



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:15 AM UTC

PDB ID : 3HG7 / pdb_00003hg7
Title : CRYSTAL STRUCTURE OF D-isomer specific 2-hydroxyacid dehydrogenase family protein from *Aeromonas salmonicida* subsp. *salmonicida* A449
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Deposited on : 2009-05-13
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
Mogul : 2022.3.0, CSD as543be (2022)
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

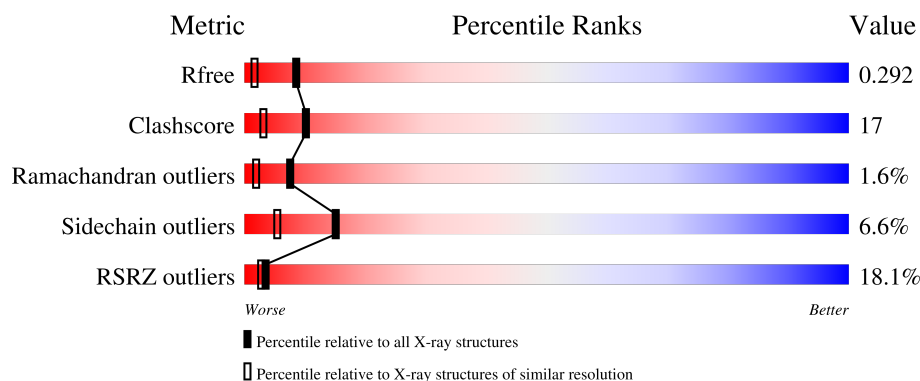
1 Overall quality at a glance

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	324	17% 73% 18% ...

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2715 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 D-isomer specific 2-hydroxyacid dehydrogenase family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	3	0
			2476	1577	456	435	8			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP A4SIK7
A	2	SER	-	expression tag	UNP A4SIK7
A	3	LEU	-	expression tag	UNP A4SIK7
A	169	VAL	ILE	engineered mutation	UNP A4SIK7
A	317	GLU	-	expression tag	UNP A4SIK7
A	318	GLY	-	expression tag	UNP A4SIK7
A	319	HIS	-	expression tag	UNP A4SIK7
A	320	HIS	-	expression tag	UNP A4SIK7
A	321	HIS	-	expression tag	UNP A4SIK7
A	322	HIS	-	expression tag	UNP A4SIK7
A	323	HIS	-	expression tag	UNP A4SIK7
A	324	HIS	-	expression tag	UNP A4SIK7

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		

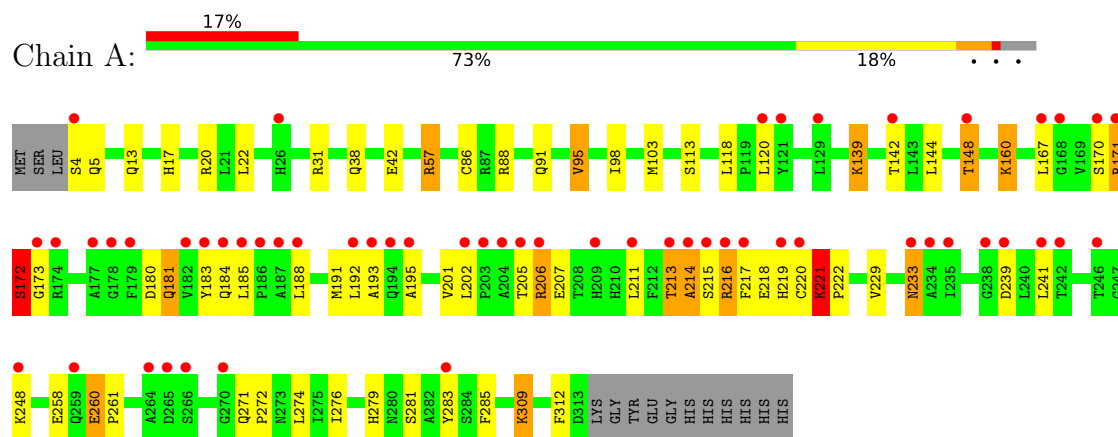
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	233	Total	O	0	0
			233	233		

