



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 01:32 PM UTC

PDB ID : 1QML / pdb_00001qml
Title : Hg complex of yeast 5-aminolaevulinic acid dehydratase
Authors : Erskine, P.T.; Senior, N.; Warren, M.J.; Wood, S.P.; Cooper, J.B.
Deposited on : 1999-10-02
Resolution : 3.00 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

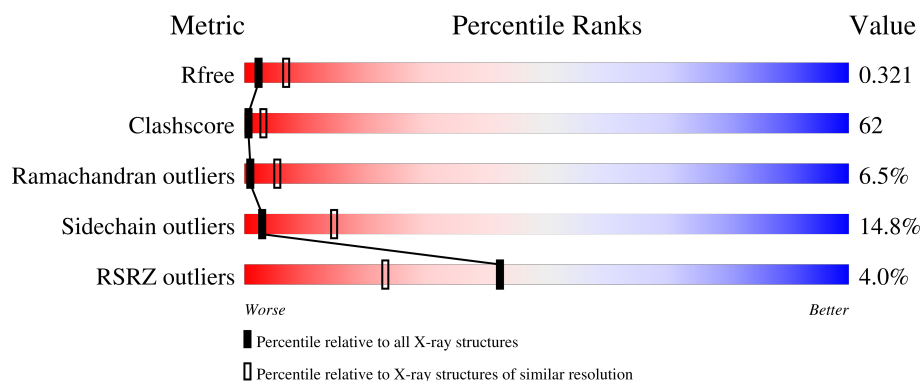
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	342	4% 26% 49% 18% • •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2812 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 5-AMINOLAEVULINIC ACID DEHYDRATASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	328	Total	C	N	O	S	0	0	0
			2546	1623	437	472	14			

- Molecule 2 is MERCURY (II) ION (CCD ID: HG) (formula: Hg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Hg	0	0
			1	1		

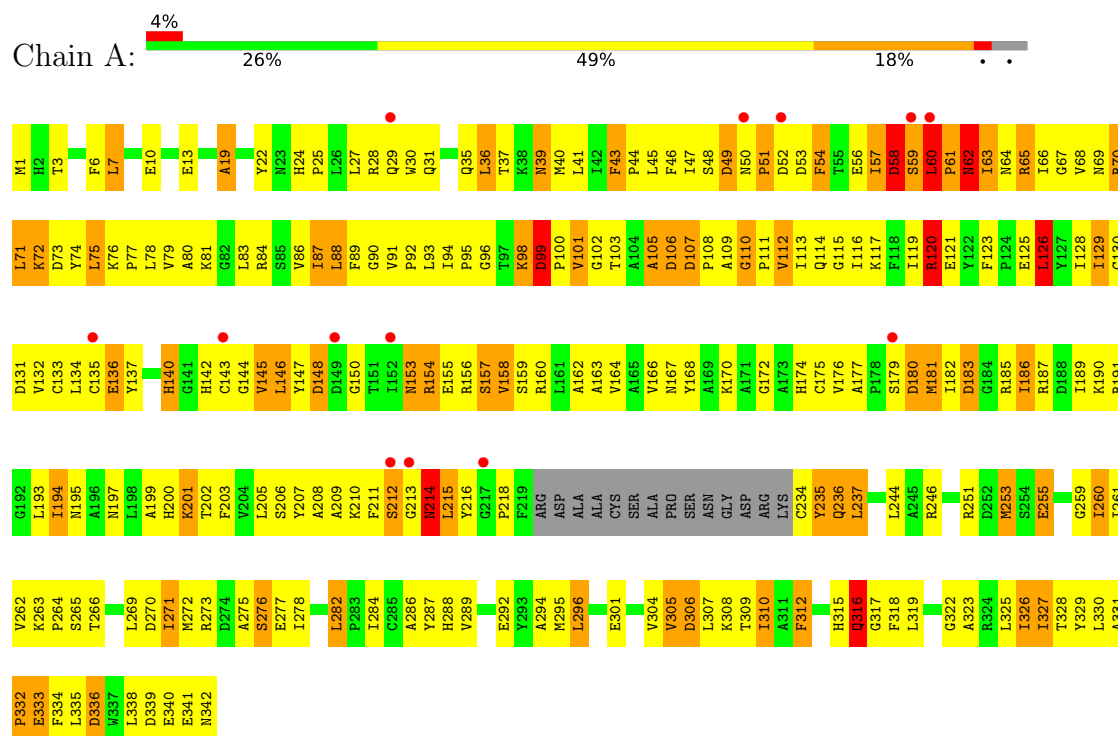
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	265	Total	O	0	4
			265	265		

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: 5-AMINOLAEVULINIC ACID DEHYDRATASE



4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	102.05Å 102.05Å 170.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.50 – 3.00 14.50 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.0 (14.50-3.00) 98.7 (14.50-3.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.71 (at 3.01Å)	Xtriage
Refinement program	CCP4	Depositor
R, R_{free}	0.249 , 0.330 0.278 , 0.321	Depositor DCC
R_{free} test set	442 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	56.8	Xtriage
Anisotropy	0.482	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.47 , 108.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	2812	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% 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: HG

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	0.81	0/2603	1.86	76/3532 (2.2%)

There are no bond length outliers.

