



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 01:52 AM UTC

PDB ID : 6ALV / pdb_00006alv
Title : Crystal structure of H107A-peptidylglycine alpha-hydroxylating monooxygenase (PHM) mutant (no CuH bound)
Authors : Maheshwari, S.; Rudzka, K.; Gabelli, S.B.; Amzel, L.M.
Deposited on : 2017-08-08
Resolution : 3.50 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 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

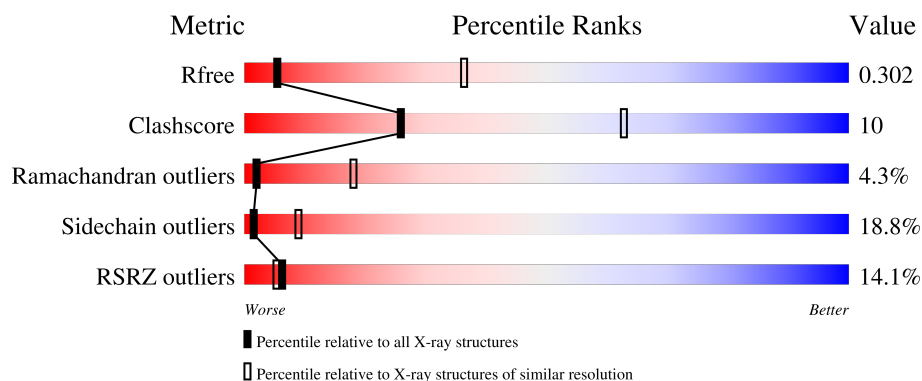
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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}	180053	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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	312	14% 63% 27% 6%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	AZI	A	1003	-	X	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 2402 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 Peptidyl-glycine alpha-amidating monooxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	305	Total	C	N	O	S	0	0	0
			2372	1511	399	436	26			

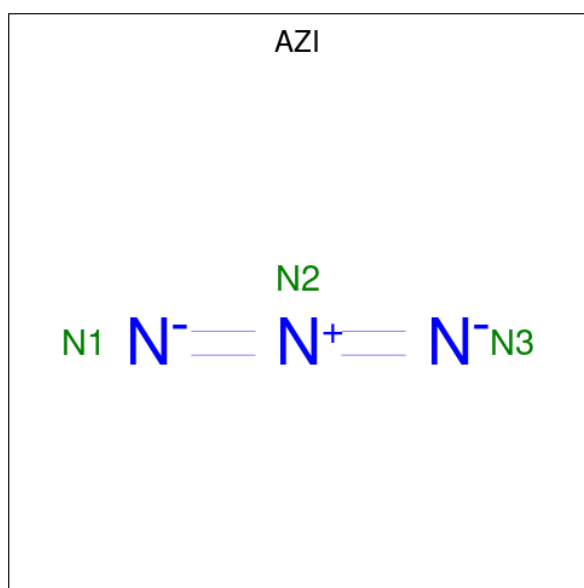
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	ALA	HIS	engineered mutation	UNP P14925

- Molecule 2 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

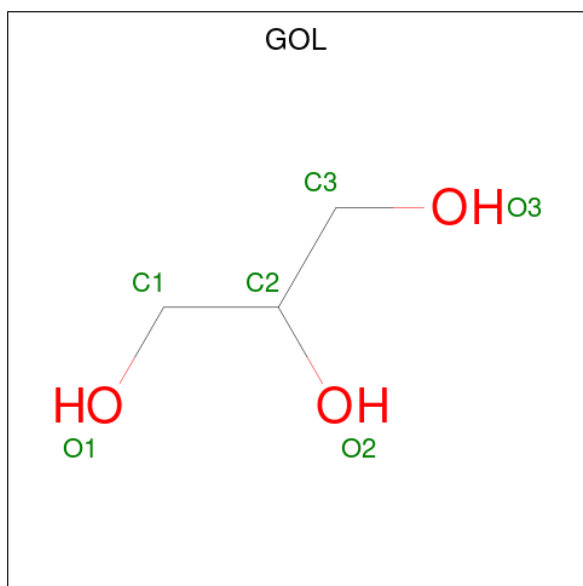
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Cu	0	0
			2	2		

