



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:45 PM UTC

PDB ID : 4IG2 / pdb_00004ig2
Title : 1.80 Angstroms X-ray crystal structure of R51A and R239A heterodimer 2-amino-3-carboxymuconate-6-semialdehyde decarboxylase from *Pseudomonas fluorescens*
Authors : Huo, L.; Davis, I.; Chen, L.; Liu, A.
Deposited on : 2012-12-15
Resolution : 1.80 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

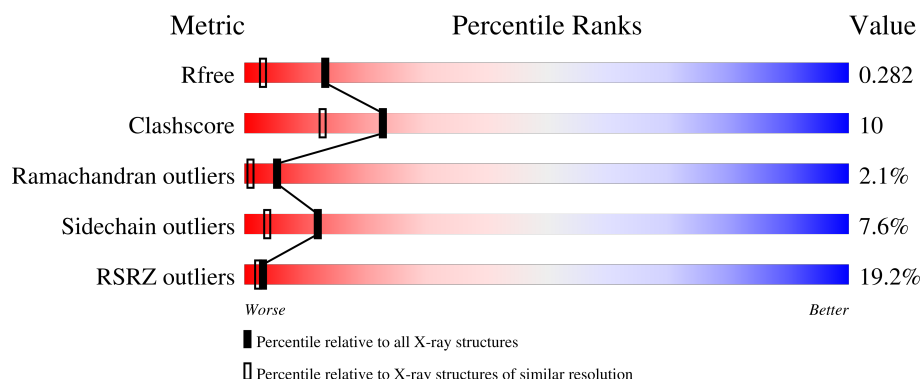
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	331	2% 90% 9%
2	B	331	36% 58% 34% 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5316 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 2-amino-3-carboxymuconate 6-semialdehyde decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	331	Total	C	N	O	S	0	1	0
			2582	1648	447	469	18			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	239	ALA	ARG	engineered mutation	UNP Q83V25

- Molecule 2 is a protein called 2-amino-3-carboxymuconate 6-semialdehyde decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	331	Total	C	N	O	S	0	2	0
			2591	1652	451	470	18			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	51	ALA	ARG	engineered mutation	UNP Q83V25

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		
3	B	1	Total	Zn	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	117	Total	O	0	0
			117	117		

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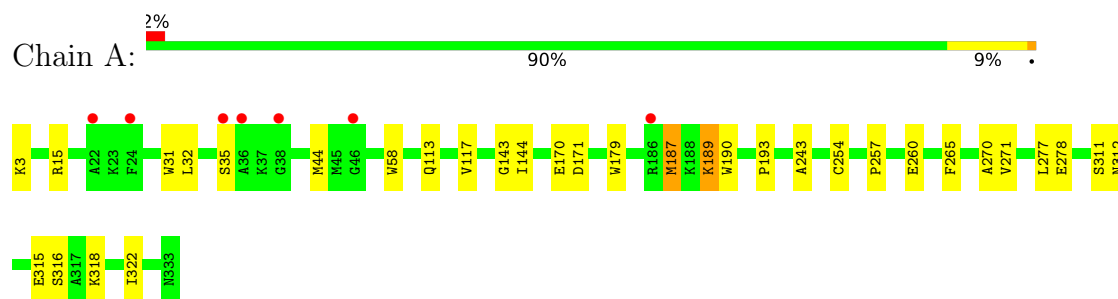
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	24	Total	O	0	0
			24	24		

