



Full wwPDB X-ray Structure Validation Report

Sep 18, 2014 – 11:14 PM EDT

PDB ID : 4PHC
Title : Crystal Structure of a human cytosolic histidyl-tRNA synthetase, histidine-bound
Authors : Koh, C.Y.; Wetzel, A.B.; de van der Schueren, W.J.; Hol, W.G.J.
Deposited on : 2014-05-06
Resolution : 2.84 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

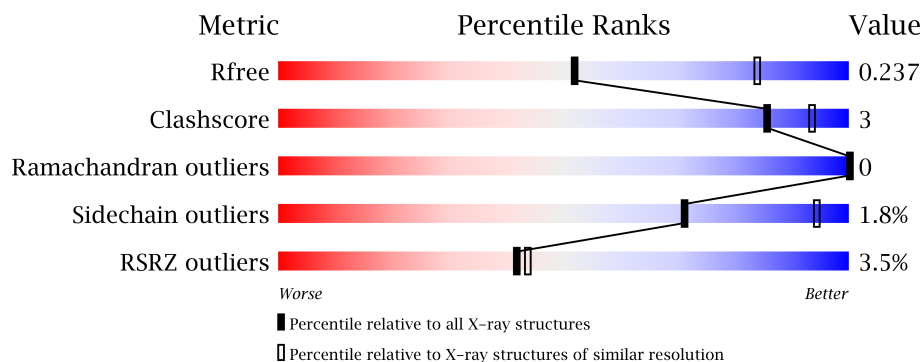
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable23489
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable23489

1 Overall quality at a glance

The reported resolution of this entry is 2.84 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}	66092	2270 (2.88-2.80)
Clashscore	79885	2848 (2.88-2.80)
Ramachandran outliers	78287	2786 (2.88-2.80)
Sidechain outliers	78261	2789 (2.88-2.80)
RSRZ outliers	66119	2274 (2.88-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	509	
1	B	509	
1	C	509	
1	D	509	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	HIS	C	1001	-	X
3	GOL	C	1002	-	X
3	GOL	C	1003	-	X

2 Entry composition i

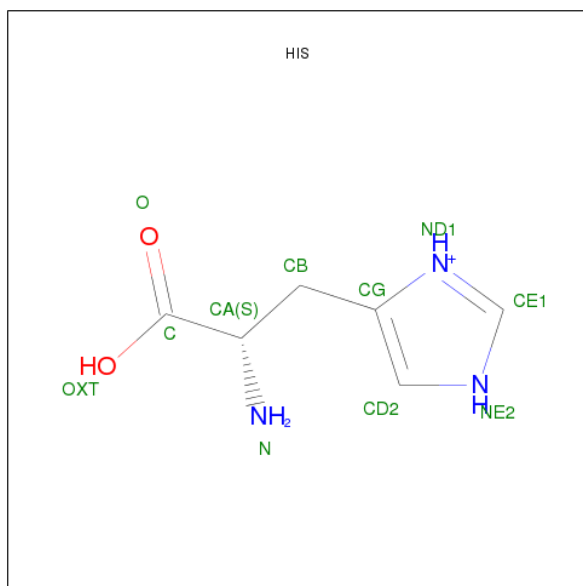
There are 4 unique types of molecules in this entry. The entry contains 14080 atoms, of which 0 are hydrogen and 0 are deuterium.

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-tRNA ligase, cytoplasmic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	444	Total	C	N	O	S	0	0	0
			3488	2222	594	655	17			
1	B	441	Total	C	N	O	S	0	0	0
			3490	2223	594	656	17			
1	C	440	Total	C	N	O	S	0	0	0
			3480	2216	592	655	17			
1	D	442	Total	C	N	O	S	0	0	0
			3499	2226	597	659	17			

- Molecule 2 is HISTIDINE (three-letter code: HIS) (formula: C₆H₁₀N₃O₂).



