



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:38 PM UTC

PDB ID : 5HY0 / pdb_00005hy0
Title : orotic acid hydrolase
Authors : Peat, T.S.; Balotra, S.; Wilding, M.; Newman, J.; Scott, C.
Deposited on : 2016-02-01
Resolution : 2.40 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

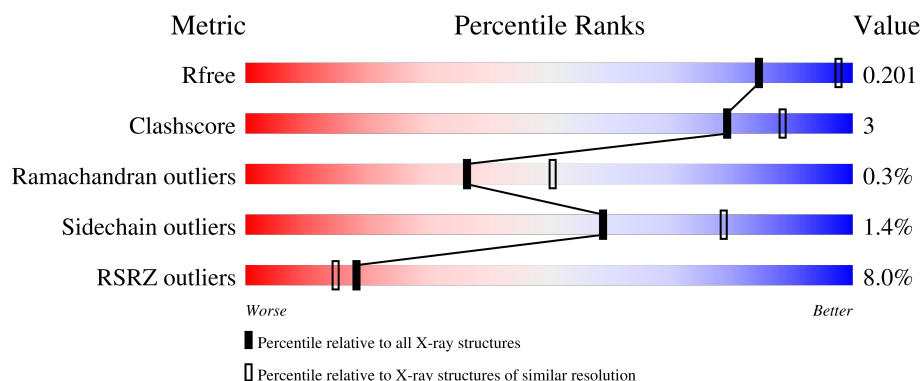
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	410	6% 81% 7% • 12%
1	B	410	8% 83% • 12%
1	C	410	7% 83% 6% 11%
1	D	410	8% 82% 6% • 11%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10739 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 Ring-opening amidohydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	362	Total	C	N	O	S	0	2	0
			2576	1599	466	500	11			
1	B	359	Total	C	N	O	S	0	5	0
			2590	1607	467	505	11			
1	C	364	Total	C	N	O	S	0	1	0
			2610	1621	474	504	11			
1	D	363	Total	C	N	O	S	0	2	0
			2601	1614	469	507	11			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP E3JD18
A	-18	GLY	-	expression tag	UNP E3JD18
A	-17	SER	-	expression tag	UNP E3JD18
A	-16	SER	-	expression tag	UNP E3JD18
A	-15	HIS	-	expression tag	UNP E3JD18
A	-14	HIS	-	expression tag	UNP E3JD18
A	-13	HIS	-	expression tag	UNP E3JD18
A	-12	HIS	-	expression tag	UNP E3JD18
A	-11	HIS	-	expression tag	UNP E3JD18
A	-10	HIS	-	expression tag	UNP E3JD18
A	-9	SER	-	expression tag	UNP E3JD18
A	-8	SER	-	expression tag	UNP E3JD18
A	-7	GLY	-	expression tag	UNP E3JD18
A	-6	LEU	-	expression tag	UNP E3JD18
A	-5	VAL	-	expression tag	UNP E3JD18
A	-4	PRO	-	expression tag	UNP E3JD18
A	-3	ARG	-	expression tag	UNP E3JD18
A	-2	GLY	-	expression tag	UNP E3JD18
A	-1	SER	-	expression tag	UNP E3JD18
A	0	HIS	-	expression tag	UNP E3JD18
B	-19	MET	-	initiating methionine	UNP E3JD18