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: D-isomer specific 2-hydroxyacid dehydrogenase family protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	117.06Å 117.06Å 64.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.80 20.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.1 (20.00-1.80) 99.0 (20.00-1.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.5.0070	Depositor
R, R_{free}	0.228 , 0.264 (Not available) , 0.292	Depositor DCC
R_{free} test set	2115 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	28.5	Xtriage
Anisotropy	0.220	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2715	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.56% 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: GOL

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	0.73	1/2542 (0.0%)	0.95	5/3440 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	95	VAL	CA-CB	5.92	1.61	1.54

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	221	LYS	CA-C-N	5.84	125.53	119.05
1	A	221	LYS	C-N-CA	5.84	125.53	119.05
1	A	233	ASN	N-CA-C	5.39	118.96	112.38
1	A	57[A]	ARG	NE-CZ-NH1	-5.08	116.42	121.50
1	A	57[B]	ARG	NE-CZ-NH1	-5.08	116.42	121.50

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	2476	0	2506	86	0
2	A	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	233	0	0	8	1
All	All	2715	0	2514	86	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 17.

All (86) 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:171:ARG:HB2	1:A:184:GLN:CG	1.57	1.34
1:A:171:ARG:CB	1:A:184:GLN:HG3	1.69	1.22
1:A:139:LYS:HG3	3:A:359:HOH:O	1.41	1.21
1:A:214:ALA:HA	1:A:239:ASP:CB	1.70	1.20
1:A:171:ARG:NE	1:A:184:GLN:HG2	1.71	1.04
1:A:173:GLY:HA2	1:A:184:GLN:OE1	1.58	1.02
1:A:213:THR:HG21	1:A:216:ARG:HD3	1.01	1.00
1:A:213:THR:HG21	1:A:216:ARG:CD	1.93	0.99
1:A:213:THR:CG2	1:A:216:ARG:HD3	1.92	0.98
1:A:206:ARG:HG2	1:A:206:ARG:HH11	1.27	0.97
1:A:214:ALA:HA	1:A:239:ASP:HB3	1.49	0.93
1:A:171:ARG:HB2	1:A:184:GLN:HG3	0.92	0.90
1:A:170:SER:OG	1:A:172:SER:HB3	1.73	0.88
1:A:171:ARG:HA	1:A:173:GLY:N	1.90	0.84
1:A:214:ALA:HA	1:A:239:ASP:HB2	1.62	0.81
1:A:173:GLY:HA2	1:A:184:GLN:CD	2.07	0.80
1:A:171:ARG:CB	1:A:184:GLN:CG	2.45	0.78
1:A:214:ALA:HA	1:A:239:ASP:CG	2.08	0.77
1:A:173:GLY:CA	1:A:184:GLN:OE1	2.33	0.76
1:A:91:GLN:OE1	1:A:309:LYS:HE2	1.86	0.75
1:A:260:GLU:HA	1:A:261:PRO:C	2.12	0.74
1:A:171:ARG:CA	1:A:184:GLN:HG3	2.18	0.74
1:A:171:ARG:HA	1:A:173:GLY:H	1.51	0.74
1:A:4:SER:HB3	1:A:31:ARG:HB2	1.70	0.72
1:A:86:CYS:SG	3:A:445:HOH:O	2.49	0.70
1:A:170:SER:OG	1:A:172:SER:CB	2.40	0.69
1:A:181:GLN:HG2	1:A:183:TYR:CZ	2.27	0.69