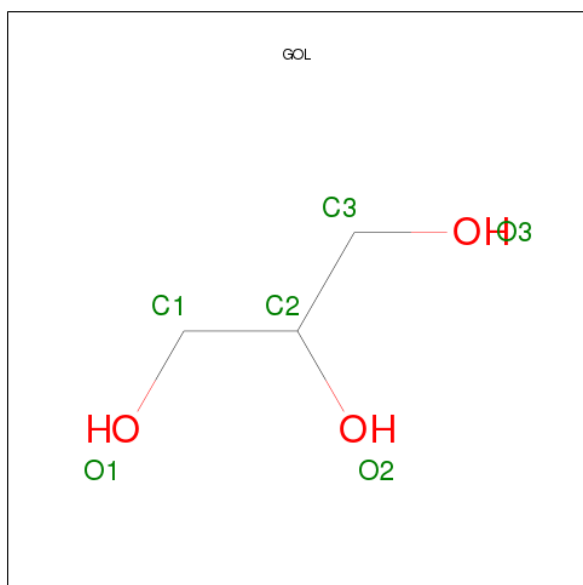
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			11	6	3	2		
2	B	1	Total	C	N	O	0	0
			11	6	3	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	N	O	0	0
			11	6	3	2		
2	D	1	Total	C	N	O	0	0
			11	6	3	2		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is water.

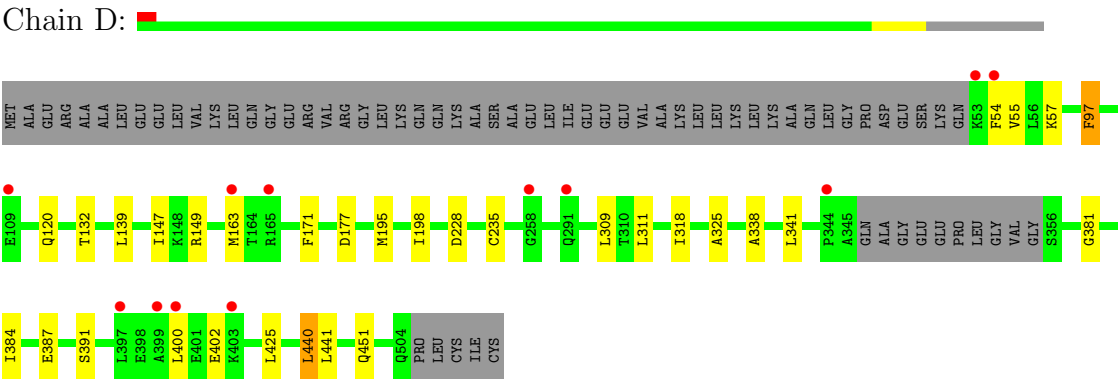
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	14	Total	O	0	0
			14	14		
4	B	19	Total	O	0	0
			19	19		
4	C	13	Total	O	0	0
			13	13		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	9	Total	O	0	0
			9	9		

● Molecule 1: Histidine–tRNA ligase, cytoplasmic



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	89.09Å 92.99Å 261.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.41 – 2.84 39.31 – 2.84	Depositor EDS
% Data completeness (in resolution range)	94.7 (39.41-2.84) 94.8 (39.31-2.84)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.76 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.201 , 0.238 0.204 , 0.237	Depositor DCC
R_{free} test set	2504 reflections (5.36%)	DCC
Wilson B-factor (Å ²)	59.5	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 29.1	EDS
Estimated twinning fraction	0.047 for k,h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	1 of 49249 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14080	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.08% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.40	0/3539	0.61	0/4768
1	B	0.37	0/3541	0.61	0/4766
1	C	0.38	0/3531	0.59	0/4753
1	D	0.37	0/3551	0.62	0/4782
All	All	0.38	0/14162	0.61	0/19069

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3488	0	3537	26	0
1	B	3490	0	3557	20	0
1	C	3480	0	3542	24	0
1	D	3499	0	3556	19	0
2	A	11	0	6	1	0
2	B	11	0	6	1	0
2	C	11	0	6	1	0
2	D	11	0	6	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	6	0	8	0	0
3	B	6	0	8	0	0
3	C	12	0	16	0	0
4	A	14	0	0	0	0
4	B	19	0	0	0	0
4	C	13	0	0	0	0
4	D	9	0	0	0	0
All	All	14080	0	14248	76	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 3.

