



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:38 PM GMT

PDB ID : 1GKM
Title : HISTIDINE AMMONIA-LYASE (HAL) FROM PSEUDOMONAS PUTIDA
INHIBITED WITH L-CYSTEINE
Authors : Baedeker, M.; Schulz, G.E.
Deposited on : 2001-08-16
Resolution : 1.00 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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

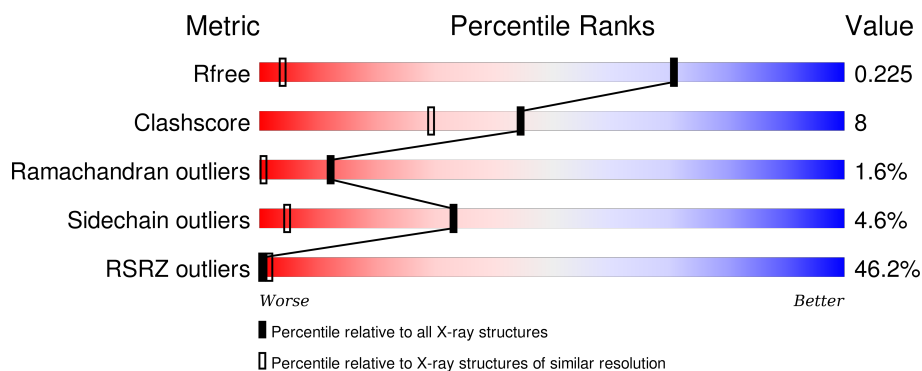
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.00 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}	91344	1235 (1.10-0.90)
Clashscore	102246	1333 (1.10-0.90)
Ramachandran outliers	100387	1247 (1.10-0.90)
Sidechain outliers	100360	1246 (1.10-0.90)
RSRZ outliers	91569	1239 (1.10-0.90)

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. 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	507	

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
2	CYS	A	1510	X	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	SO4	A	1512	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4360 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.

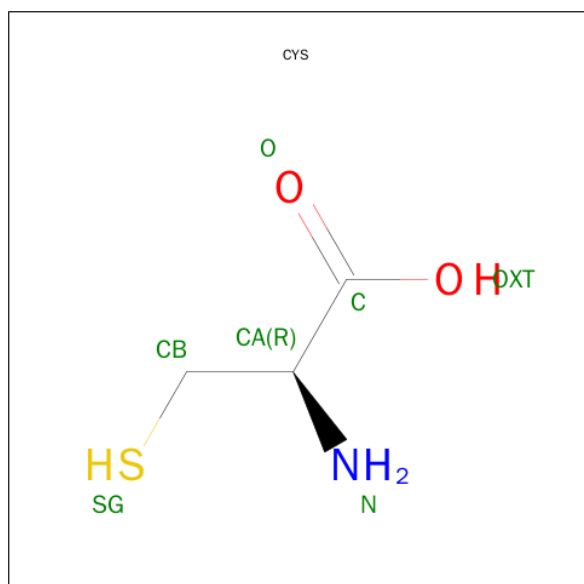
- Molecule 1 is a protein called HISTIDINE AMMONIA-LYASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	507	3796	2376	674	728	18	0	12	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	273	ALA	CYS	ENGINEERED MUTATION	UNP P21310
A	142	MDO	ALA	CHROMOPHORE	UNP P21310
A	142	MDO	SER	CHROMOPHORE	UNP P21310
A	142	MDO	GLY	CHROMOPHORE	UNP P21310

- Molecule 2 is CYSTEINE (three-letter code: CYS) (formula: $C_3H_7NO_2S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	7	3	1	2	1	0	0

- Molecule 3 is OXYGEN ATOM (three-letter code: O) (formula: O).