All (76) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	62	ASN	CA-C-N	10.34	136.43	123.10
1	A	62	ASN	C-N-CA	10.34	136.43	123.10
1	A	58	ASP	CA-C-N	10.22	141.06	121.54
1	A	58	ASP	C-N-CA	10.22	141.06	121.54
1	A	64	ASN	CA-C-N	10.15	136.39	122.79
1	A	64	ASN	C-N-CA	10.15	136.39	122.79
1	A	340	GLU	CA-C-N	9.53	139.75	121.54
1	A	340	GLU	C-N-CA	9.53	139.75	121.54
1	A	150	GLY	CA-C-N	9.50	139.68	121.54
1	A	150	GLY	C-N-CA	9.50	139.68	121.54
1	A	235	TYR	CA-CB-CG	9.46	130.93	113.90
1	A	99	ASP	CA-C-N	8.70	128.35	119.82
1	A	99	ASP	C-N-CA	8.70	128.35	119.82
1	A	61	PRO	CA-C-N	8.47	134.49	121.53
1	A	61	PRO	C-N-CA	8.47	134.49	121.53
1	A	236	GLN	CA-C-N	8.42	132.72	120.51
1	A	236	GLN	C-N-CA	8.42	132.72	120.51
1	A	312	PHE	CA-CB-CG	8.41	122.21	113.80
1	A	128	ILE	N-CA-C	7.95	120.39	108.23
1	A	317	GLY	N-CA-C	-7.83	102.75	112.77
1	A	62	ASN	O-C-N	7.79	129.89	122.18
1	A	60	LEU	CA-C-N	7.74	129.51	119.84
1	A	60	LEU	C-N-CA	7.74	129.51	119.84
1	A	88	LEU	CA-C-N	7.70	134.04	122.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	88	LEU	C-N-CA	7.70	134.04	122.95
1	A	342	ASN	CA-CB-CG	7.37	119.97	112.60
1	A	322	GLY	CA-C-N	6.93	131.41	121.50
1	A	322	GLY	C-N-CA	6.93	131.41	121.50
1	A	35	GLN	CA-C-N	6.80	132.27	121.66
1	A	35	GLN	C-N-CA	6.80	132.27	121.66
1	A	39	ASN	CA-CB-CG	6.77	119.37	112.60
1	A	74	TYR	CA-CB-CG	6.42	125.45	113.90
1	A	237	LEU	CA-C-N	6.37	126.94	120.38
1	A	237	LEU	C-N-CA	6.37	126.94	120.38
1	A	316	GLN	N-CA-C	-6.33	105.52	113.18
1	A	322	GLY	N-CA-C	6.31	128.14	113.18
1	A	112	VAL	N-CA-C	6.31	116.79	110.23
1	A	135	CYS	CA-C-N	6.23	130.57	120.60
1	A	135	CYS	C-N-CA	6.23	130.57	120.60
1	A	29	GLN	N-CA-C	-6.14	106.42	114.04
1	A	323	ALA	N-CA-C	6.08	119.42	109.76
1	A	43	PHE	CA-CB-CG	6.03	119.83	113.80
1	A	145	VAL	CA-C-N	5.99	133.90	121.32
1	A	145	VAL	C-N-CA	5.99	133.90	121.32
1	A	305	VAL	CA-CB-CG1	5.82	120.29	110.40
1	A	306	ASP	CA-CB-CG	-5.78	106.82	112.60
1	A	10	GLU	CA-CB-CG	5.78	125.65	114.10
1	A	129	ILE	CA-C-N	-5.46	115.29	123.00
1	A	129	ILE	C-N-CA	-5.46	115.29	123.00
1	A	301	GLU	CA-CB-CG	5.39	124.88	114.10
1	A	140	HIS	O-C-N	5.38	127.82	122.12
1	A	49	ASP	N-CA-CB	5.35	119.12	110.40
1	A	187	ARG	CA-C-N	5.33	127.85	120.29
1	A	187	ARG	C-N-CA	5.33	127.85	120.29
1	A	106	ASP	CA-C-N	5.26	134.64	121.80
1	A	106	ASP	C-N-CA	5.26	134.64	121.80
1	A	259	GLY	CA-C-N	-5.26	115.22	122.69
1	A	259	GLY	C-N-CA	-5.26	115.22	122.69
1	A	70	ARG	CA-C-N	5.22	131.51	121.54
1	A	70	ARG	C-N-CA	5.22	131.51	121.54
1	A	136	GLU	N-CA-C	5.20	118.73	112.38
1	A	336	ASP	CA-CB-CG	5.18	117.78	112.60
1	A	332	PRO	CA-C-N	5.14	127.62	120.63
1	A	332	PRO	C-N-CA	5.14	127.62	120.63
1	A	6	PHE	CA-CB-CG	5.13	118.93	113.80
1	A	244	LEU	O-C-N	5.12	127.35	122.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	255	GLU	CA-C-N	-5.12	116.17	123.08
1	A	255	GLU	C-N-CA	-5.12	116.17	123.08
1	A	333	GLU	N-CA-C	5.11	116.70	111.03
1	A	110	GLY	CA-C-N	5.09	126.20	119.84
1	A	110	GLY	C-N-CA	5.09	126.20	119.84
1	A	146	LEU	N-CA-C	5.07	117.39	110.55
1	A	29	GLN	CA-C-O	5.04	125.36	119.06
1	A	148	ASP	CA-CB-CG	-5.02	107.58	112.60
1	A	83	LEU	CA-C-N	-5.00	114.48	122.29
1	A	83	LEU	C-N-CA	-5.00	114.48	122.29

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	2546	0	2523	316	1
2	A	1	0	0	0	0
3	A	265	0	0	10	1
All	All	2812	0	2523	316	2

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 62.