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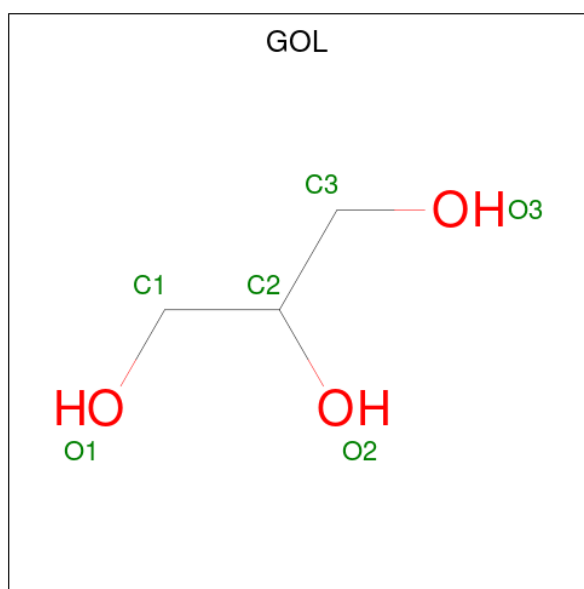
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP E3JD18
B	-17	SER	-	expression tag	UNP E3JD18
B	-16	SER	-	expression tag	UNP E3JD18
B	-15	HIS	-	expression tag	UNP E3JD18
B	-14	HIS	-	expression tag	UNP E3JD18
B	-13	HIS	-	expression tag	UNP E3JD18
B	-12	HIS	-	expression tag	UNP E3JD18
B	-11	HIS	-	expression tag	UNP E3JD18
B	-10	HIS	-	expression tag	UNP E3JD18
B	-9	SER	-	expression tag	UNP E3JD18
B	-8	SER	-	expression tag	UNP E3JD18
B	-7	GLY	-	expression tag	UNP E3JD18
B	-6	LEU	-	expression tag	UNP E3JD18
B	-5	VAL	-	expression tag	UNP E3JD18
B	-4	PRO	-	expression tag	UNP E3JD18
B	-3	ARG	-	expression tag	UNP E3JD18
B	-2	GLY	-	expression tag	UNP E3JD18
B	-1	SER	-	expression tag	UNP E3JD18
B	0	HIS	-	expression tag	UNP E3JD18
C	-19	MET	-	initiating methionine	UNP E3JD18
C	-18	GLY	-	expression tag	UNP E3JD18
C	-17	SER	-	expression tag	UNP E3JD18
C	-16	SER	-	expression tag	UNP E3JD18
C	-15	HIS	-	expression tag	UNP E3JD18
C	-14	HIS	-	expression tag	UNP E3JD18
C	-13	HIS	-	expression tag	UNP E3JD18
C	-12	HIS	-	expression tag	UNP E3JD18
C	-11	HIS	-	expression tag	UNP E3JD18
C	-10	HIS	-	expression tag	UNP E3JD18
C	-9	SER	-	expression tag	UNP E3JD18
C	-8	SER	-	expression tag	UNP E3JD18
C	-7	GLY	-	expression tag	UNP E3JD18
C	-6	LEU	-	expression tag	UNP E3JD18
C	-5	VAL	-	expression tag	UNP E3JD18
C	-4	PRO	-	expression tag	UNP E3JD18
C	-3	ARG	-	expression tag	UNP E3JD18
C	-2	GLY	-	expression tag	UNP E3JD18
C	-1	SER	-	expression tag	UNP E3JD18
C	0	HIS	-	expression tag	UNP E3JD18
D	-19	MET	-	initiating methionine	UNP E3JD18
D	-18	GLY	-	expression tag	UNP E3JD18
D	-17	SER	-	expression tag	UNP E3JD18

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP E3JD18
D	-15	HIS	-	expression tag	UNP E3JD18
D	-14	HIS	-	expression tag	UNP E3JD18
D	-13	HIS	-	expression tag	UNP E3JD18
D	-12	HIS	-	expression tag	UNP E3JD18
D	-11	HIS	-	expression tag	UNP E3JD18
D	-10	HIS	-	expression tag	UNP E3JD18
D	-9	SER	-	expression tag	UNP E3JD18
D	-8	SER	-	expression tag	UNP E3JD18
D	-7	GLY	-	expression tag	UNP E3JD18
D	-6	LEU	-	expression tag	UNP E3JD18
D	-5	VAL	-	expression tag	UNP E3JD18
D	-4	PRO	-	expression tag	UNP E3JD18
D	-3	ARG	-	expression tag	UNP E3JD18
D	-2	GLY	-	expression tag	UNP E3JD18
D	-1	SER	-	expression tag	UNP E3JD18
D	0	HIS	-	expression tag	UNP E3JD18