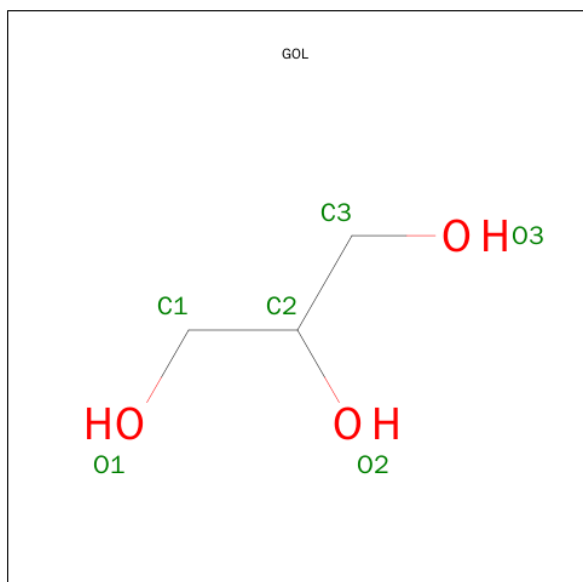
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	O	0	0
			1	1		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

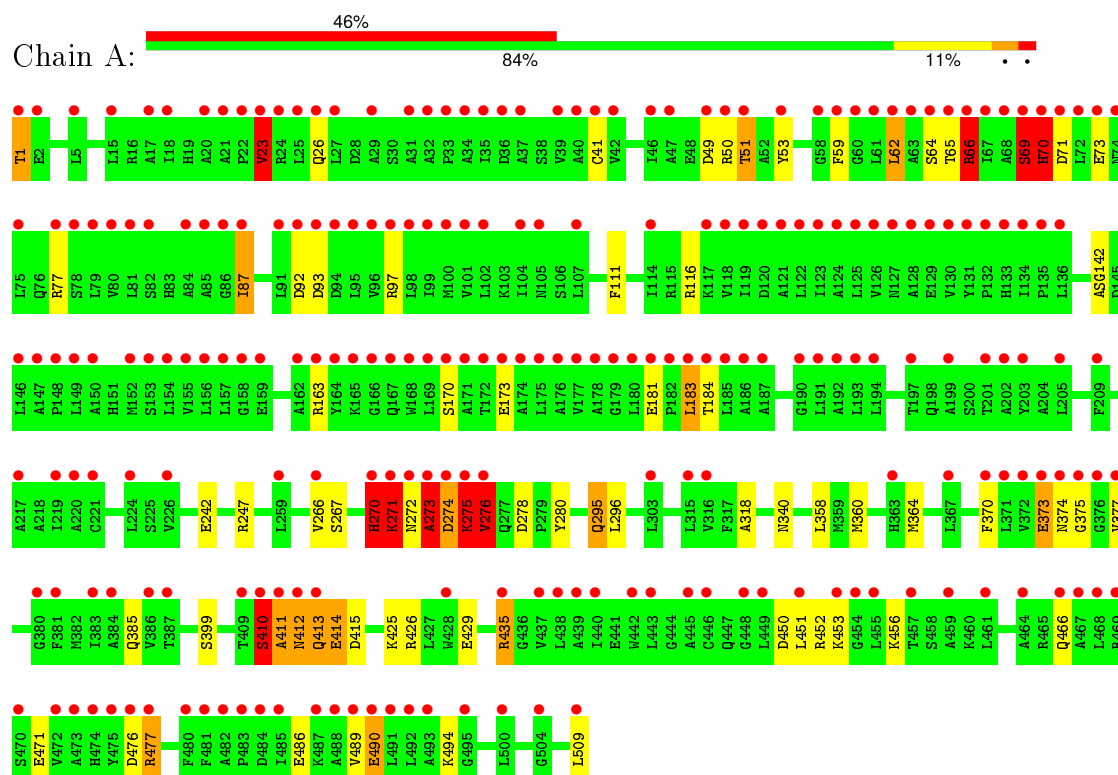
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	545	Total	O	0	0
			545	545		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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: HISTIDINE AMMONIA-LYASE



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	79.27Å 116.79Å 129.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 1.00 29.26 – 1.01	Depositor EDS
% Data completeness (in resolution range)	96.0 (40.00-1.00) 95.8 (29.26-1.01)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 1.01Å)	Xtriage
Refinement program	SHELX	Depositor
R, R_{free}	0.119 , 0.135 0.229 , 0.225	Depositor DCC
R_{free} test set	15248 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	6.9	Xtriage
Anisotropy	0.312	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 72.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 301144 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4360	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.26% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, SO4, O, MDO