- Molecule 3 is AZIDE ION (CCD ID: AZI) (formula: N₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total N 3 3	0	0

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

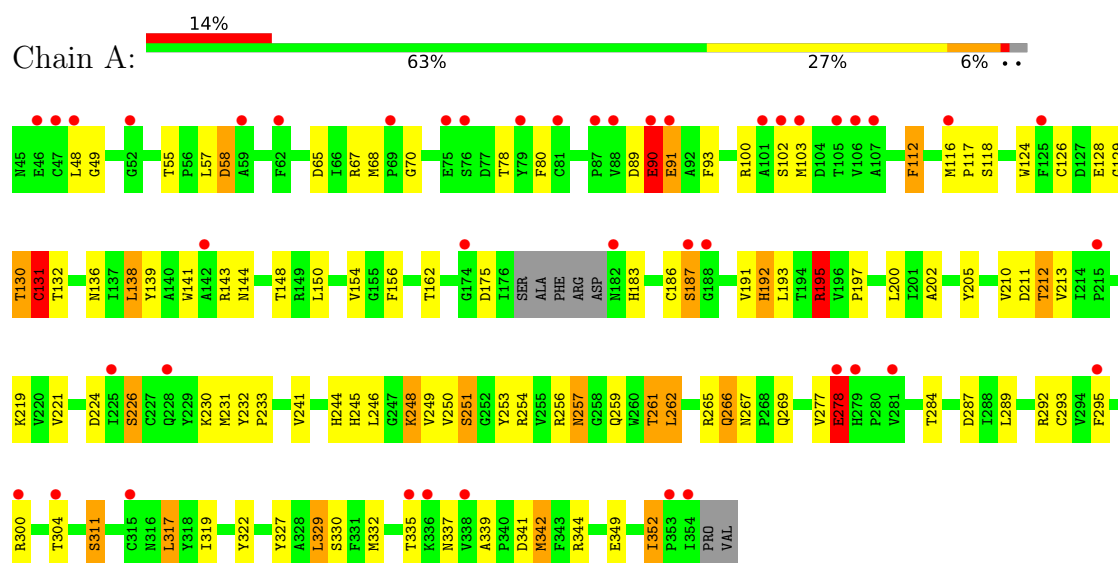
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O 1 1	0	0

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: Peptidyl-glycine alpha-amidating monooxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	69.05Å 68.86Å 81.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.50 50.00 – 3.50	Depositor EDS
% Data completeness (in resolution range)	87.3 (50.00-3.50) 87.3 (50.00-3.50)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.46 (at 3.46Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.275 , 0.298 0.282 , 0.302	Depositor DCC
R_{free} test set	239 reflections (4.56%)	wwPDB-VP
Wilson B-factor (Å ²)	21.8	Xtriage
Anisotropy	0.376	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 41.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	0.054 for k,h,-l	Xtriage
F_o, F_c correlation	0.75	EDS
Total number of atoms	2402	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.32% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CU, GOL, AZI

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	0.90	0/2437	1.08	5/3314 (0.2%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	248	LYS	N-CA-C	-7.19	103.12	112.68
1	A	249	VAL	N-CA-C	6.32	116.15	108.06
1	A	195	ARG	N-CA-C	-6.31	105.07	112.89
1	A	90	GLU	N-CA-C	6.05	117.34	108.14
1	A	89	ASP	N-CA-C	-5.28	104.00	110.65