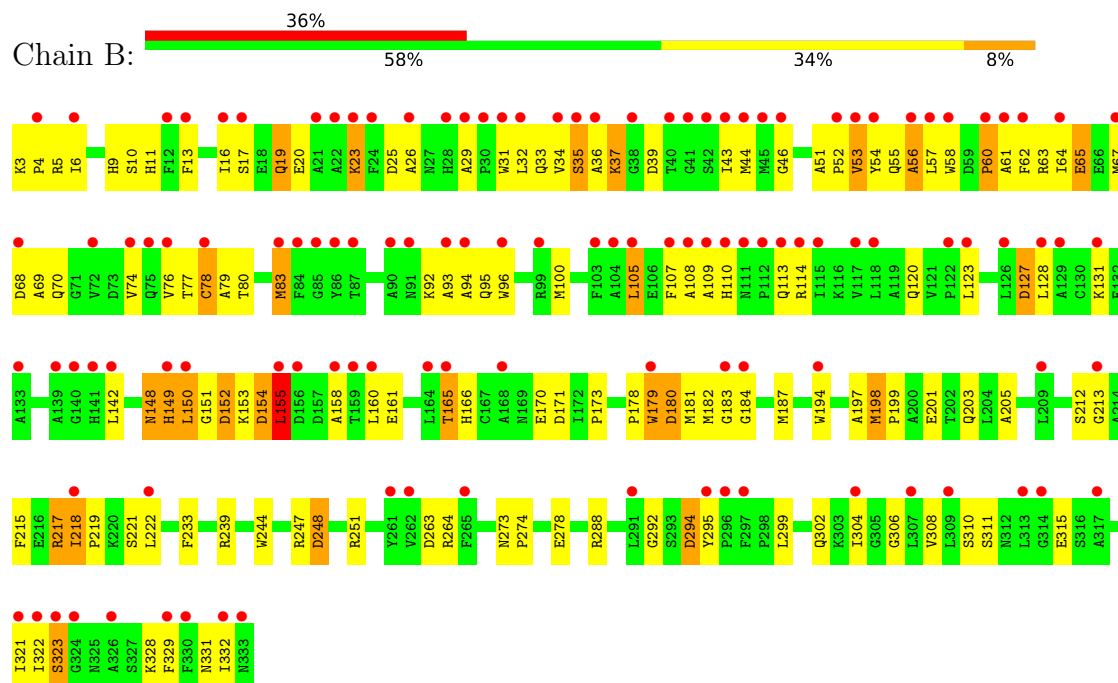
3 Residue-property plots

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: 2-amino-3-carboxymuconate 6-semialdehyde decarboxylase



- Molecule 2: 2-amino-3-carboxymuconate 6-semialdehyde decarboxylase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	153.10Å 48.52Å 109.83Å 90.00° 126.80° 90.00°	Depositor
Resolution (Å)	20.78 – 1.80 20.78 – 1.80	Depositor EDS
% Data completeness (in resolution range)	86.0 (20.78-1.80) 81.1 (20.78-1.80)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 1.80Å)	Xtriage
Refinement program	PHENIX 1.7.3 _928	Depositor
R, R_{free}	0.232 , 0.282 0.233 , 0.282	Depositor DCC
R_{free} test set	2591 reflections (4.30%)	wwPDB-VP
Wilson B-factor (Å ²)	27.9	Xtriage
Anisotropy	0.645	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 33.3	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	0.95	EDS
Total number of atoms	5316	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.24% 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	0.58	0/2656	0.89	4/3599 (0.1%)
2	B	0.48	1/2667 (0.0%)	0.92	7/3614 (0.2%)
All	All	0.53	1/5323 (0.0%)	0.91	11/7213 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	332	ILE	C-N	9.45	1.46	1.33

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	182	MET	N-CA-C	7.33	122.35	113.41
2	B	155	LEU	N-CA-C	6.49	119.36	109.62
1	A	254	CYS	CA-C-N	6.28	126.40	119.87
1	A	254	CYS	C-N-CA	6.28	126.40	119.87
2	B	34	VAL	N-CA-C	-6.15	101.62	109.80
2	B	29	ALA	CA-C-N	6.05	126.40	119.92
2	B	29	ALA	C-N-CA	6.05	126.40	119.92
2	B	179	TRP	N-CA-C	5.21	116.33	108.46
2	B	78	CYS	N-CA-C	5.13	115.31	108.38
1	A	265	PHE	N-CA-C	5.11	115.79	108.74
1	A	117	VAL	N-CA-C	5.03	115.72	108.48

There are no chirality outliers.

There are no planarity outliers.