All (316) 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:24:HIS:CD2	1:A:25:PRO:HD2	1.38	1.57
1:A:60:LEU:H	1:A:61:PRO:CD	1.49	1.21
1:A:60:LEU:H	1:A:61:PRO:HD2	0.98	1.14
1:A:145:VAL:HG11	1:A:156:ARG:HG2	1.30	1.12
1:A:65:ARG:HG2	1:A:65:ARG:HH11	1.16	1.11
1:A:24:HIS:CD2	1:A:25:PRO:CD	2.34	1.09
1:A:253:MET:HG3	1:A:282:LEU:HD21	1.33	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:ILE:O	1:A:58:ASP:HB2	1.49	1.07
1:A:99:ASP:HB2	1:A:100:PRO:CD	1.84	1.07
1:A:260:ILE:HD12	1:A:261:ILE:N	1.69	1.06
1:A:99:ASP:HB2	1:A:100:PRO:HD2	1.38	1.04
1:A:59:SER:H	1:A:61:PRO:HD2	1.23	1.03
1:A:57:ILE:HG22	1:A:58:ASP:H	1.21	1.02
1:A:177:ALA:HB1	1:A:207:TYR:HE1	1.25	1.01
1:A:180:ASP:HB2	1:A:182:ILE:HD12	1.41	0.99
1:A:58:ASP:HA	1:A:61:PRO:HG2	1.45	0.97
1:A:98:LYS:O	1:A:99:ASP:HB3	1.64	0.96
1:A:327:ILE:HG22	1:A:327:ILE:O	1.64	0.95
1:A:60:LEU:N	1:A:61:PRO:CD	2.24	0.94
1:A:60:LEU:N	1:A:61:PRO:HD2	1.83	0.92
1:A:145:VAL:CG1	1:A:156:ARG:HG2	2.01	0.91
1:A:214:ASN:O	1:A:214:ASN:ND2	2.02	0.91
1:A:51:PRO:HB2	1:A:69:ASN:ND2	1.86	0.91
1:A:48:SER:HB2	1:A:65:ARG:HG3	1.53	0.90
1:A:41:LEU:HD11	1:A:334:PHE:HB2	1.53	0.89
1:A:253:MET:HG3	1:A:282:LEU:CD2	2.02	0.88
1:A:177:ALA:HB1	1:A:207:TYR:CE1	2.08	0.88
1:A:99:ASP:CB	1:A:100:PRO:CD	2.48	0.88
1:A:260:ILE:HD12	1:A:260:ILE:C	2.01	0.85
1:A:59:SER:N	1:A:61:PRO:HD2	1.93	0.83
1:A:181:MET:HE1	1:A:237:LEU:CD1	2.07	0.83
1:A:57:ILE:O	1:A:58:ASP:CB	2.25	0.83
1:A:205:LEU:CD2	1:A:261:ILE:HD11	2.08	0.83
1:A:99:ASP:CB	1:A:100:PRO:HD2	2.07	0.83
1:A:40:MET:SD	1:A:319:LEU:HD21	2.21	0.81
1:A:263:LYS:HA	1:A:264:PRO:C	2.05	0.80
1:A:185:ARG:O	1:A:189:ILE:HG13	1.82	0.80
1:A:140:HIS:HD2	1:A:142:HIS:H	1.29	0.79
1:A:310:ILE:HD12	1:A:310:ILE:O	1.82	0.79
1:A:51:PRO:HB2	1:A:69:ASN:HD22	1.46	0.79
1:A:58:ASP:HA	1:A:61:PRO:CG	2.11	0.79
1:A:44:PRO:HA	1:A:87:ILE:HG23	1.63	0.79
1:A:65:ARG:HD2	1:A:91:VAL:HG11	1.65	0.79
1:A:90:GLY:HA3	1:A:112:VAL:HG23	1.65	0.78
1:A:57:ILE:HG22	1:A:58:ASP:N	1.95	0.78
1:A:65:ARG:HG2	1:A:65:ARG:NH1	1.94	0.78
1:A:24:HIS:HD2	1:A:25:PRO:CD	1.84	0.78
1:A:180:ASP:CB	1:A:182:ILE:HD12	2.12	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:ASP:CG	1:A:93:LEU:H	1.92	0.77
1:A:66:ILE:HG23	1:A:70:ARG:HB2	1.68	0.75
1:A:176:VAL:HG23	1:A:176:VAL:O	1.86	0.75
1:A:72:LYS:O	1:A:72:LYS:HD3	1.87	0.75
1:A:111:PRO:HD2	3:A:2172:HOH:O	1.87	0.74
1:A:94:ILE:HG23	1:A:95:PRO:HD2	1.67	0.74
1:A:177:ALA:CB	1:A:207:TYR:HE1	2.00	0.74
1:A:99:ASP:HB2	1:A:100:PRO:HD3	1.67	0.73
1:A:145:VAL:O	1:A:153:ASN:HB3	1.90	0.72
1:A:216:TYR:HE1	1:A:263:LYS:HE3	1.55	0.72
1:A:1:MET:O	1:A:3:THR:HG23	1.90	0.72
1:A:155:GLU:HA	1:A:158:VAL:CG2	2.20	0.72
1:A:66:ILE:HG22	1:A:67:GLY:N	2.04	0.71
1:A:327:ILE:O	1:A:327:ILE:CG2	2.37	0.71