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

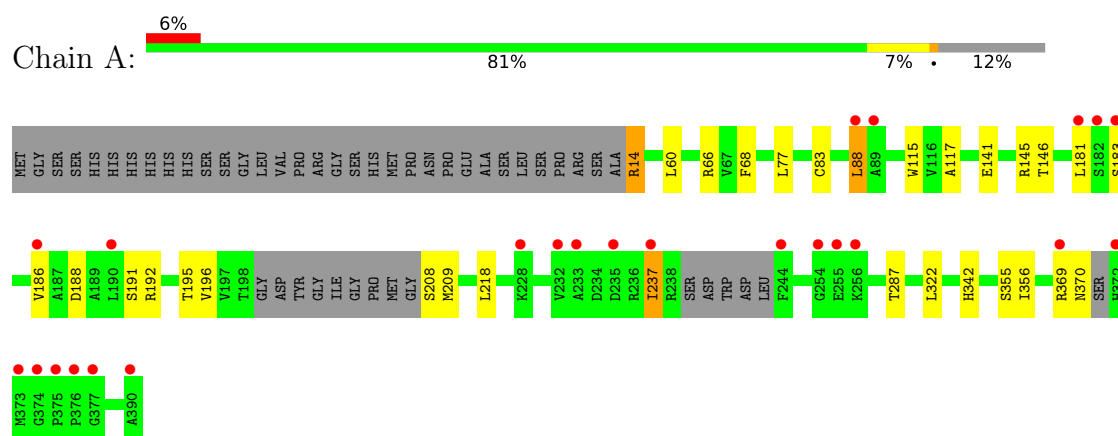
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	75	Total 75	O 75	0	0
3	B	81	Total 81	O 81	0	0
3	C	105	Total 105	O 105	0	0
3	D	89	Total 89	O 89	0	0

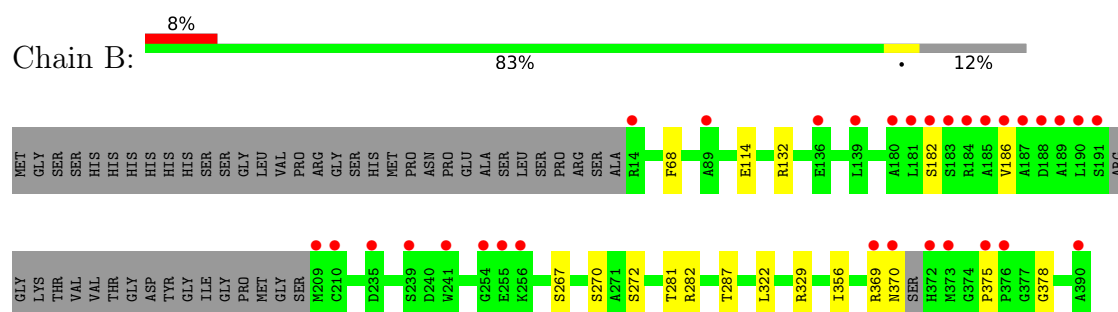
3 Residue-property plots [i](#)

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.

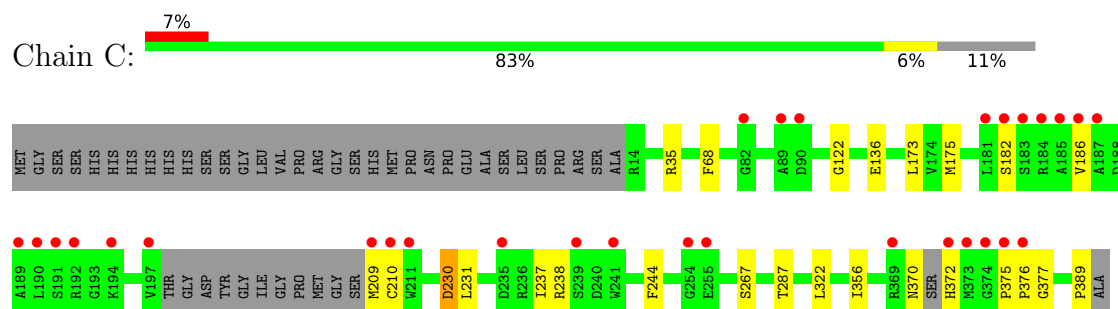
- Molecule 1: Ring-opening amidohydrolase