All (76) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:65:TYR:HB2	1:A:70:MET:HE3	1.52	0.91
1:A:70:MET:HE1	1:B:93:ASP:CB	2.08	0.84
1:A:70:MET:HE1	1:B:93:ASP:HB2	1.62	0.82
1:A:65:TYR:HB2	1:A:70:MET:CE	2.13	0.79
1:C:132:THR:HG1	2:C:1001:HIS:N	1.87	0.72
1:C:137:ARG:HD2	1:C:141:MET:HE3	1.73	0.71
1:A:70:MET:CE	1:B:93:ASP:HB3	2.22	0.69
1:A:70:MET:CE	1:B:93:ASP:CB	2.73	0.66
1:D:171:PHE:HB2	1:D:387:GLU:HG3	1.79	0.64
1:A:65:TYR:CG	1:A:70:MET:HE2	2.33	0.64
1:A:70:MET:HE1	1:B:93:ASP:HB3	1.78	0.63
1:B:132:THR:HG1	2:B:1001:HIS:N	1.97	0.63
1:C:137:ARG:CD	1:C:141:MET:HE3	2.29	0.62
1:A:65:TYR:CB	1:A:70:MET:CE	2.78	0.61
1:A:132:THR:HG1	2:A:1001:HIS:N	1.99	0.60
1:D:132:THR:HG1	2:D:1001:HIS:N	1.99	0.60
1:A:139:LEU:HD21	1:A:147:ILE:CG2	2.33	0.59
1:C:422:GLU:HG3	1:D:311:LEU:HD11	1.85	0.59
1:B:139:LEU:HD21	1:B:147:ILE:CG2	2.33	0.58
1:D:139:LEU:HD21	1:D:147:ILE:CG2	2.33	0.57
1:C:139:LEU:HD21	1:C:147:ILE:CG2	2.34	0.57
1:A:65:TYR:CB	1:A:70:MET:HE2	2.37	0.55
1:C:141:MET:HE2	1:D:57:LYS:N	2.23	0.53
1:A:139:LEU:HD21	1:A:147:ILE:HG21	1.91	0.53
1:D:309:LEU:HD13	1:D:318:ILE:HG13	1.91	0.52
1:C:470:GLU:OE2	1:C:477:LYS:HE3	2.10	0.52
1:A:309:LEU:HD13	1:A:318:ILE:HG13	1.91	0.51
1:C:139:LEU:HD21	1:C:147:ILE:HG21	1.93	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:139:LEU:HD21	1:D:147:ILE:HG21	1.91	0.51
1:C:468:GLU:HA	1:C:468:GLU:OE1	2.11	0.51
1:B:139:LEU:HD21	1:B:147:ILE:HG21	1.91	0.51
1:B:309:LEU:HD13	1:B:318:ILE:HG13	1.92	0.50
1:B:464:ALA:HB1	1:B:476:ILE:HD13	1.93	0.50
1:A:259:LEU:HG	1:A:263:VAL:CG2	2.42	0.49
1:C:309:LEU:HD13	1:C:318:ILE:HG13	1.92	0.49
1:A:311:LEU:HD11	1:B:422:GLU:HG3	1.95	0.48
1:C:62:THR:HG21	1:D:97:PHE:HE1	1.78	0.48
1:A:259:LEU:HD11	1:A:263:VAL:HG21	1.95	0.48
1:A:70:MET:CE	1:B:93:ASP:HB2	2.37	0.48
1:C:464:ALA:HB1	1:C:476:ILE:HD13	1.94	0.48
1:D:400:LEU:HD23	1:D:402:GLU:OE2	2.13	0.48
1:C:235:CYS:SG	1:C:325:ALA:HB1	2.53	0.47
1:B:235:CYS:SG	1:B:325:ALA:HB1	2.55	0.46
1:D:441:LEU:HD22	1:D:451:GLN:HG2	1.98	0.46
1:B:214:ARG:NH1	1:B:232:ARG:HH22	2.14	0.46
1:C:137:ARG:HH11	1:C:141:MET:HE3	1.81	0.46
1:A:441:LEU:HD22	1:A:451:GLN:HG2	1.98	0.46
1:D:235:CYS:SG	1:D:325:ALA:HB1	2.56	0.46
1:D:341:LEU:HD23	1:D:341:LEU:HA	1.71	0.45
1:B:441:LEU:HD22	1:B:451:GLN:HG2	1.98	0.45
1:B:177:ASP:OD2	1:B:381:GLY:HA3	2.17	0.45
1:C:441:LEU:HD22	1:C:451:GLN:HG2	1.99	0.44
1:A:352:LEU:HA	1:A:352:LEU:HD12	1.85	0.44
1:D:55:VAL:HG13	1:D:55:VAL:O	2.16	0.44
1:A:195:MET:CE	1:A:338:ALA:HB2	2.48	0.43
1:B:195:MET:CE	1:B:338:ALA:HB2	2.48	0.43
1:D:177:ASP:OD2	1:D:381:GLY:HA3	2.18	0.43
1:D:195:MET:CE	1:D:338:ALA:HB2	2.49	0.43
1:B:198:ILE:HG21	1:B:384:ILE:HD13	2.01	0.43
1:C:177:ASP:OD2	1:C:381:GLY:HA3	2.18	0.43
1:C:195:MET:CE	1:C:338:ALA:HB2	2.49	0.43
1:B:425:LEU:HD23	1:B:440:LEU:HD21	2.02	0.42
1:C:137:ARG:CD	1:C:141:MET:CE	2.98	0.42
1:A:261:PRO:HG3	1:C:143:LYS:HB2	2.01	0.42
1:A:198:ILE:HG21	1:A:384:ILE:HD13	2.02	0.42
1:C:158:ARG:NH1	1:D:120:GLN:HB3	2.35	0.42
1:D:425:LEU:HD23	1:D:440:LEU:HD21	2.02	0.41
1:D:400:LEU:HG	1:D:402:GLU:HB3	2.02	0.41
1:A:55:VAL:O	1:A:55:VAL:HG13	2.21	0.41
1:C:425:LEU:HD23	1:C:440:LEU:HD21	2.03	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:198:ILE:HG21	1:D:384:ILE:HD13	2.02	0.41
1:A:177:ASP:OD2	1:A:381:GLY:HA3	2.20	0.41
1:C:198:ILE:HG21	1:C:384:ILE:HD13	2.03	0.41
1:C:146:ASN:OD1	1:C:146:ASN:C	2.59	0.41
1:C:137:ARG:HD3	1:C:141:MET:CE	2.51	0.40
1:A:57:LYS:HE3	1:B:123:GLU:OE2	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	438/509 (86%)	432 (99%)	6 (1%)	0	100	100
1	B	435/509 (86%)	430 (99%)	5 (1%)	0	100	100
1	C	434/509 (85%)	430 (99%)	4 (1%)	0	100	100
1	D	438/509 (86%)	431 (98%)	7 (2%)	0	100	100
All	All	1745/2036 (86%)	1723 (99%)	22 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	376/438 (86%)	368 (98%)	8 (2%)	66	93
1	B	379/438 (86%)	373 (98%)	6 (2%)	75	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	378/438 (86%)	372 (98%)	6 (2%)	75	95
1	D	379/438 (86%)	372 (98%)	7 (2%)	71	94
All	All	1512/1752 (86%)	1485 (98%)	27 (2%)	71	94

