG:HH22	2.33	0.40
1:B:177:ASN:OD1	1:B:178:PRO:HD2	2.21	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	382/461 (83%)	369 (97%)	9 (2%)	4 (1%)	15 17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	361/461 (78%)	334 (92%)	17 (5%)	10 (3%)	5	3
All	All	743/922 (81%)	703 (95%)	26 (4%)	14 (2%)	8	7

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	233	PRO
1	A	266	LYS
1	B	195	PRO
1	B	233	PRO
1	B	250	TYR
1	B	264	ARG
1	A	264	ARG
1	B	157	ARG
1	A	234	HIS
1	B	196	SER
1	B	249	GLN
1	B	400	ALA
1	B	275	PHE
1	B	32	VAL

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	291/381 (76%)	275 (94%)	16 (6%)	21	30
1	B	250/381 (66%)	239 (96%)	11 (4%)	28	39
All	All	541/762 (71%)	514 (95%)	27 (5%)	24	34

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	6	ASN

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Mol	Chain	Res	Type
1	A	30	ILE
1	A	42	ARG
1	A	70	ILE
1	A	116	HIS
1	A	145	ASP
1	A	146	VAL
1	A	147	PRO
1	A	187	SER
1	A	202	ARG
1	A	233	PRO
1	A	299	ARG
1	A	326	THR
1	A	329	THR
1	A	380	MET
1	B	1	MET
1	B	6	ASN
1	B	42	ARG
1	B	107	ARG
1	B	116	HIS
1	B	148	THR
1	B	195	PRO
1	B	197	PRO
1	B	216	GLN
1	B	223	ILE
1	B	249	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	ASN
1	A	37	HIS
1	A	97	HIS
1	A	177	ASN
1	A	219	ASN
1	A	220	HIS
1	A	224	HIS
1	A	235	HIS
1	A	241	GLN
1	A	246	HIS
1	A	256	HIS
1	A	297	HIS
1	A	308	ASN

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Mol	Chain	Res	Type
1	A	383	HIS
1	A	396	GLN
1	B	6	ASN
1	B	37	HIS
1	B	97	HIS
1	B	177	ASN
1	B	219	ASN
1	B	220	HIS
1	B	224	HIS
1	B	235	HIS
1	B	241	GLN
1	B	246	HIS
1	B	297	HIS
1	B	308	ASN
1	B	383	HIS

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 2 ligands modelled in this entry, 2 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	386/461 (83%)	-0.03	3 (0%) 86 89	19, 32, 46, 54	0
1	B	369/461 (80%)	0.19	14 (3%) 40 47	19, 42, 62, 78	0
All	All	755/922 (81%)	0.08	17 (2%) 60 67	19, 35, 60, 78	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	248	GLY	6.9
1	B	190	GLY	3.9
1	B	274	PHE	3.8
1	B	267	MET	3.6
1	A	134	ALA	3.5
1	B	176	ARG	3.1
1	B	265	GLU	3.0
1	B	371	ALA	3.0
1	B	184	TRP	2.9
1	B	263	ASP	2.7
1	B	32	VAL	2.6
1	B	132	GLY	2.5
1	A	147	PRO	2.3
1	A	146	VAL	2.2
1	B	33	TYR	2.1
1	B	284	TYR	2.1
1	B	304	TYR	2.1

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 [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	A	963	1/1	0.98	0.10	32,32,32,32	0
2	ZN	B	964	1/1	0.98	0.06	36,36,36,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.