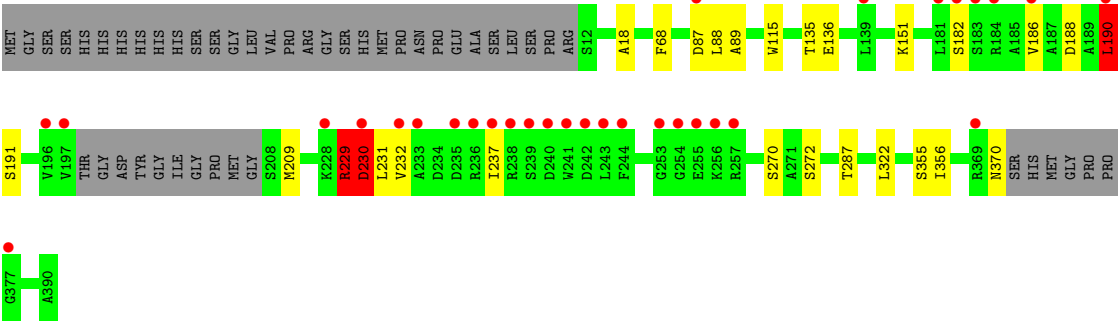
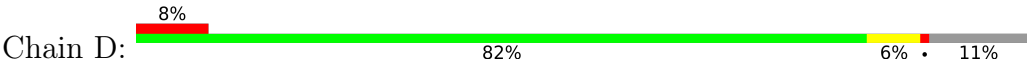
- Molecule 1: Ring-opening amidohydrolase



- Molecule 1: Ring-opening amidohydrolase



- Molecule 1: Ring-opening amidohydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	73.58Å 85.66Å 87.23Å 96.47° 114.94° 111.77°	Depositor
Resolution (Å)	41.50 – 2.40 41.50 – 2.40	Depositor EDS
% Data completeness (in resolution range)	96.8 (41.50-2.40) 97.0 (41.50-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.72 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.194 , 0.236 (Not available) , 0.201	Depositor DCC
R_{free} test set	3266 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	20.3	Xtriage
Anisotropy	0.093	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 33.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.009 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	10739	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.60% 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	1.02	1/2616 (0.0%)	1.03	3/3565 (0.1%)
1	B	0.97	0/2633	0.99	2/3591 (0.1%)
1	C	1.07	1/2653 (0.0%)	1.04	4/3616 (0.1%)
1	D	1.04	1/2642 (0.0%)	1.03	3/3601 (0.1%)
All	All	1.03	3/10544 (0.0%)	1.02	12/14373 (0.1%)

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	1
1	C	0	1
1	D	0	1
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	355	SER	C-O	-5.69	1.17	1.24
1	C	231	LEU	N-CA	-5.19	1.39	1.46
1	D	355	SER	C-O	-5.07	1.17	1.24

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	237	ILE	N-CA-C	8.90	119.70	110.62
1	B	375	PRO	CA-C-N	-6.80	112.65	119.93
1	B	375	PRO	C-N-CA	-6.80	112.65	119.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	375	PRO	N-CA-C	5.85	117.83	110.70
1	A	83	CYS	CA-C-N	-5.79	114.00	119.85
1	A	83	CYS	C-N-CA	-5.79	114.00	119.85
1	D	230	ASP	N-CA-C	5.57	122.67	110.80
1	C	136	GLU	CA-C-N	-5.54	114.05	119.76
1	C	136	GLU	C-N-CA	-5.54	114.05	119.76
1	A	209	MET	N-CA-C	-5.50	105.36	111.36
1	C	237	ILE	N-CA-C	5.49	116.88	110.62
1	D	190	LEU	N-CA-C	-5.08	104.72	112.04

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	237	ILE	Peptide
1	C	376	PRO	Peptide
1	D	229	ARG	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	2576	0	2549	16	0
1	B	2590	0	2546	9	0
1	C	2610	0	2590	14	0
1	D	2601	0	2574	17	0
2	A	6	0	8	2	0
2	B	6	0	8	0	0
3	A	75	0	0	2	0
3	B	81	0	0	1	0
3	C	105	0	0	2	0
3	D	89	0	0	1	0
All	All	10739	0	10275	55	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 3.