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	2582	0	2521	19	0
2	B	2591	0	2535	91	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	117	0	0	3	0
4	B	24	0	0	6	0
All	All	5316	0	5056	106	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 (106) 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)
2:B:158:ALA:HA	2:B:161:GLU:HB2	1.51	0.89
1:A:170:GLU:OE1	4:A:599:HOH:O	1.93	0.84
1:A:113:GLN:O	4:A:570:HOH:O	1.97	0.82
2:B:78:CYS:SG	4:B:515:HOH:O	2.38	0.81
2:B:123:LEU:HB3	2:B:150:LEU:HD11	1.62	0.81
2:B:215:PHE:O	2:B:264:ARG:NH1	2.17	0.78
2:B:10:SER:O	4:B:515:HOH:O	2.05	0.73
2:B:53:VAL:HG21	2:B:57:LEU:HD22	1.68	0.73
2:B:105:LEU:O	2:B:109:ALA:N	2.21	0.73
1:A:189:LYS:HE3	1:A:190:TRP:H	1.53	0.72
2:B:70:GLN:NE2	2:B:302:GLN:O	2.23	0.72
2:B:150:LEU:HB2	2:B:153:LYS:HD2	1.72	0.71
2:B:248:ASP:OD1	2:B:248:ASP:N	2.21	0.71
2:B:60:PRO:O	2:B:63:ARG:N	2.21	0.70
2:B:127:ASP:OD1	2:B:127:ASP:N	2.22	0.70
2:B:79:ALA:HA	2:B:83:MET:HE2	1.71	0.70
2:B:161:GLU:O	2:B:165:THR:OG1	2.10	0.69
2:B:67:MET:HE2	2:B:114:ARG:HH21	1.60	0.66
2:B:110:HIS:NE2	4:B:522:HOH:O	2.29	0.66
2:B:263:ASP:O	2:B:288:ARG:NH2	2.31	0.64
2:B:94:ALA:HB2	2:B:128:LEU:HD13	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:198:MET:HG3	2:B:199:PRO:HD3	1.80	0.62
1:A:270:ALA:O	2:B:239[A]:ARG:NH2	2.33	0.61
2:B:53:VAL:HG22	2:B:54:TYR:H	1.66	0.61
2:B:11:HIS:O	2:B:63:ARG:NH2	2.33	0.60
2:B:148:ASN:HD21	2:B:178:PRO:HA	1.66	0.60
2:B:212:SER:O	4:B:506:HOH:O	2.16	0.59
2:B:149:HIS:NE2	2:B:180:ASP:O	2.36	0.58
2:B:244:TRP:CE2	2:B:251:ARG:HG2	2.38	0.58
2:B:149:HIS:HE1	2:B:201:GLU:CD	2.12	0.57
2:B:306:GLY:O	2:B:310:SER:OG	2.21	0.57
2:B:37:LYS:NZ	2:B:39:ASP:OD2	2.36	0.57
2:B:292:GLY:O	4:B:510:HOH:O	2.17	0.57
2:B:213:GLY:O	2:B:217:ARG:HD2	2.05	0.56
1:A:278:GLU:OE2	1:A:312:ASN:ND2	2.30	0.56
2:B:17:SER:OG	2:B:19:GLN:HG3	2.05	0.56
1:A:15:ARG:HD3	1:A:58:TRP:CD1	2.41	0.56
1:A:315:GLU:OE2	4:A:560:HOH:O	2.18	0.55
2:B:68:ASP:OD1	2:B:114:ARG:NH2	2.26	0.55
1:A:277:LEU:HD23	1:A:311:SER:OG	2.07	0.54
2:B:153:LYS:NZ	2:B:160:LEU:HD23	2.23	0.54
2:B:110:HIS:CE1	4:B:522:HOH:O	2.61	0.53
1:A:271:VAL:HG12	2:B:239[B]:ARG:HH21	1.76	0.51
2:B:183:GLY:HA3	2:B:187:MET:HE3	1.92	0.51
2:B:93:ALA:HA	2:B:96:TRP:HB3	1.93	0.51
1:A:257:PRO:HG2	1:A:260:GLU:HG3	1.92	0.50
2:B:35:SER:OG	2:B:36:ALA:N	2.41	0.50
2:B:154:ASP:OD2	2:B:154:ASP:N	2.44	0.50
2:B:60:PRO:O	2:B:62:PHE:N	2.45	0.49
2:B:153:LYS:HG2	2:B:154:ASP:N	2.27	0.49
1:A:15:ARG:HD2	1:A:32:LEU:HD23	1.94	0.49
2:B:96:TRP:O	2:B:100:MET:HG2	2.12	0.49