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	0.89	5/3899 (0.1%)	1.36	55/5284 (1.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	509	LEU	C-OXT	9.98	1.42	1.23
1	A	413	GLN	C-O	6.41	1.35	1.23
1	A	273	ALA	N-CA	5.91	1.58	1.46
1	A	399[A]	SER	CB-OG	-5.86	1.34	1.42
1	A	399[B]	SER	CB-OG	-5.86	1.34	1.42

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	53	TYR	CB-CG-CD2	17.73	131.64	121.00
1	A	97	ARG	NE-CZ-NH2	-14.53	113.04	120.30
1	A	87	ILE	CG1-CB-CG2	-12.93	82.95	111.40
1	A	97	ARG	NE-CZ-NH1	11.46	126.03	120.30
1	A	370	PHE	CB-CG-CD2	-10.82	113.23	120.80
1	A	66	ARG	NE-CZ-NH1	10.60	125.60	120.30
1	A	77	ARG	NE-CZ-NH1	-9.22	115.69	120.30
1	A	53	TYR	CB-CG-CD1	-8.88	115.67	121.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	429[A]	GLU	OE1-CD-OE2	8.69	133.73	123.30
1	A	429[B]	GLU	OE1-CD-OE2	8.69	133.73	123.30
1	A	66	ARG	CD-NE-CZ	8.41	135.37	123.60
1	A	116	ARG	NE-CZ-NH2	-7.80	116.40	120.30
1	A	413	GLN	N-CA-CB	-7.57	96.97	110.60
1	A	414[A]	GLU	N-CA-CB	7.55	124.19	110.60
1	A	414[B]	GLU	N-CA-CB	7.55	124.19	110.60
1	A	296	LEU	CB-CA-C	7.54	124.52	110.20
1	A	435[A]	ARG	NE-CZ-NH2	7.47	124.04	120.30
1	A	435[B]	ARG	NE-CZ-NH2	7.47	124.04	120.30
1	A	77	ARG	NH1-CZ-NH2	7.39	127.53	119.40
1	A	53	TYR	CG-CD2-CE2	7.24	127.09	121.30
1	A	163	ARG	NE-CZ-NH2	-7.19	116.70	120.30
1	A	77	ARG	NE-CZ-NH2	-7.04	116.78	120.30
1	A	1	THR	CA-CB-CG2	-6.90	102.74	112.40
1	A	414[A]	GLU	CA-CB-CG	6.76	128.28	113.40
1	A	414[B]	GLU	CA-CB-CG	6.76	128.28	113.40
1	A	247	ARG	NE-CZ-NH1	6.55	123.58	120.30
1	A	273	ALA	N-CA-CB	6.47	119.16	110.10
1	A	50	ARG	NE-CZ-NH1	-6.38	117.11	120.30
1	A	373	GLU	OE1-CD-OE2	-6.34	115.69	123.30
1	A	66	ARG	NE-CZ-NH2	-6.30	117.15	120.30
1	A	87	ILE	CA-CB-CG2	6.16	123.22	110.90
1	A	49	ASP	CB-CG-OD2	-6.09	112.81	118.30
1	A	116	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	A	70	HIS	N-CA-CB	-5.87	100.03	110.60
1	A	370	PHE	CG-CD2-CE2	-5.84	114.37	120.80
1	A	278	ASP	CB-CG-OD2	-5.83	113.05	118.30
1	A	23	VAL	CG1-CB-CG2	-5.67	101.82	110.90
1	A	435[A]	ARG	NH1-CZ-NH2	-5.59	113.26	119.40
1	A	435[B]	ARG	NH1-CZ-NH2	-5.59	113.26	119.40
1	A	69	SER	CA-C-O	5.55	131.76	120.10
1	A	413	GLN	CA-C-O	5.43	131.50	120.10
1	A	111	PHE	CB-CG-CD1	-5.42	117.01	120.80
1	A	471	GLU	OE1-CD-OE2	5.35	129.72	123.30
1	A	93	ASP	CB-CG-OD2	-5.34	113.50	118.30
1	A	490	GLU	OE1-CD-OE2	5.31	129.67	123.30
1	A	280	TYR	CB-CG-CD1	5.31	124.18	121.00
1	A	276	VAL	CB-CA-C	-5.29	101.36	111.40
1	A	370	PHE	CD1-CE1-CZ	-5.27	113.78	120.10
1	A	59	PHE	CB-CG-CD2	-5.23	117.14	120.80
1	A	270	HIS	ND1-CG-CD2	-5.14	98.80	106.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	276	VAL	C-N-CA	5.13	134.53	121.70
1	A	425	LYS	CB-CG-CD	5.13	124.94	111.60
1	A	452	ARG	CD-NE-CZ	5.10	130.74	123.60
1	A	92	ASP	CB-CG-OD1	5.03	122.83	118.30
1	A	242	GLU	OE1-CD-OE2	5.00	129.31	123.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	142	MDO	Mainchain,Peptide