All (55) 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:D:135:THR:HG22	1:D:136:GLU:O	1.77	0.83
1:C:173:LEU:HD21	1:C:175:MET:HG3	1.59	0.83
1:C:230:ASP:OD1	1:C:230:ASP:N	2.22	0.63
1:C:370:ASN:ND2	3:C:403:HOH:O	2.34	0.60
1:B:132:ARG:HD3	3:B:507:HOH:O	2.01	0.60
1:D:87:ASP:O	1:D:89:ALA:N	2.35	0.59
1:C:210:CYS:HB3	1:C:238:ARG:HH12	1.68	0.58
1:B:68:PHE:CD1	1:D:68:PHE:CD1	2.92	0.57
1:A:188:ASP:OD2	1:A:192:ARG:NH1	2.39	0.55
1:D:135:THR:HG23	1:D:151:LYS:HB3	1.89	0.54
1:B:322:LEU:O	1:B:370:ASN:HB2	2.08	0.54
1:D:186:VAL:O	1:D:190:LEU:HB2	2.07	0.53
1:D:135:THR:CG2	1:D:151:LYS:HB3	2.38	0.53
1:A:68:PHE:CD1	1:C:68:PHE:CD1	2.97	0.53
1:D:182:SER:O	1:D:186:VAL:HG23	2.09	0.52
1:A:145:ARG:NH2	1:A:195:THR:O	2.42	0.51
2:A:401:GOL:O1	3:A:501:HOH:O	2.06	0.51
1:C:182:SER:O	1:C:186:VAL:HG23	2.11	0.51
1:D:87:ASP:C	1:D:89:ALA:H	2.19	0.51
1:D:322:LEU:O	1:D:370:ASN:HB2	2.12	0.50
1:A:14:ARG:NH2	1:A:117:ALA:HB2	2.27	0.50
1:B:182:SER:O	1:B:186:VAL:HG23	2.12	0.50
1:C:238:ARG:O	1:C:238:ARG:HG2	2.12	0.50
1:D:229:ARG:O	1:D:232:VAL:N	2.40	0.48
1:C:322:LEU:O	1:C:370:ASN:HB2	2.13	0.48
1:D:287:THR:HB	1:D:356:ILE:HD11	1.96	0.47
1:A:287:THR:HB	1:A:356:ILE:HD11	1.96	0.47
1:C:173:LEU:C	1:C:173:LEU:HD23	2.40	0.47
1:A:322:LEU:O	1:A:370:ASN:HB2	2.15	0.46
1:A:188:ASP:O	1:A:191:SER:HB2	2.16	0.46
1:B:287:THR:HB	1:B:356:ILE:HD11	1.98	0.45
1:A:237:ILE:HG22	1:A:237:ILE:O	2.17	0.45
1:A:181:LEU:HD12	1:A:208:SER:HB2	1.98	0.45
1:C:287:THR:HB	1:C:356:ILE:HD11	1.99	0.44
1:A:115:TRP:HE1	2:A:401:GOL:H12	1.84	0.43
1:D:188:ASP:O	1:D:191:SER:HB2	2.19	0.43
1:D:229:ARG:C	1:D:231:LEU:H	2.27	0.43
1:D:270:SER:OG	1:D:272:SER:HB3	2.19	0.43
1:A:77:LEU:HD23	1:A:88:LEU:HD21	1.99	0.42
1:D:18:ALA:H	1:D:272:SER:HB2	1.84	0.42
1:D:87:ASP:C	1:D:89:ALA:N	2.77	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:270:SER:OG	1:B:272[A]:SER:HB3	2.18	0.42
1:B:114:GLU:H	1:B:114:GLU:HG2	1.78	0.41
1:C:122:GLY:O	1:C:389:PRO:HA	2.20	0.41
1:A:60:LEU:O	1:A:66[A]:ARG:NH2	2.53	0.41
1:A:237:ILE:O	1:A:237:ILE:CG2	2.68	0.41
1:C:244:PHE:HA	1:C:372:HIS:O	2.21	0.41
1:D:115:TRP:NE1	3:D:403:HOH:O	2.41	0.41
1:C:210:CYS:HB3	1:C:238:ARG:NH1	2.35	0.41
1:A:342:HIS:ND1	3:A:502:HOH:O	2.37	0.41
1:B:281:THR:O	1:B:378:GLY:HA2	2.21	0.41
1:C:35[A]:ARG:HH11	1:C:35[A]:ARG:HD2	1.75	0.41
1:A:141:GLU:OE1	1:A:192:ARG:NH2	2.54	0.40
1:A:186:VAL:HG22	1:A:196:VAL:HG11	2.03	0.40
1:B:329:ARG:HD2	3:C:477:HOH:O	2.20	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	356/410 (87%)	343 (96%)	13 (4%)	0	100	100
1	B	358/410 (87%)	351 (98%)	7 (2%)	0	100	100
1	C	359/410 (88%)	349 (97%)	9 (2%)	1 (0%)	36	50
1	D	359/410 (88%)	347 (97%)	9 (2%)	3 (1%)	16	25
All	All	1432/1640 (87%)	1390 (97%)	38 (3%)	4 (0%)	36	50