1:A:192:LEU:C	1:A:220:CYS:SG	2.78	0.66
1:A:139:LYS:CG	3:A:359:HOH:O	2.16	0.66
1:A:171:ARG:CD	1:A:184:GLN:HG2	2.25	0.66
1:A:184:GLN:NE2	3:A:439:HOH:O	2.28	0.65
1:A:214:ALA:CA	1:A:239:ASP:HB3	2.23	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:ARG:HH11	1:A:206:ARG:CG	2.06	0.63
1:A:171:ARG:HB2	1:A:184:GLN:HG2	1.73	0.62
1:A:192:LEU:HB3	1:A:220:CYS:SG	2.41	0.60
1:A:213:THR:O	1:A:214:ALA:C	2.45	0.59
1:A:160:LYS:NZ	1:A:180:ASP:OD2	2.36	0.58
1:A:171:ARG:HB2	1:A:184:GLN:CB	2.32	0.58
1:A:160:LYS:NZ	1:A:180:ASP:OD1	2.36	0.58
1:A:167:LEU:HD13	1:A:191:MET:SD	2.46	0.56
1:A:148:THR:O	1:A:148:THR:OG1	2.24	0.56
1:A:181:GLN:HG2	1:A:183:TYR:CE2	2.42	0.55
1:A:202:LEU:CD1	1:A:211:LEU:HD12	2.37	0.55
1:A:214:ALA:O	1:A:239:ASP:HB3	2.07	0.54
1:A:148:THR:HG21	1:A:170:SER:OG	2.08	0.53
1:A:193:ALA:HA	1:A:220:CYS:SG	2.47	0.53
1:A:103:MET:HE1	1:A:281:SER:OG	2.08	0.53
1:A:160:LYS:NZ	1:A:180:ASP:CG	2.67	0.53
1:A:206:ARG:HG2	1:A:206:ARG:NH1	2.07	0.52
1:A:221:LYS:HG2	1:A:222:PRO:HD2	1.91	0.52
1:A:171:ARG:CZ	1:A:184:GLN:HG2	2.38	0.52
1:A:103:MET:HE1	1:A:229:VAL:HB	1.94	0.50
1:A:215:SER:O	1:A:216:ARG:C	2.54	0.50
1:A:185:LEU:O	1:A:185:LEU:HD23	2.13	0.49
1:A:214:ALA:C	1:A:239:ASP:HB3	2.38	0.48
1:A:195:ALA:O	3:A:375:HOH:O	2.20	0.48
1:A:113:SER:HA	1:A:118:LEU:HG	1.97	0.47
1:A:91:GLN:HG3	3:A:334:HOH:O	2.13	0.47
1:A:188:LEU:HD23	1:A:217:PHE:CE1	2.50	0.47
1:A:205:THR:HG22	1:A:207:GLU:H	1.80	0.47
1:A:120:LEU:C	1:A:120:LEU:HD23	2.40	0.47
1:A:218:GLU:O	1:A:220:CYS:N	2.47	0.47
1:A:13:GLN:HE21	1:A:57[B]:ARG:HH22	1.63	0.47
1:A:171:ARG:N	1:A:184:GLN:HG3	2.30	0.46
1:A:144:LEU:HD23	1:A:192:LEU:HD23	1.97	0.46
1:A:103:MET:CE	1:A:281:SER:OG	2.63	0.46
1:A:283:TYR:HB3	1:A:285:PHE:CE2	2.51	0.46
1:A:171:ARG:HE	1:A:184:GLN:HG2	1.74	0.45
1:A:188:LEU:HD23	1:A:217:PHE:CZ	2.52	0.45
1:A:17:HIS:CD2	1:A:20[A]:ARG:NH2	2.85	0.45
1:A:88:ARG:HG2	1:A:312:PHE:CG	2.52	0.44
1:A:170:SER:HG	1:A:172:SER:HB3	1.75	0.44
1:A:260:GLU:OE2	1:A:279:HIS:ND1	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:GLN:O	1:A:42:GLU:HG2	2.18	0.44
1:A:142:THR:HG23	3:A:482:HOH:O	2.18	0.43
1:A:216:ARG:H	1:A:216:ARG:HG3	1.54	0.42
1:A:202:LEU:CD1	1:A:211:LEU:CD1	2.98	0.42
1:A:171:ARG:H	1:A:184:GLN:HG3	1.85	0.42
1:A:192:LEU:C	1:A:220:CYS:HG	2.27	0.42
1:A:233:ASN:HD22	1:A:233:ASN:HA	1.61	0.41
1:A:274:LEU:HD22	1:A:276:ILE:HG13	2.02	0.41
1:A:271:GLN:HA	1:A:272:PRO:HD3	1.93	0.41
1:A:193:ALA:N	1:A:220:CYS:SG	2.94	0.40
1:A:95:VAL:HG11	1:A:98:ILE:HD11	2.03	0.40
1:A:148:THR:HG23	3:A:481:HOH:O	2.21	0.40
1:A:205:THR:HG22	1:A:206:ARG:N	2.36	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)
3:A:391:HOH:O	3:A:391:HOH:O[7_555]	1.98	0.22