2:B:151:GLY:HA2	2:B:179:TRP:CH2	2.48	0.48
2:B:5:ARG:HA	2:B:322:ILE:HG22	1.95	0.48
1:A:243:ALA:HA	2:B:299:LEU:HD22	1.95	0.48
2:B:63:ARG:HD3	2:B:295:TYR:HE2	1.79	0.48
2:B:10:SER:OG	2:B:76:VAL:O	2.30	0.48
1:A:143:GLY:O	1:A:144:ILE:HD13	2.14	0.48
1:A:271:VAL:HG12	2:B:239[B]:ARG:NH2	2.30	0.47
2:B:65:GLU:O	2:B:69:ALA:N	2.44	0.47
2:B:155:LEU:HD12	2:B:155:LEU:H	1.79	0.47
2:B:181:MET:HB3	2:B:197:ALA:HB1	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:123:LEU:CB	2:B:150:LEU:HD11	2.40	0.46
2:B:150:LEU:HA	2:B:150:LEU:HD13	1.55	0.46
1:A:187:MET:O	1:A:193:PRO:HD3	2.16	0.46
2:B:150:LEU:HD23	2:B:153:LYS:NZ	2.31	0.46
2:B:218:ILE:HG21	2:B:222:LEU:HD22	1.98	0.46
2:B:274:PRO:O	2:B:278:GLU:HG3	2.15	0.46
2:B:3:LYS:HB3	2:B:4:PRO:HD2	1.99	0.45
2:B:13:PHE:CE2	2:B:32:LEU:HB2	2.51	0.45
2:B:203:GLN:HG3	2:B:233:PHE:HA	1.99	0.45
2:B:218:ILE:HD13	2:B:218:ILE:HA	1.78	0.45
2:B:37:LYS:HZ3	2:B:39:ASP:H	1.65	0.45
2:B:273:ASN:HA	2:B:274:PRO:HD3	1.86	0.44
2:B:9:HIS:NE2	2:B:294:ASP:OD1	2.50	0.44
2:B:153:LYS:HD3	2:B:155:LEU:HA	1.98	0.44
2:B:153:LYS:HZ3	2:B:160:LEU:HD23	1.81	0.44
1:A:31:TRP:CE2	1:A:44:MET:HB2	2.52	0.44
2:B:58:TRP:HA	2:B:107:PHE:CE1	2.53	0.44
1:A:318:LYS:O	1:A:322:ILE:HG12	2.18	0.44
2:B:13:PHE:HE2	2:B:32:LEU:HB2	1.83	0.44
2:B:165:THR:HG23	2:B:219:PRO:HD3	2.00	0.44
2:B:17:SER:HG	2:B:20:GLU:H	1.64	0.44
2:B:54:TYR:O	2:B:56:ALA:N	2.48	0.44
2:B:105:LEU:HA	2:B:108:ALA:HB3	1.99	0.43
2:B:4:PRO:HG2	2:B:323:SER:HB3	1.98	0.43
2:B:31:TRP:CZ2	2:B:44:MET:HG3	2.54	0.43
2:B:53:VAL:CG2	2:B:57:LEU:HD22	2.44	0.43
2:B:17:SER:OG	2:B:20:GLU:HG2	2.19	0.43
1:A:189:LYS:HD2	1:A:189:LYS:HA	1.63	0.43
2:B:148:ASN:HB3	2:B:205:ALA:HB2	2.01	0.42
2:B:173:PRO:HB3	2:B:329:PHE:CE1	2.54	0.42
2:B:166:HIS:O	2:B:170:GLU:HG2	2.20	0.41
2:B:92:LYS:HA	2:B:95:GLN:HB2	2.03	0.41
2:B:150:LEU:H	2:B:153:LYS:HB3	1.85	0.41
2:B:181:MET:HB3	2:B:197:ALA:CB	2.50	0.41
2:B:23:LYS:HD3	2:B:23:LYS:HA	1.80	0.41
2:B:51:ALA:HA	2:B:52:PRO:HD2	1.91	0.41
2:B:60:PRO:HG3	2:B:107:PHE:CE1	2.56	0.41
2:B:328:LYS:HE3	2:B:328:LYS:HB2	1.61	0.41
2:B:64:ILE:HA	2:B:67:MET:HB2	2.03	0.40
1:A:44:MET:HE3	1:A:44:MET:HB3	1.86	0.40
2:B:219:PRO:HB2	2:B:221:SER:OG	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:155:LEU:HD21	2:B:205:ALA:HA	2.02	0.40
2:B:26:ALA:O	2:B:46:GLY:HA3	2.21	0.40
2:B:308:VAL:O	2:B:311:SER:OG	2.25	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	330/331 (100%)	321 (97%)	8 (2%)	1 (0%)	36	25
2	B	331/331 (100%)	295 (89%)	22 (7%)	14 (4%)	2	0
All	All	661/662 (100%)	616 (93%)	30 (4%)	15 (2%)	5	1