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	3796	0	3843	60	0
2	A	7	0	3	1	0
3	A	1	0	0	0	0
4	A	5	0	0	1	0
5	A	6	0	8	0	0
6	A	545	0	0	12	0
All	All	4360	0	3854	61	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 8.

All (61) 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:A:1510:CYS:O	4:A:1512:SO4:O3	1.83	0.94
1:A:276:VAL:O	1:A:276:VAL:HG22	1.80	0.81
1:A:270:HIS:ND1	1:A:273:ALA:HB2	1.98	0.78
1:A:1:THR:OG1	1:A:23:VAL:HG23	1.89	0.72
1:A:267:SER:HA	1:A:270:HIS:CD2	2.25	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:267:SER:HA	1:A:270:HIS:NE2	2.05	0.71
1:A:51:THR:HG22	1:A:66:ARG:HH21	1.57	0.70
1:A:364:MET:HG3	6:A:2399:HOH:O	1.92	0.68
1:A:377:VAL:HG13	6:A:2413:HOH:O	1.92	0.68
1:A:170:SER:OG	1:A:173:GLU:HG3	1.95	0.66
1:A:270:HIS:ND1	1:A:273:ALA:CB	2.59	0.65
1:A:410:SER:OG	1:A:414[B]:GLU:OE1	2.13	0.65
1:A:270:HIS:CG	1:A:273:ALA:HB2	2.34	0.62
1:A:271:LYS:C	1:A:273:ALA:H	2.02	0.61
1:A:435[B]:ARG:HE	1:A:489:VAL:HG13	1.66	0.60
1:A:413:GLN:HG3	6:A:2441:HOH:O	2.02	0.60
1:A:62:LEU:HD12	1:A:65:THR:HG21	1.84	0.60
1:A:51:THR:HG22	1:A:66:ARG:HE	1.68	0.59
1:A:51:THR:CG2	1:A:66:ARG:HH21	2.15	0.59
1:A:490:GLU:OE2	1:A:494:LYS:HE3	2.03	0.59
1:A:276:VAL:CG2	6:A:2356:HOH:O	2.51	0.58
1:A:276:VAL:HG21	6:A:2356:HOH:O	2.04	0.57
1:A:271:LYS:C	1:A:273:ALA:N	2.59	0.56
1:A:270:HIS:C	1:A:271:LYS:HG2	2.27	0.55
1:A:486:GLU:HB3	6:A:2514:HOH:O	2.05	0.55
1:A:270:HIS:CE1	1:A:273:ALA:HB3	2.42	0.54
1:A:466:GLN:NE2	6:A:2488:HOH:O	2.39	0.54
1:A:69:SER:HG	1:A:70:HIS:CD2	2.24	0.54
1:A:1:THR:HG23	6:A:2069:HOH:O	2.08	0.54
1:A:295:GLN:HE21	1:A:340:ASN:HB3	1.73	0.54
1:A:41[B]:CYS:SG	1:A:318:ALA:HA	2.48	0.53
1:A:375:GLY:HA3	6:A:2408:HOH:O	2.09	0.53
1:A:271:LYS:O	1:A:273:ALA:N	2.44	0.50
1:A:181:GLU:O	1:A:183:LEU:HD23	2.11	0.50
1:A:373:GLU:O	1:A:374:ASN:HB2	2.12	0.49
1:A:476:ASP:OD1	1:A:477:ARG:HG2	2.13	0.49
1:A:411:ALA:O	1:A:413:GLN:N	2.46	0.48
1:A:87:ILE:HD13	1:A:87:ILE:HA	1.56	0.48
1:A:266:VAL:HG12	6:A:2291:HOH:O	2.14	0.48
1:A:26:GLN:HB3	6:A:2079:HOH:O	2.14	0.47
1:A:71:ASP:OD1	1:A:71:ASP:N	2.47	0.47
1:A:70:HIS:H	1:A:70:HIS:CD2	2.18	0.47
1:A:412:ASN:O	1:A:415:ASP:HB3	2.14	0.46
1:A:270:HIS:HD1	1:A:270:HIS:C	2.18	0.46
1:A:451:LEU:HA	1:A:453:LYS:HE3	1.98	0.46
1:A:477:ARG:NH2	6:A:2500:HOH:O	2.49	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:360:MET:HG3	1:A:385:GLN:OE1	2.17	0.44
1:A:270:HIS:C	1:A:270:HIS:ND1	2.72	0.43
1:A:450:ASP:O	1:A:453:LYS:HD3	2.18	0.43
1:A:358:LEU:CD1	1:A:364:MET:HB3	2.49	0.42
1:A:266:VAL:HG23	1:A:456:LYS:O	2.20	0.42
1:A:73:GLU:OE1	1:A:184:THR:HG21	2.20	0.42
1:A:273:ALA:O	1:A:275:LYS:N	2.53	0.42
1:A:51:THR:HG22	1:A:66:ARG:NH2	2.30	0.41
1:A:183:LEU:N	1:A:183:LEU:HD23	2.34	0.41
1:A:87:ILE:HD12	1:A:87:ILE:HG23	0.83	0.41
1:A:267:SER:O	1:A:270:HIS:CE1	2.73	0.41
1:A:295:GLN:HE21	1:A:340:ASN:CB	2.32	0.41
1:A:410:SER:HG	1:A:414[B]:GLU:CD	2.20	0.41
1:A:69:SER:OG	1:A:70:HIS:NE2	2.49	0.41
1:A:412:ASN:N	1:A:412:ASN:ND2	2.69	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	516/507 (102%)	497 (96%)	11 (2%)	8 (2%)	12 1