1:A:162:ALA:O	1:A:166:VAL:HG23	1.91	0.71
1:A:332:PRO:HG2	1:A:333:GLU:OE1	1.89	0.71
1:A:22:TYR:O	1:A:22:TYR:CD1	2.44	0.71
1:A:269:LEU:HD23	1:A:272:MET:HE3	1.73	0.71
1:A:275:ALA:HB1	1:A:284:ILE:HD13	1.73	0.70
1:A:212:SER:HB3	1:A:236:GLN:OE1	1.92	0.70
1:A:154:ARG:HB2	3:A:2202:HOH:O	1.90	0.70
1:A:75:LEU:C	1:A:77:PRO:HD2	2.16	0.70
1:A:140:HIS:CD2	1:A:142:HIS:H	2.08	0.70
1:A:47:ILE:O	1:A:111:PRO:HB3	1.92	0.69
1:A:27:LEU:O	1:A:31:GLN:HG2	1.92	0.69
1:A:200:HIS:HD2	1:A:201:LYS:HG2	1.56	0.69
1:A:140:HIS:CD2	1:A:146:LEU:HD11	2.26	0.69
1:A:331:ALA:N	1:A:332:PRO:HD2	2.07	0.69
1:A:58:ASP:CA	1:A:61:PRO:HG2	2.21	0.69
1:A:24:HIS:HD2	1:A:25:PRO:HD2	0.94	0.69
1:A:325:LEU:C	1:A:326:ILE:HG12	2.18	0.69
1:A:205:LEU:HG	1:A:261:ILE:CD1	2.23	0.68
1:A:263:LYS:HG3	1:A:289:VAL:HG13	1.75	0.68
1:A:61:PRO:C	1:A:62:ASN:HD22	2.01	0.68
1:A:190:LYS:O	1:A:194:ILE:HD12	1.92	0.68
1:A:47:ILE:HG22	1:A:111:PRO:HB3	1.75	0.68
1:A:84:ARG:HH11	1:A:84:ARG:HG3	1.59	0.68
1:A:216:TYR:HE1	1:A:263:LYS:CE	2.06	0.67
1:A:66:ILE:CG2	1:A:67:GLY:N	2.57	0.67
1:A:94:ILE:HG22	1:A:96:GLY:H	1.57	0.67
1:A:269:LEU:HD23	1:A:272:MET:CE	2.25	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:LEU:HG	1:A:261:ILE:HD11	1.76	0.66
1:A:60:LEU:N	1:A:61:PRO:HD3	2.10	0.66
1:A:251:ARG:O	1:A:255:GLU:HG3	1.94	0.66
1:A:180:ASP:CG	1:A:181:MET:H	2.03	0.66
1:A:68:VAL:HG12	1:A:68:VAL:O	1.96	0.66
1:A:200:HIS:CD2	1:A:201:LYS:HG2	2.31	0.65
1:A:90:GLY:HA3	1:A:112:VAL:CG2	2.26	0.65
1:A:263:LYS:HA	1:A:264:PRO:O	1.95	0.65
1:A:336:ASP:O	1:A:339:ASP:HB2	1.97	0.65
1:A:115:GLY:O	1:A:119:ILE:HD12	1.97	0.64
1:A:265:SER:OG	1:A:266:THR:N	2.30	0.64
1:A:40:MET:HE1	1:A:319:LEU:CD2	2.29	0.63
1:A:260:ILE:HD12	1:A:261:ILE:CA	2.28	0.63
1:A:50:ASN:C	1:A:52:ASP:H	2.07	0.62
1:A:73:ASP:O	1:A:77:PRO:HD3	1.99	0.62
1:A:72:LYS:HE3	1:A:76:LYS:NZ	2.15	0.62
1:A:205:LEU:CG	1:A:261:ILE:HD11	2.29	0.62
1:A:160:ARG:O	1:A:163:ALA:HB3	2.00	0.61
1:A:78:LEU:O	1:A:81:LYS:HB2	1.99	0.61
1:A:140:HIS:CD2	1:A:142:HIS:HB2	2.34	0.61
1:A:80:ALA:HB2	3:A:2155:HOH:O	2.00	0.61
1:A:194:ILE:HG13	1:A:199:ALA:HB2	1.82	0.61
1:A:51:PRO:O	1:A:69:ASN:HB2	2.01	0.61
1:A:98:LYS:O	1:A:99:ASP:CB	2.42	0.60
1:A:107:ASP:C	1:A:107:ASP:OD1	2.45	0.59
1:A:331:ALA:O	1:A:335:LEU:HD12	2.01	0.59
1:A:50:ASN:O	1:A:52:ASP:N	2.35	0.59
1:A:50:ASN:C	1:A:50:ASN:OD1	2.45	0.59
1:A:181:MET:HE1	1:A:237:LEU:HD12	1.85	0.59
1:A:53:ASP:O	1:A:70:ARG:HG3	2.02	0.59
1:A:41:LEU:HD11	1:A:334:PHE:CB	2.29	0.59
1:A:36:LEU:HG	1:A:338:LEU:HD21	1.85	0.59
1:A:47:ILE:O	1:A:47:ILE:HG22	2.02	0.59
1:A:60:LEU:CB	1:A:294:ALA:HB1	2.32	0.59
1:A:199:ALA:HB3	3:A:2217:HOH:O	2.02	0.59
1:A:140:HIS:HD2	1:A:142:HIS:HB2	1.68	0.58
1:A:153:ASN:ND2	1:A:156:ARG:HB2	2.18	0.58