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	61	ALA
2	B	35	SER
2	B	55	GLN
2	B	56	ALA
2	B	60	PRO
2	B	184	GLY
2	B	304	ILE
1	A	35	SER
2	B	37	LYS
2	B	149	HIS
2	B	152	ASP
2	B	331[A]	ASN
2	B	331[B]	ASN
2	B	180	ASP
2	B	53	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	271/270 (100%)	265 (98%)	6 (2%)	45	34
2	B	272/270 (101%)	237 (87%)	35 (13%)	4	1
All	All	543/540 (101%)	502 (92%)	41 (8%)	12	4

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	171	ASP
1	A	179	TRP
1	A	187	MET
1	A	189	LYS
1	A	316	SER
2	B	6	ILE
2	B	16	ILE
2	B	19	GLN
2	B	23	LYS
2	B	25	ASP
2	B	33	GLN
2	B	43	ILE
2	B	65	GLU
2	B	74	VAL
2	B	77	THR
2	B	80	THR
2	B	83	MET
2	B	105	LEU
2	B	113	GLN
2	B	120	GLN
2	B	127	ASP
2	B	131	LYS
2	B	142	LEU
2	B	148	ASN
2	B	150	LEU
2	B	152	ASP

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Mol	Chain	Res	Type
2	B	154	ASP
2	B	155	LEU
2	B	165	THR
2	B	171	ASP
2	B	194	TRP
2	B	198	MET
2	B	217	ARG
2	B	218	ILE
2	B	247	ARG
2	B	248	ASP
2	B	294	ASP
2	B	315	GLU
2	B	321	ILE
2	B	323	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	228	HIS
2	B	11	HIS
2	B	145	GLN
2	B	148	ASN
2	B	166	HIS
2	B	333	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 oligosaccharides 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

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	331/331 (100%)	0.39	7 (2%) 63 64	22, 34, 57, 82	1 (0%)
2	B	331/331 (100%)	1.76	120 (36%) 1 0	19, 63, 84, 94	2 (0%)
All	All	662/662 (100%)	1.07	127 (19%) 3 2	19, 45, 81, 94	3 (0%)

All (127) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	74	VAL	5.5
2	B	333	ASN	5.5
2	B	61	ALA	5.3
2	B	107	PHE	4.7
2	B	58	TRP	4.7
2	B	179	TRP	4.6
2	B	36	ALA	4.5
2	B	304	ILE	4.5
2	B	317	ALA	4.3
2	B	31	TRP	4.1
2	B	99	ARG	4.0
2	B	24	PHE	4.0
2	B	112	PRO	4.0
2	B	155	LEU	3.8
2	B	309	LEU	3.8
2	B	90	ALA	3.8
2	B	93	ALA	3.8
2	B	332	ILE	3.7
1	A	36	ALA	3.7
2	B	321	ILE	3.7
2	B	34	VAL	3.7
2	B	72	VAL	3.6
2	B	16	ILE	3.6
2	B	62	PHE	3.5