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	273	ALA
1	A	274	ASP
1	A	412	ASN
1	A	272	ASN
1	A	275	LYS
1	A	410	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	411	ALA
1	A	271	LYS

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	399/387 (103%)	382 (96%)	17 (4%)	35 5

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

Mol	Chain	Res	Type
1	A	23	VAL
1	A	51	THR
1	A	62	LEU
1	A	64	SER
1	A	66	ARG
1	A	69	SER
1	A	70	HIS
1	A	183	LEU
1	A	270	HIS
1	A	271	LYS
1	A	274	ASP
1	A	275	LYS
1	A	276	VAL
1	A	295	GLN
1	A	410	SER
1	A	426	ARG
1	A	477	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	195	ASN
1	A	466	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue 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	$\# Z > 2$
1	MDO	A	142	1,3,2	11,13,14	1.18	0	13,18,20	1.67	3 (23%)

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
1	MDO	A	142	1,3,2	-	0/4/23/24	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	142	MDO	CA3-N3-C2	-2.18	120.44	123.99
1	A	142	MDO	CA2-C2-N3	-2.10	102.30	103.39
1	A	142	MDO	O2-C2-CA2	3.85	133.03	130.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	$\# Z > 2$
2	CYS	A	1510	1	3,6,6	2.81	2 (66%)	1,7,7	1.02	0
4	SO4	A	1512	-	4,4,4	0.91	0	6,6,6	1.16	1 (16%)
5	GOL	A	1513	-	5,5,5	0.83	0	5,5,5	0.55	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	CYS	A	1510	1	1/1/2/2	0/2/6/6	0/0/0/0
4	SO4	A	1512	-	-	0/0/0/0	0/0/0/0
5	GOL	A	1513	-	-	0/4/4/4	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1510	CYS	CB-CA	-2.21	1.50	1.53
2	A	1510	CYS	CA-N	4.23	1.66	1.48

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1512	SO4	O2-S-O1	2.35	116.94	109.50

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1510	CYS	CA

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1510	CYS	1	0
4	A	1512	SO4	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	506/507 (99%)	2.25	234 (46%) 0 2	4, 8, 40, 79	0