1:A:260:ILE:HD11	1:A:262:VAL:HG23	1.85	0.58
1:A:65:ARG:CD	1:A:91:VAL:HG11	2.33	0.58
1:A:68:VAL:O	1:A:68:VAL:CG1	2.51	0.58
1:A:75:LEU:O	1:A:79:VAL:HG23	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:LEU:HD23	1:A:126:LEU:N	2.18	0.57
1:A:140:HIS:HD2	1:A:142:HIS:N	1.99	0.57
1:A:107:ASP:O	1:A:109:ALA:N	2.36	0.57
1:A:132:VAL:O	1:A:132:VAL:HG12	2.03	0.57
1:A:62:ASN:C	1:A:63:ILE:HD13	2.29	0.57
1:A:101:VAL:O	1:A:102:GLY:C	2.48	0.57
1:A:155:GLU:HA	1:A:158:VAL:HG22	1.85	0.57
1:A:133:CYS:HB2	1:A:179:SER:OG	2.04	0.56
1:A:263:LYS:HE3	1:A:289:VAL:CG1	2.35	0.56
1:A:176:VAL:O	1:A:176:VAL:CG2	2.51	0.56
1:A:181:MET:HE1	1:A:237:LEU:HG	1.87	0.56
1:A:181:MET:HE1	1:A:237:LEU:CG	2.36	0.56
1:A:54:PHE:HD1	1:A:54:PHE:O	1.88	0.56
1:A:72:LYS:HE3	1:A:76:LYS:CE	2.36	0.55
1:A:1:MET:HE3	3:A:2009[B]:HOH:O	2.06	0.55
1:A:66:ILE:CG2	1:A:67:GLY:H	2.19	0.55
1:A:275:ALA:CB	1:A:284:ILE:HD13	2.37	0.55
1:A:263:LYS:CG	1:A:289:VAL:HG13	2.36	0.55
1:A:186:ILE:HD11	1:A:206:SER:HB2	1.87	0.55
1:A:47:ILE:HG22	1:A:111:PRO:CB	2.37	0.55
1:A:65:ARG:HH11	1:A:65:ARG:CG	2.02	0.55
1:A:270:ASP:OD2	1:A:271:ILE:HD13	2.06	0.55
1:A:203:PHE:HE1	1:A:205:LEU:HD13	1.72	0.55
1:A:216:TYR:CE1	1:A:263:LYS:HE3	2.41	0.54
1:A:260:ILE:C	1:A:260:ILE:CD1	2.70	0.54
1:A:56:GLU:HG3	3:A:2128:HOH:O	2.07	0.54
1:A:76:LYS:N	1:A:77:PRO:HD2	2.22	0.54
1:A:76:LYS:N	1:A:77:PRO:CD	2.70	0.54
1:A:102:GLY:HA2	1:A:137:TYR:O	2.07	0.54
1:A:47:ILE:HG21	1:A:111:PRO:O	2.08	0.54
1:A:195:ASN:C	1:A:197:ASN:H	2.16	0.54
1:A:331:ALA:N	1:A:332:PRO:CD	2.70	0.54
1:A:45:LEU:O	1:A:89:PHE:HB2	2.08	0.53
1:A:57:ILE:CG2	1:A:58:ASP:N	2.70	0.53
1:A:41:LEU:CD1	1:A:334:PHE:HB2	2.33	0.53
1:A:131:ASP:OD1	1:A:179:SER:HB3	2.09	0.53
1:A:181:MET:CE	1:A:237:LEU:HG	2.38	0.52
1:A:155:GLU:CA	1:A:158:VAL:HG22	2.39	0.52
1:A:316:GLN:HA	1:A:319:LEU:HD12	1.91	0.52
1:A:65:ARG:NH1	1:A:65:ARG:CG	2.68	0.52
1:A:186:ILE:CD1	1:A:206:SER:HB2	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:ASP:OD2	1:A:235:TYR:HE2	1.92	0.52
1:A:304:VAL:O	1:A:305:VAL:HG13	2.10	0.52
1:A:287:TYR:CZ	1:A:327:ILE:HG21	2.45	0.51
1:A:318:PHE:HD2	1:A:326:ILE:HG21	1.76	0.51
1:A:315:HIS:CD2	1:A:334:PHE:CZ	2.98	0.51
1:A:126:LEU:HD23	1:A:126:LEU:H	1.74	0.51
1:A:260:ILE:HD12	1:A:261:ILE:C	2.35	0.51
1:A:119:ILE:HG23	1:A:123:PHE:HB2	1.93	0.50
1:A:44:PRO:HB3	1:A:89:PHE:HE2	1.75	0.50
1:A:94:ILE:HG23	1:A:95:PRO:CD	2.39	0.50
1:A:66:ILE:HG22	1:A:67:GLY:O	2.11	0.50
1:A:88:LEU:HD12	1:A:116:ILE:CG1	2.41	0.50
1:A:296:LEU:HD21	3:A:2239:HOH:O	2.10	0.50
1:A:304:VAL:O	1:A:304:VAL:CG1	2.60	0.50
1:A:52:ASP:HB3	3:A:2121:HOH:O	2.12	0.50
1:A:145:VAL:H	1:A:157:SER:CB	2.25	0.50
1:A:287:TYR:CD1	1:A:327:ILE:HG22	2.47	0.50
1:A:180:ASP:HB2	1:A:182:ILE:CD1	2.29	0.50