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Mol	Chain	Res	Type	RSRZ
2	B	41	GLY	3.5
2	B	4	PRO	3.5
2	B	117	VAL	3.4
2	B	150	LEU	3.4
2	B	40	THR	3.4
2	B	45	MET	3.4
2	B	115	ILE	3.3
2	B	183	GLY	3.3
2	B	21	ALA	3.2
2	B	109	ALA	3.2
2	B	322	ILE	3.2
1	A	38	GLY	3.1
2	B	118	LEU	3.1
2	B	326	ALA	3.1
2	B	149	HIS	3.1
2	B	32	LEU	3.1
2	B	128	LEU	3.1
2	B	194	TRP	3.0
2	B	57	LEU	3.0
2	B	67	MET	3.0
2	B	46	GLY	3.0
2	B	96	TRP	3.0
2	B	123	LEU	2.9
2	B	126	LEU	2.9
2	B	103	PHE	2.9
2	B	78	CYS	2.9
2	B	110	HIS	2.9
2	B	222	LEU	2.9
2	B	26	ALA	2.9
2	B	184	GLY	2.9
2	B	131	LYS	2.8
2	B	64	ILE	2.8
2	B	13	PHE	2.8
2	B	84	PHE	2.8
2	B	22	ALA	2.8
2	B	329	PHE	2.8
2	B	142	LEU	2.7
2	B	75	GLN	2.7
2	B	76	VAL	2.7
2	B	108	ALA	2.7
2	B	160	LEU	2.7
2	B	209	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	60	PRO	2.7
2	B	297	PHE	2.7
2	B	313	LEU	2.6
2	B	56	ALA	2.6
2	B	129	ALA	2.6
2	B	159	THR	2.6
2	B	30	PRO	2.6
2	B	6	ILE	2.5
2	B	133	ALA	2.5
2	B	323	SER	2.5
2	B	86	TYR	2.5
2	B	139	ALA	2.5
2	B	307	LEU	2.5
2	B	43	ILE	2.5
2	B	330	PHE	2.4
2	B	94	ALA	2.4
1	A	22	ALA	2.4
1	A	186	ARG	2.4
2	B	53	VAL	2.4
2	B	314	GLY	2.4
2	B	295	TYR	2.4
2	B	12	PHE	2.3
2	B	165	THR	2.3
2	B	296	PRO	2.3
2	B	83	MET	2.3
2	B	218	ILE	2.3
2	B	85	GLY	2.3
2	B	35	SER	2.3
2	B	87	THR	2.3
2	B	111	ASN	2.3
2	B	158	ALA	2.3
2	B	54	TYR	2.2
2	B	168	ALA	2.2
2	B	262	VAL	2.2
2	B	141	HIS	2.2
1	A	35	SER	2.2
2	B	156	ASP	2.2
2	B	114	ARG	2.2
2	B	113	GLN	2.2
1	A	46	GLY	2.2
2	B	42	SER	2.2
2	B	29	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	68	ASP	2.2
2	B	17	SER	2.2
2	B	140	GLY	2.2
2	B	324	GLY	2.2
2	B	104	ALA	2.2
2	B	213	GLY	2.1
2	B	291	LEU	2.1
2	B	44	MET	2.1
1	A	24	PHE	2.1
2	B	38	GLY	2.1
2	B	23	LYS	2.1
2	B	105	LEU	2.1
2	B	265	PHE	2.1
2	B	91	ASN	2.1
2	B	261	TYR	2.0
2	B	28	HIS	2.0
2	B	122	PRO	2.0
2	B	164	LEU	2.0
2	B	52	PRO	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
3	ZN	B	401	1/1	0.97	0.05	46,46,46,46	0
3	ZN	A	401	1/1	0.99	0.04	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.