All (234) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	272	ASN	21.2
1	A	273	ALA	19.7
1	A	276	VAL	16.4
1	A	274	ASP	13.4
1	A	61	LEU	10.8
1	A	375	GLY	10.1
1	A	275	LYS	7.3
1	A	271	LYS	6.8
1	A	130	VAL	6.7
1	A	410	SER	6.6
1	A	180	LEU	6.2
1	A	177	VAL	6.2
1	A	62	LEU	6.1
1	A	376	GLY	6.0
1	A	64	SER	5.9
1	A	411	ALA	5.8
1	A	377	VAL	5.7
1	A	374	ASN	5.7
1	A	477	ARG	5.6
1	A	70	HIS	5.5
1	A	174	ALA	5.4
1	A	270	HIS	5.4
1	A	71	ASP	5.3
1	A	412	ASN	5.3
1	A	169	LEU	5.1
1	A	66	ARG	5.0
1	A	175	LEU	5.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	183	LEU	4.8
1	A	69	SER	4.8
1	A	168	TRP	4.7
1	A	164	TYR	4.6
1	A	442	TRP	4.6
1	A	65	THR	4.6
1	A	123	ILE	4.5
1	A	131	TYR	4.5
1	A	81	LEU	4.5
1	A	122	LEU	4.5
1	A	176	ALA	4.5
1	A	154	LEU	4.3
1	A	60	GLY	4.3
1	A	126	VAL	4.3
1	A	171	ALA	4.3
1	A	178	ALA	4.3
1	A	172	THR	4.2
1	A	67	ILE	4.2
1	A	134	ILE	4.2
1	A	491	LEU	4.2
1	A	472	VAL	4.2
1	A	128	ALA	4.2
1	A	179	GLY	4.1
1	A	118	VAL	4.1
1	A	125	LEU	4.1
1	A	96	VAL	4.1
1	A	119	ILE	4.1
1	A	104	ILE	4.0
1	A	485	ILE	4.0
1	A	72	LEU	4.0
1	A	181	GLU	4.0
1	A	1	THR	4.0
1	A	87	ILE	4.0
1	A	63	ALA	4.0
1	A	35	ILE	3.9
1	A	107	LEU	3.9
1	A	74	ASN	3.9
1	A	156	LEU	3.9
1	A	468	LEU	3.8
1	A	185	LEU	3.8
1	A	446	CYS	3.8
1	A	193	LEU	3.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	480	PHE	3.7
1	A	25	LEU	3.7
1	A	461	LEU	3.7
1	A	372	VAL	3.7
1	A	162	ALA	3.7
1	A	170	SER	3.7
1	A	492	LEU	3.7
1	A	155	VAL	3.7
1	A	489	VAL	3.7
1	A	184	THR	3.6
1	A	194	LEU	3.6
1	A	413	GLN	3.6
1	A	166	GLY	3.6
1	A	481	PHE	3.6
1	A	124	ALA	3.5
1	A	453	LYS	3.5
1	A	99	ILE	3.5
1	A	476	ASP	3.5
1	A	149	LEU	3.5
1	A	114	ILE	3.5
1	A	59	PHE	3.4
1	A	27	LEU	3.4
1	A	167	GLN	3.3
1	A	192	ALA	3.3
1	A	316	VAL	3.3
1	A	102	LEU	3.3
1	A	483	PRO	3.3
1	A	85	ALA	3.3
1	A	158	GLY	3.3
1	A	101	VAL	3.3
1	A	370	PHE	3.3
1	A	32	ALA	3.3
1	A	440	ILE	3.2
1	A	224	LEU	3.2
1	A	488	ALA	3.2
1	A	51	THR	3.2
1	A	79	LEU	3.2
1	A	121	ALA	3.2
1	A	84	ALA	3.2
1	A	150	ALA	3.2
1	A	373	GLU	3.2
1	A	473	ALA	3.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	75	LEU	3.2
1	A	91	LEU	3.2
1	A	157	LEU	3.2
1	A	443	LEU	3.2
1	A	20	ALA	3.1
1	A	482	ALA	3.1
1	A	451	LEU	3.1
1	A	509	LEU	3.1
1	A	409	THR	3.1
1	A	23	VAL	3.1
1	A	21	ALA	3.1
1	A	50	ARG	3.1
1	A	98	LEU	3.1
1	A	80	VAL	3.0
1	A	475	TYR	3.0