1:A:205:LEU:HD23	1:A:261:ILE:HD11	1.92	0.49
1:A:106:ASP:HB3	1:A:164:VAL:HA	1.95	0.49
1:A:269:LEU:CD2	1:A:272:MET:HE3	2.41	0.49
1:A:63:ILE:HD13	1:A:63:ILE:N	2.28	0.49
1:A:306:ASP:O	1:A:309:THR:HB	2.12	0.49
1:A:133:CYS:SG	1:A:143:CYS:HB3	2.53	0.49
1:A:166:VAL:HG12	1:A:170:LYS:HE3	1.94	0.49
1:A:200:HIS:CD2	1:A:201:LYS:CG	2.95	0.49
1:A:275:ALA:HB1	1:A:284:ILE:CD1	2.42	0.49
1:A:41:LEU:HD13	1:A:331:ALA:HA	1.94	0.49
1:A:27:LEU:HA	1:A:30:TRP:HB2	1.95	0.49
1:A:276:SER:OG	1:A:277:GLU:N	2.46	0.49
1:A:287:TYR:CE1	1:A:327:ILE:HG21	2.47	0.49
1:A:333:GLU:O	1:A:336:ASP:HB2	2.13	0.49
1:A:13:GLU:HA	3:A:2053:HOH:O	2.11	0.48
1:A:65:ARG:CZ	1:A:93:LEU:HD11	2.43	0.48
1:A:318:PHE:CD2	1:A:326:ILE:HG21	2.48	0.48
1:A:175:CYS:SG	1:A:203:PHE:HD1	2.37	0.48
1:A:315:HIS:CD2	1:A:334:PHE:CE2	3.01	0.48
1:A:330:LEU:C	1:A:332:PRO:HD2	2.39	0.48
1:A:287:TYR:CD1	1:A:327:ILE:CG2	2.97	0.48
1:A:275:ALA:C	1:A:284:ILE:HD11	2.38	0.48
1:A:153:ASN:C	1:A:153:ASN:OD1	2.55	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:ASP:OD2	1:A:65:ARG:HG2	2.13	0.48
1:A:180:ASP:O	1:A:181:MET:HB2	2.13	0.48
1:A:207:TYR:HA	1:A:261:ILE:HB	1.95	0.48
1:A:253:MET:HE3	1:A:253:MET:HB3	1.72	0.47
1:A:153:ASN:HD21	1:A:156:ARG:HB2	1.79	0.47
1:A:110:GLY:O	1:A:114:GLN:HB2	2.13	0.47
1:A:19:ALA:HA	1:A:22:TYR:CE2	2.48	0.47
1:A:304:VAL:O	1:A:304:VAL:HG12	2.14	0.47
1:A:46:PHE:CE1	1:A:89:PHE:CD2	3.03	0.47
1:A:91:VAL:O	1:A:91:VAL:HG12	2.14	0.47
1:A:106:ASP:CB	1:A:167:ASN:HD22	2.28	0.47
1:A:129:ILE:HG13	1:A:175:CYS:HB3	1.97	0.47
1:A:44:PRO:CG	1:A:329:TYR:CE1	2.98	0.46
1:A:77:PRO:HG2	1:A:78:LEU:H	1.80	0.46
1:A:49:ASP:O	1:A:51:PRO:HD3	2.15	0.46
1:A:287:TYR:CE1	1:A:327:ILE:CG2	2.99	0.46
1:A:206:SER:O	1:A:261:ILE:HD12	2.16	0.46
1:A:54:PHE:O	1:A:54:PHE:CD1	2.67	0.46
1:A:116:ILE:HG22	1:A:116:ILE:O	2.14	0.46
1:A:329:TYR:O	1:A:332:PRO:HD2	2.14	0.46
1:A:36:LEU:HD12	1:A:37:THR:O	2.15	0.46
1:A:84:ARG:HG3	1:A:84:ARG:NH1	2.27	0.46
1:A:140:HIS:CD2	1:A:146:LEU:CD1	2.96	0.46
1:A:263:LYS:HB2	1:A:287:TYR:HB3	1.98	0.46
1:A:325:LEU:O	1:A:326:ILE:HG12	2.16	0.46
1:A:181:MET:HE1	1:A:237:LEU:HD11	1.95	0.46
1:A:134:LEU:HD12	1:A:144:GLY:HA2	1.98	0.46
1:A:185:ARG:HD3	1:A:186:ILE:HG12	1.98	0.46
1:A:263:LYS:CA	1:A:264:PRO:O	2.64	0.46
1:A:113:ILE:O	1:A:113:ILE:HG22	2.16	0.45
1:A:147:TYR:HB3	1:A:148:ASP:H	1.54	0.45
1:A:191:ARG:O	1:A:194:ILE:HB	2.16	0.45
1:A:58:ASP:HA	1:A:61:PRO:CD	2.47	0.45
1:A:116:ILE:HD11	1:A:130:CYS:SG	2.57	0.45
1:A:129:ILE:HA	1:A:175:CYS:HB3	1.98	0.45
1:A:24:HIS:CG	1:A:25:PRO:HD2	2.28	0.45
1:A:194:ILE:HG22	1:A:195:ASN:N	2.30	0.45
1:A:205:LEU:HD21	1:A:261:ILE:HD11	1.92	0.45
1:A:145:VAL:CB	1:A:156:ARG:HG2	2.47	0.45
1:A:308:LYS:O	1:A:312:PHE:HD1	2.00	0.45