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	377	GLY

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Mol	Chain	Res	Type
1	D	230	ASP
1	D	88	LEU
1	D	229	ARG

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	265/310 (86%)	259 (98%)	6 (2%)	44	66
1	B	267/310 (86%)	264 (99%)	3 (1%)	65	82
1	C	270/310 (87%)	267 (99%)	3 (1%)	65	82
1	D	269/310 (87%)	266 (99%)	3 (1%)	65	82
All	All	1071/1240 (86%)	1056 (99%)	15 (1%)	59	79

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	ARG
1	A	88	LEU
1	A	146	THR
1	A	183	SER
1	A	218	LEU
1	A	369	ARG
1	B	267	SER
1	B	282	ARG
1	B	369	ARG
1	C	209	MET
1	C	230	ASP
1	C	267	SER
1	D	190	LEU
1	D	209	MET
1	D	230	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	339	HIS
1	C	339	HIS
1	D	269	GLN

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 ⓘ

2 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	GOL	A	401	-	5,5,5	0.49	0	5,5,5	1.17	0
2	GOL	B	401	-	5,5,5	0.51	0	5,5,5	1.16	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	401	-	-	4/4/4/4	-
2	GOL	B	401	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	GOL	O1-C1-C2-O2
2	A	401	GOL	O1-C1-C2-C3
2	A	401	GOL	C1-C2-C3-O3
2	B	401	GOL	O1-C1-C2-O2
2	B	401	GOL	O1-C1-C2-C3
2	A	401	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	GOL	2	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	362/410 (88%)	0.12	24 (6%)	24	20	7, 22, 65, 109	2 (0%)
1	B	359/410 (87%)	0.15	31 (8%)	16	13	8, 20, 73, 104	5 (1%)
1	C	364/410 (88%)	0.09	30 (8%)	17	14	7, 18, 66, 93	1 (0%)
1	D	363/410 (88%)	0.08	31 (8%)	16	13	8, 20, 71, 100	2 (0%)
All	All	1448/1640 (88%)	0.11	116 (8%)	18	15	7, 20, 69, 109	10 (0%)