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	311/324 (96%)	292 (94%)	14 (4%)	5 (2%)	7 2

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	214	ALA
1	A	171	ARG
1	A	172	SER

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Mol	Chain	Res	Type
1	A	221	LYS
1	A	219	HIS

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	262/271 (97%)	245 (94%)	17 (6%)	15 5

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	22	LEU
1	A	139	LYS
1	A	148	THR
1	A	160	LYS
1	A	172	SER
1	A	181	GLN
1	A	201	VAL
1	A	206	ARG
1	A	213	THR
1	A	216	ARG
1	A	221	LYS
1	A	241	LEU
1	A	248	LYS
1	A	258	GLU
1	A	260	GLU
1	A	309	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	13	GLN

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Mol	Chain	Res	Type
1	A	131	GLN
1	A	181	GLN
1	A	210	HIS
1	A	233	ASN
1	A	271	GLN
1	A	291	GLN

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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	GOL	A	501	-	5,5,5	0.41	0	5,5,5	0.61	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	A	501	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	GOL	C1-C2-C3-O3
2	A	501	GOL	O2-C2-C3-O3

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	310/324 (95%)	1.05	56 (18%) 3 3	7, 20, 42, 57	3 (0%)

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	217	PHE	8.0
1	A	214	ALA	7.5
1	A	215	SER	5.1
1	A	213	THR	4.7
1	A	216	ARG	4.4
1	A	219	HIS	4.4
1	A	168	GLY	4.3
1	A	233	ASN	4.2
1	A	173	GLY	4.1
1	A	183	TYR	3.8
1	A	177	ALA	3.7
1	A	179	PHE	3.7
1	A	264	ALA	3.6
1	A	185	LEU	3.5
1	A	239	ASP	3.3
1	A	206	ARG	3.3
1	A	204	ALA	3.2
1	A	171	ARG	3.1
1	A	246	THR	3.1
1	A	238	GLY	2.9
1	A	26[A]	HIS	2.8
1	A	195	ALA	2.8
1	A	167	LEU	2.8
1	A	186	PRO	2.8
1	A	242	THR	2.7
1	A	184	GLN	2.7
1	A	193	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	121	TYR	2.7
1	A	259	GLN	2.7
1	A	4	SER	2.7
1	A	182	VAL	2.7
1	A	187	ALA	2.6
1	A	220	CYS	2.6
1	A	170	SER	2.5
1	A	205	THR	2.5
1	A	188	LEU	2.5
1	A	241	LEU	2.5
1	A	235	ILE	2.4
1	A	209	HIS	2.4
1	A	265	ASP	2.3
1	A	202	LEU	2.3
1	A	129	LEU	2.3
1	A	148	THR	2.3
1	A	211	LEU	2.2
1	A	203	PRO	2.2
1	A	234	ALA	2.2
1	A	192	LEU	2.2
1	A	283	TYR	2.2
1	A	194	GLN	2.2
1	A	178	GLY	2.2
1	A	270	GLY	2.2
1	A	120	LEU	2.1
1	A	174	ARG	2.1
1	A	266	SER	2.1
1	A	142	THR	2.1
1	A	248	LYS	2.0

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 ⓘ

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	GOL	A	501	6/6	0.65	0.21	50,50,53,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.