1:A:260:ILE:CD1	1:A:261:ILE:N	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:147:TYR:CE1	1:A:153:ASN:HB2	2.52	0.44
1:A:195:ASN:C	1:A:197:ASN:N	2.75	0.44
1:A:205:LEU:HG	1:A:261:ILE:HD12	1.98	0.44
1:A:40:MET:HE1	1:A:319:LEU:HD21	2.00	0.44
1:A:43:PHE:O	1:A:86:VAL:HA	2.17	0.44
1:A:46:PHE:CD1	1:A:89:PHE:CB	3.00	0.44
1:A:310:ILE:HD13	1:A:310:ILE:HA	1.86	0.44
1:A:119:ILE:C	1:A:121:GLU:H	2.25	0.44
1:A:153:ASN:OD1	1:A:153:ASN:O	2.34	0.44
1:A:210:LYS:HD2	1:A:263:LYS:HE2	1.98	0.44
1:A:54:PHE:HB3	1:A:70:ARG:NH2	2.33	0.44
1:A:40:MET:CE	1:A:319:LEU:HD21	2.47	0.44
1:A:44:PRO:HG2	1:A:329:TYR:CE1	2.53	0.44
1:A:72:LYS:O	1:A:72:LYS:CD	2.60	0.44
1:A:94:ILE:CG2	1:A:95:PRO:N	2.81	0.44
1:A:189:ILE:O	1:A:193:LEU:HG	2.17	0.43
1:A:132:VAL:HG22	1:A:168:TYR:CE2	2.53	0.43
1:A:214:ASN:ND2	1:A:218:PRO:HA	2.33	0.43
1:A:213:GLY:C	1:A:215:LEU:H	2.26	0.43
1:A:106:ASP:OD1	1:A:106:ASP:N	2.49	0.43
1:A:47:ILE:HD11	1:A:71:LEU:HD21	2.01	0.43
1:A:36:LEU:HB2	1:A:319:LEU:HD11	2.01	0.43
1:A:77:PRO:CG	1:A:78:LEU:H	2.32	0.43
1:A:174:HIS:O	1:A:202:THR:HG23	2.19	0.43
1:A:203:PHE:HE1	1:A:205:LEU:CD1	2.31	0.42
1:A:272:MET:HB2	1:A:272:MET:HE2	1.76	0.42
1:A:288:HIS:HD2	1:A:292:GLU:OE1	2.02	0.42
1:A:44:PRO:CA	1:A:87:ILE:HG23	2.41	0.42
1:A:103:THR:C	1:A:105:ALA:H	2.26	0.42
1:A:183:ASP:HA	1:A:251:ARG:HH12	1.85	0.42
1:A:286:ALA:HB3	1:A:326:ILE:HG23	2.01	0.42
1:A:22:TYR:O	1:A:22:TYR:CG	2.67	0.42
1:A:66:ILE:CG2	1:A:70:ARG:HB2	2.46	0.42
1:A:287:TYR:CE2	1:A:327:ILE:HG21	2.54	0.42
1:A:153:ASN:O	1:A:153:ASN:CG	2.63	0.42
1:A:209:ALA:HB1	1:A:211:PHE:HE1	1.85	0.42
1:A:272:MET:O	1:A:275:ALA:HB3	2.20	0.42
1:A:246:ARG:HG2	1:A:278:ILE:HD11	2.02	0.42
1:A:154:ARG:O	1:A:158:VAL:HG22	2.18	0.42
1:A:113:ILE:O	1:A:117:LYS:HG3	2.20	0.42
1:A:75:LEU:CB	1:A:123:PHE:CE2	3.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:ARG:HD3	1:A:172:GLY:O	2.20	0.41
1:A:100:PRO:O	1:A:101:VAL:HG13	2.20	0.41
1:A:140:HIS:CG	1:A:146:LEU:HD11	2.55	0.41
1:A:46:PHE:CD1	1:A:89:PHE:HB2	2.56	0.41
1:A:46:PHE:HA	1:A:89:PHE:O	2.19	0.41
1:A:75:LEU:HB2	1:A:123:PHE:CE2	2.55	0.41
1:A:182:ILE:O	1:A:185:ARG:HB3	2.21	0.41
1:A:119:ILE:C	1:A:121:GLU:N	2.78	0.41
1:A:43:PHE:CD1	1:A:331:ALA:HB3	2.55	0.41
1:A:81:LYS:HE2	1:A:336:ASP:OD1	2.21	0.41
1:A:153:ASN:ND2	1:A:156:ARG:CB	2.83	0.41
1:A:88:LEU:HD12	1:A:116:ILE:HG12	2.03	0.41
1:A:90:GLY:CA	1:A:112:VAL:CG2	2.97	0.41
1:A:91:VAL:HA	1:A:92:PRO:HD2	1.95	0.41
1:A:214:ASN:HD21	1:A:218:PRO:HA	1.84	0.41
1:A:292:GLU:O	1:A:295:MET:HB3	2.20	0.41
1:A:318:PHE:CD2	1:A:326:ILE:CG2	3.03	0.41
1:A:84:ARG:HD2	3:A:2162:HOH:O	2.21	0.40
1:A:126:LEU:N	1:A:126:LEU:CD2	2.83	0.40
1:A:44:PRO:CB	1:A:89:PHE:HE2	2.33	0.40
1:A:191:ARG:HH21	1:A:194:ILE:HG21	1.86	0.40
1:A:200:HIS:CD2	1:A:200:HIS:C	2.99	0.40