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	2372	0	2298	45	0
2	A	2	0	0	0	0
3	A	3	0	0	0	0
4	A	24	0	31	1	0
5	A	1	0	0	0	0
All	All	2402	0	2329	45	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 (45) 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:329:LEU:HD11	1:A:332:MET:HE2	1.77	0.64
1:A:117:PRO:HA	1:A:131:CYS:HA	1.83	0.61
1:A:138:LEU:N	1:A:138:LEU:HD23	2.18	0.59
1:A:156:PHE:CD1	1:A:202:ALA:HB3	2.39	0.58
1:A:205:TYR:CZ	1:A:289:LEU:HD12	2.39	0.57
1:A:154:VAL:HA	1:A:200:LEU:O	2.03	0.57
1:A:251:SER:HB3	1:A:265:ARG:HG2	1.87	0.57
1:A:186:CYS:O	1:A:187:SER:O	2.24	0.56
1:A:154:VAL:HG22	1:A:200:LEU:HB2	1.90	0.53
1:A:254:ARG:NH2	1:A:261:THR:OG1	2.43	0.51
1:A:224:ASP:OD2	1:A:292:ARG:NH2	2.45	0.50
1:A:341:ASP:O	1:A:342:MET:C	2.55	0.49
1:A:245:HIS:O	1:A:269:GLN:NE2	2.47	0.47
1:A:90:GLU:OE1	1:A:195:ARG:NH2	2.48	0.47
1:A:139:TYR:CE1	1:A:141:TRP:HB2	2.49	0.47
1:A:226:SER:HB3	1:A:337:ASN:OD1	2.15	0.46
1:A:257:ASN:OD1	1:A:257:ASN:N	2.49	0.46
1:A:124:TRP:NE1	1:A:129:GLY:O	2.48	0.46
1:A:241:VAL:HG21	1:A:266:GLN:HB3	1.98	0.46
1:A:250:VAL:HG13	1:A:293:CYS:SG	2.56	0.45
1:A:300:ARG:NH1	1:A:311:SER:O	2.49	0.45
1:A:139:TYR:HE1	1:A:141:TRP:HB2	1.81	0.45
1:A:267:ASN:OD1	1:A:267:ASN:C	2.61	0.44
1:A:211:ASP:O	1:A:212:THR:C	2.61	0.44
1:A:191:VAL:O	1:A:192:HIS:CB	2.66	0.43
1:A:253:TYR:CD2	1:A:262:LEU:HA	2.54	0.43
1:A:93:PHE:CE1	1:A:197:PRO:HA	2.54	0.43
1:A:112:PHE:CE2	1:A:130:THR:HG21	2.54	0.43
1:A:277:VAL:O	1:A:278:GLU:C	2.62	0.42
1:A:317:LEU:HD12	1:A:317:LEU:C	2.43	0.42
1:A:91:GLU:HG2	1:A:93:PHE:CE1	2.54	0.42
1:A:132:THR:O	1:A:132:THR:HG22	2.20	0.42
1:A:156:PHE:CE1	1:A:202:ALA:CB	3.03	0.42
1:A:57:LEU:O	1:A:58:ASP:HB3	2.20	0.42
1:A:80:PHE:C	1:A:126:CYS:SG	3.02	0.41
1:A:341:ASP:HB3	1:A:344:ARG:NH2	2.35	0.41
1:A:349:GLU:HA	1:A:352:ILE:CD1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:TYR:CG	1:A:327:TYR:HB3	2.55	0.41
1:A:226:SER:HA	1:A:289:LEU:O	2.20	0.41
1:A:48:LEU:HD11	1:A:67:ARG:HH21	1.86	0.41
1:A:246:LEU:O	1:A:295:PHE:HA	2.21	0.41
1:A:330:SER:HB3	4:A:1006:GOL:H2	2.02	0.41
1:A:205:TYR:CD2	1:A:332:MET:HB2	2.56	0.41
1:A:322:TYR:CD1	1:A:322:TYR:C	2.99	0.40
1:A:339:ALA:O	1:A:342:MET:HB3	2.22	0.40

There are no symmetry-related clashes.

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	301/312 (96%)	249 (83%)	39 (13%)	13 (4%)	2	18

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	58	ASP
1	A	187	SER
1	A	278	GLU
1	A	49	GLY
1	A	70	GLY
1	A	91	GLU
1	A	131	CYS
1	A	192	HIS
1	A	244	HIS
1	A	342	MET
1	A	212	THR
1	A	262	LEU
1	A	233	PRO

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	260/266 (98%)	211 (81%)	49 (19%)	1 9

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	THR
1	A	65	ASP
1	A	68	MET
1	A	78	THR
1	A	90	GLU
1	A	100	ARG
1	A	102	SER
1	A	103	MET
1	A	112	PHE
1	A	116	MET
1	A	118	SER
1	A	128	GLU
1	A	130	THR
1	A	131	CYS
1	A	136	ASN
1	A	138	LEU
1	A	143	ARG
1	A	144	ASN
1	A	148	THR
1	A	150	LEU
1	A	162	THR
1	A	175	ASP
1	A	183	HIS
1	A	193	LEU
1	A	195	ARG
1	A	210	VAL
1	A	213	VAL
1	A	219	LYS
1	A	221	VAL
1	A	226	SER