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	PHE
1	A	149	ARG
1	A	164	THR
1	A	165	ARG
1	A	228	ASP
1	A	233	THR
1	A	391	SER
1	A	440	LEU
1	B	97	PHE
1	B	149	ARG
1	B	163	MET
1	B	228	ASP
1	B	391	SER
1	B	440	LEU
1	C	97	PHE
1	C	149	ARG
1	C	163	MET
1	C	228	ASP
1	C	391	SER
1	C	440	LEU
1	D	54	PHE
1	D	97	PHE
1	D	149	ARG
1	D	163	MET
1	D	228	ASP
1	D	391	SER
1	D	440	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

8 ligands are 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	HIS	A	1001	-	11,11,11	0.79	1 (9%)	14,14,14	1.00	1 (7%)
3	GOL	A	1002	-	5,5,5	0.26	0	5,5,5	0.40	0
2	HIS	B	1001	-	11,11,11	0.75	0	14,14,14	0.77	1 (7%)
3	GOL	B	1002	-	5,5,5	0.38	0	5,5,5	0.73	0
2	HIS	C	1001	-	11,11,11	0.80	1 (9%)	14,14,14	0.81	1 (7%)
3	GOL	C	1002	-	5,5,5	0.13	0	5,5,5	0.74	0
3	GOL	C	1003	-	5,5,5	0.31	0	5,5,5	0.34	0
2	HIS	D	1001	-	11,11,11	0.71	0	14,14,14	0.75	1 (7%)