All (2) 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)
3:A:2164:HOH:O	3:A:2164:HOH:O[7_555]	1.64	0.56
1:A:7:LEU:O	1:A:159:SER:OG[7_555]	2.09	0.11

5.3 Torsion angles

5.3.1 Protein backbone

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	324/342 (95%)	251 (78%)	52 (16%)	21 (6%)	1 5

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	ALA
1	A	54	PHE
1	A	60	LEU
1	A	99	ASP
1	A	154	ARG
1	A	181	MET
1	A	58	ASP
1	A	59	SER
1	A	208	ALA
1	A	214	ASN
1	A	51	PRO
1	A	108	PRO
1	A	105	ALA
1	A	126	LEU
1	A	180	ASP
1	A	183	ASP
1	A	120	ARG
1	A	307	LEU
1	A	107	ASP
1	A	57	ILE
1	A	101	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	270/282 (96%)	230 (85%)	40 (15%)	3 15

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	28	ARG
1	A	36	LEU
1	A	39	ASN
1	A	62	ASN
1	A	63	ILE
1	A	65	ARG
1	A	71	LEU
1	A	72	LYS
1	A	75	LEU
1	A	87	ILE
1	A	98	LYS
1	A	99	ASP
1	A	120	ARG
1	A	125	GLU
1	A	126	LEU
1	A	136	GLU
1	A	153	ASN
1	A	157	SER
1	A	158	VAL
1	A	186	ILE
1	A	194	ILE
1	A	201	LYS
1	A	212	SER
1	A	214	ASN
1	A	215	LEU
1	A	234	CYS
1	A	253	MET
1	A	260	ILE
1	A	271	ILE
1	A	273	ARG
1	A	276	SER
1	A	282	LEU
1	A	296	LEU
1	A	310	ILE
1	A	316	GLN
1	A	326	ILE
1	A	327	ILE
1	A	328	THR
1	A	341	GLU

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

Mol	Chain	Res	Type
1	A	24	HIS
1	A	29	GLN
1	A	39	ASN
1	A	62	ASN
1	A	69	ASN
1	A	140	HIS
1	A	167	ASN
1	A	288	HIS
1	A	315	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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 1 ligands modelled in this entry, 1 is 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 ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	328/342 (95%)	0.43	13 (3%) 42 23	30, 30, 30, 30	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	60	LEU	5.1
1	A	59	SER	3.6
1	A	212	SER	3.4
1	A	149	ASP	3.3
1	A	217	GLY	2.8
1	A	179	SER	2.8
1	A	135	CYS	2.6
1	A	152	ILE	2.5
1	A	213	GLY	2.4
1	A	143	CYS	2.4
1	A	52	ASP	2.3
1	A	29	GLN	2.3
1	A	50	ASN	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 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	HG	A	400	1/1	0.97	0.13	29,29,29,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.