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Mol	Chain	Res	Type
1	A	230	LYS
1	A	231	MET
1	A	248	LYS
1	A	251	SER
1	A	256	ARG
1	A	257	ASN
1	A	259	GLN
1	A	261	THR
1	A	266	GLN
1	A	278	GLU
1	A	284	THR
1	A	287	ASP
1	A	304	THR
1	A	311	SER
1	A	317	LEU
1	A	319	ILE
1	A	329	LEU
1	A	335	THR
1	A	352	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	170	GLN
1	A	266	GLN
1	A	279	HIS
1	A	316	ASN
1	A	351	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 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 for Mogul analysis.

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
4	GOL	A	1005	-	5,5,5	0.64	0	5,5,5	0.69	0
4	GOL	A	1006	-	5,5,5	0.64	0	5,5,5	0.78	0
3	AZI	A	1003	-	2,2,2	3.99	2 (100%)	0,1,1	-	-
4	GOL	A	1007	-	5,5,5	0.45	0	5,5,5	0.41	0
4	GOL	A	1004	2	5,5,5	0.39	0	5,5,5	0.88	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
4	GOL	A	1005	-	-	2/4/4/4	-
4	GOL	A	1007	-	-	2/4/4/4	-
4	GOL	A	1004	2	-	2/4/4/4	-
4	GOL	A	1006	-	-	1/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1003	AZI	N1-N2	4.06	1.31	1.23
3	A	1003	AZI	N3-N2	3.91	1.31	1.23

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1004	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
4	A	1005	GOL	O1-C1-C2-C3
4	A	1005	GOL	O1-C1-C2-O2
4	A	1007	GOL	O1-C1-C2-C3
4	A	1007	GOL	O1-C1-C2-O2
4	A	1006	GOL	C1-C2-C3-O3
4	A	1004	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1006	GOL	1	0

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	305/312 (97%)	1.26	43 (14%) 6 5	23, 44, 69, 104	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	90	GLU	3.5
1	A	174	GLY	3.4
1	A	279	HIS	3.4
1	A	101	ALA	3.2
1	A	76	SER	3.1
1	A	188	GLY	3.0
1	A	47	CYS	3.0
1	A	354	ILE	2.8
1	A	79	TYR	2.8
1	A	304	THR	2.8
1	A	48	LEU	2.7
1	A	59	ALA	2.7
1	A	75	GLU	2.6
1	A	228	GLN	2.6
1	A	315	CYS	2.6
1	A	187	SER	2.5
1	A	338	VAL	2.5
1	A	225	ILE	2.5
1	A	46	GLU	2.4
1	A	336	LYS	2.4
1	A	103	MET	2.4
1	A	182	ASN	2.3
1	A	353	PRO	2.3
1	A	107	ALA	2.3
1	A	335	THR	2.3
1	A	88	VAL	2.3
1	A	278	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	69	PRO	2.3
1	A	215	PRO	2.3
1	A	52	GLY	2.3
1	A	105	THR	2.2
1	A	87	PRO	2.2
1	A	106	VAL	2.2
1	A	295	PHE	2.2
1	A	81	CYS	2.1
1	A	300	ARG	2.1
1	A	102	SER	2.1
1	A	142	ALA	2.1
1	A	116	MET	2.1
1	A	125	PHE	2.1
1	A	281	VAL	2.0
1	A	62	PHE	2.0
1	A	91	GLU	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	AZI	A	1003	3/3	0.75	0.20	42,42,44,46	0
4	GOL	A	1006	6/6	0.75	0.27	53,55,57,57	0
4	GOL	A	1007	6/6	0.75	0.33	59,66,67,68	0
4	GOL	A	1004	6/6	0.80	0.19	27,32,35,38	0
4	GOL	A	1005	6/6	0.80	0.17	38,45,46,46	0
2	CU	A	1002	1/1	0.95	0.06	34,34,34,34	0
2	CU	A	1001	1/1	0.98	0.06	31,31,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.