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	HIS	A	1001	-	-	0/8/8/8	0/1/1/1
3	GOL	A	1002	-	-	0/4/4/4	0/0/0/0
2	HIS	B	1001	-	-	0/8/8/8	0/1/1/1
3	GOL	B	1002	-	-	0/4/4/4	0/0/0/0
2	HIS	C	1001	-	-	0/8/8/8	0/1/1/1
3	GOL	C	1002	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	C	1003	-	-	0/4/4/4	0/0/0/0
2	HIS	D	1001	-	-	0/8/8/8	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	HIS	OXT-C	-2.11	1.22	1.30
2	C	1001	HIS	OXT-C	-2.09	1.23	1.30

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	HIS	OXT-C-O	-2.74	117.89	124.05
2	C	1001	HIS	OXT-C-O	-2.29	118.90	124.05
2	D	1001	HIS	OXT-C-O	-2.10	119.34	124.05
2	B	1001	HIS	OXT-C-O	-2.02	119.52	124.05

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	444/509 (87%)	-0.03	13 (2%) 49 52	30, 58, 97, 121	0
1	B	441/509 (86%)	-0.09	14 (3%) 45 48	33, 55, 98, 130	0
1	C	440/509 (86%)	0.06	23 (5%) 26 27	38, 62, 111, 135	0
1	D	442/509 (86%)	-0.05	12 (2%) 52 54	38, 61, 95, 134	0
All	All	1767/2036 (86%)	-0.03	62 (3%) 42 44	30, 59, 101, 135	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	162	ALA	7.2
1	C	399	ALA	6.3
1	C	164	THR	5.2
1	C	404	ILE	4.8
1	B	399	ALA	4.6
1	C	400	LEU	4.5
1	A	231	PHE	4.0
1	B	164	THR	3.9
1	A	228	ASP	3.6
1	C	163	MET	3.4
1	C	285	GLN	3.4
1	A	234	ILE	3.2
1	B	163	MET	3.2
1	D	163	MET	3.2
1	A	53	LYS	3.0
1	A	399	ALA	3.0
1	A	396	ARG	3.0
1	A	397	LEU	2.9
1	B	162	ALA	2.9
1	B	404	ILE	2.9
1	B	289	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	229	SER	2.9
1	C	265	ASP	2.8
1	B	403	LYS	2.8
1	D	397	LEU	2.8
1	C	247	GLU	2.8
1	C	121	GLY	2.7
1	C	165	ARG	2.7
1	C	161	PRO	2.6
1	C	397	LEU	2.6
1	D	54	PHE	2.5
1	D	109	GLU	2.5
1	A	232	ARG	2.5
1	C	269	ASP	2.5
1	C	251	ASN	2.4
1	A	351	PRO	2.4
1	D	400	LEU	2.4
1	C	396	ARG	2.4
1	A	400	LEU	2.4
1	B	161	PRO	2.4
1	D	291	GLN	2.3
1	B	396	ARG	2.3
1	B	269	ASP	2.3
1	A	404	ILE	2.2
1	D	344	PRO	2.2
1	D	165	ARG	2.2
1	B	243	LYS	2.2
1	C	244	VAL	2.2
1	C	504	GLN	2.1
1	D	403	LYS	2.1
1	D	258	GLY	2.1
1	A	403	LYS	2.1
1	C	292	ASN	2.1
1	C	166	GLY	2.1
1	D	53	LYS	2.0
1	B	247	GLU	2.0
1	B	248	GLU	2.0
1	B	287	PRO	2.0
1	C	355	GLY	2.0
1	C	159	ASP	2.0
1	D	399	ALA	2.0
1	C	289	LEU	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 carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	GOL	C	1003	6/6	0.24	2.33	51,53,56,61	0
3	GOL	C	1002	6/6	0.22	2.30	50,56,58,59	0
2	HIS	C	1001	11/11	0.21	2.25	57,59,61,61	0
2	HIS	A	1001	11/11	0.22	1.13	41,43,46,48	0
3	GOL	A	1002	6/6	0.17	0.83	53,58,59,61	0
2	HIS	D	1001	11/11	0.22	0.81	42,46,51,51	0
3	GOL	B	1002	6/6	0.18	0.28	39,46,48,48	0
2	HIS	B	1001	11/11	0.16	-0.26	36,41,43,44	0

6.5 Other polymers ⓘ

There are no such residues in this entry.