1	A	449	LEU	3.0
1	A	500	LEU	3.0
1	A	41[A]	CYS	2.9
1	A	2	GLU	2.9
1	A	495	GLY	2.9
1	A	470	SER	2.9
1	A	428	TRP	2.9
1	A	132	PRO	2.9
1	A	165	LYS	2.8
1	A	191	LEU	2.8
1	A	437	VAL	2.8
1	A	466	GLN	2.8
1	A	18	ILE	2.8
1	A	439	ALA	2.8
1	A	459	ALA	2.8
1	A	153	SER	2.8
1	A	26	GLN	2.8
1	A	31	ALA	2.8
1	A	40	ALA	2.8
1	A	95	LEU	2.8
1	A	146	LEU	2.8
1	A	221	CYS	2.7
1	A	438	LEU	2.7
1	A	39	VAL	2.7
1	A	100[A]	MET	2.7
1	A	383	ILE	2.7
1	A	136	LEU	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	22	PRO	2.7
1	A	435[A]	ARG	2.7
1	A	133	HIS	2.7
1	A	187	ALA	2.6
1	A	127	ASN	2.6
1	A	29	ALA	2.6
1	A	186	ALA	2.6
1	A	93	ASP	2.6
1	A	205	LEU	2.6
1	A	17	ALA	2.6
1	A	77	ARG	2.6
1	A	219	ILE	2.6
1	A	34	ALA	2.5
1	A	220	ALA	2.5
1	A	464	ALA	2.5
1	A	490	GLU	2.5
1	A	173	GLU	2.5
1	A	190	GLY	2.5
1	A	5	LEU	2.5
1	A	33	PRO	2.5
1	A	68	ALA	2.5
1	A	209	PHE	2.5
1	A	384	ALA	2.5
1	A	148	PRO	2.5
1	A	380	GLY	2.4
1	A	117	LYS	2.4
1	A	73	GLU	2.4
1	A	46	ILE	2.4
1	A	226	VAL	2.4
1	A	135	PRO	2.4
1	A	147	ALA	2.4
1	A	202	ALA	2.4
1	A	49	ASP	2.4
1	A	120	ASP	2.4
1	A	454	GLY	2.4
1	A	387	THR	2.4
1	A	457	THR	2.4
1	A	474	HIS	2.4
1	A	445	ALA	2.4
1	A	58	GLY	2.4
1	A	203	TYR	2.4
1	A	37	ALA	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	315	LEU	2.4
1	A	467	ALA	2.4
1	A	152	MET	2.3
1	A	82	SER	2.3
1	A	217	ALA	2.3
1	A	129	GLU	2.3
1	A	15	LEU	2.3
1	A	36	ASP	2.3
1	A	92	ASP	2.3
1	A	86	GLY	2.3
1	A	24	ARG	2.2
1	A	455	LEU	2.2
1	A	363	HIS	2.2
1	A	199	ALA	2.2
1	A	487	LYS	2.2
1	A	105	ASN	2.2
1	A	53	TYR	2.2
1	A	493	ALA	2.1
1	A	266	VAL	2.1
1	A	484	ASP	2.1
1	A	182	PRO	2.1
1	A	259	LEU	2.1
1	A	371	LEU	2.1
1	A	42	VAL	2.1
1	A	381	PHE	2.1
1	A	197	THR	2.1
1	A	78	SER	2.1
1	A	504	GLY	2.1
1	A	47	ALA	2.1
1	A	94	ASP	2.1
1	A	97	ARG	2.1
1	A	303	LEU	2.0
1	A	159	GLU	2.0
1	A	201	THR	2.0
1	A	448	GLY	2.0
1	A	163	ARG	2.0
1	A	469	ARG	2.0
1	A	367	LEU	2.0
1	A	386	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
1	MDO	A	142	13/14	0.94	0.12	-	4,6,11,16	0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	CYS	A	1510	7/7	0.67	0.31	7.71	14,16,39,40	7
4	SO4	A	1512	5/5	0.79	0.22	4.23	26,27,30,33	5
5	GOL	A	1513	6/6	0.90	0.12	-1.33	10,12,16,20	0
3	O	A	1511	1/1	0.74	0.25	-	21,21,21,21	1

6.5 Other polymers [i](#)

There are no such residues in this entry.