All (116) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	241	TRP	7.2
1	C	241	TRP	6.2
1	B	241	TRP	6.0
1	A	376	PRO	5.9
1	A	372	HIS	5.8
1	C	372	HIS	5.7
1	B	390	ALA	5.0
1	B	190	LEU	5.0
1	D	197	VAL	4.5
1	D	243	LEU	4.2
1	C	182	SER	4.2
1	C	190	LEU	4.2
1	C	373	MET	4.1
1	C	255	GLU	4.1
1	B	372	HIS	4.0
1	D	244	PHE	4.0
1	A	244	PHE	3.9
1	B	189	ALA	3.9
1	A	375	PRO	3.9
1	B	182	SER	3.9
1	D	255	GLU	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	190	LEU	3.6
1	A	390	ALA	3.5
1	C	189	ALA	3.5
1	B	183	SER	3.5
1	B	185	ALA	3.5
1	C	374	GLY	3.5
1	D	253	GLY	3.5
1	B	184	ARG	3.4
1	C	375	PRO	3.4
1	A	373	MET	3.4
1	B	256	LYS	3.3
1	D	236	ARG	3.3
1	C	90	ASP	3.3
1	B	235	ASP	3.3
1	D	238	ARG	3.3
1	A	186	VAL	3.2
1	B	369	ARG	3.2
1	D	254	GLY	3.2
1	B	376	PRO	3.2
1	B	89	ALA	3.1
1	A	255	GLU	3.1
1	B	139	LEU	3.1
1	B	209	MET	3.1
1	D	196	VAL	3.1
1	A	181	LEU	3.1
1	C	197	VAL	3.0
1	B	375	PRO	3.0
1	D	242	ASP	3.0
1	C	82	GLY	3.0
1	C	89	ALA	3.0
1	D	369	ARG	3.0
1	A	256	LYS	3.0
1	D	232	VAL	2.9
1	C	376	PRO	2.9
1	D	183	SER	2.9
1	B	373	MET	2.9
1	C	209	MET	2.9
1	A	182	SER	2.9
1	B	254	GLY	2.9
1	D	233	ALA	2.9
1	C	185	ALA	2.8
1	B	181	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	254	GLY	2.8
1	C	186	VAL	2.8
1	D	181	LEU	2.8
1	A	183	SER	2.8
1	D	239	SER	2.8
1	A	235	ASP	2.8
1	B	191	SER	2.7
1	D	237	ILE	2.7
1	D	190	LEU	2.6
1	B	180	ALA	2.6
1	B	210	CYS	2.6
1	C	254	GLY	2.6
1	A	374	GLY	2.6
1	C	369	ARG	2.5
1	D	235	ASP	2.5
1	B	187	ALA	2.5
1	D	186	VAL	2.5
1	D	240	ASP	2.5
1	C	184	ARG	2.5
1	A	369	ARG	2.4
1	D	182	SER	2.4
1	A	232	VAL	2.4
1	B	186	VAL	2.4
1	B	14	ARG	2.4
1	D	256	LYS	2.4
1	D	139	LEU	2.3
1	D	230	ASP	2.3
1	A	237	ILE	2.3
1	C	235	ASP	2.3
1	D	377	GLY	2.3
1	B	370	ASN	2.2
1	D	184	ARG	2.2
1	C	239	SER	2.2
1	C	192	ARG	2.2
1	C	187	ALA	2.1
1	A	88	LEU	2.1
1	C	194	LYS	2.1
1	D	228	LYS	2.1
1	A	89	ALA	2.1
1	A	228	LYS	2.1
1	C	191	SER	2.1
1	D	87	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	211	TRP	2.1
1	B	239	SER	2.1
1	C	210	CYS	2.1
1	D	257	ARG	2.0
1	A	377	GLY	2.0
1	B	255	GLU	2.0
1	B	188	ASP	2.0
1	A	233	ALA	2.0
1	B	136	GLU	2.0
1	C	181	LEU	2.0
1	C	183	SER	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(Å ²)	Q<0.9
2	GOL	A	401	6/6	0.85	0.13	30,33,35,50	0
2	GOL	B	401	6/6	0.88	0.13	29,30,33,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.