



wwPDB X-ray Structure Validation Summary Report ⓘ

May 16, 2020 – 03:35 am BST

PDB ID : 3SXX
Title : Hansenula polymorpha copper amine oxidase-1 in complex with Co(II)
Authors : Klema, V.J.; Wilmot, C.M.
Deposited on : 2011-07-15
Resolution : 1.27 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

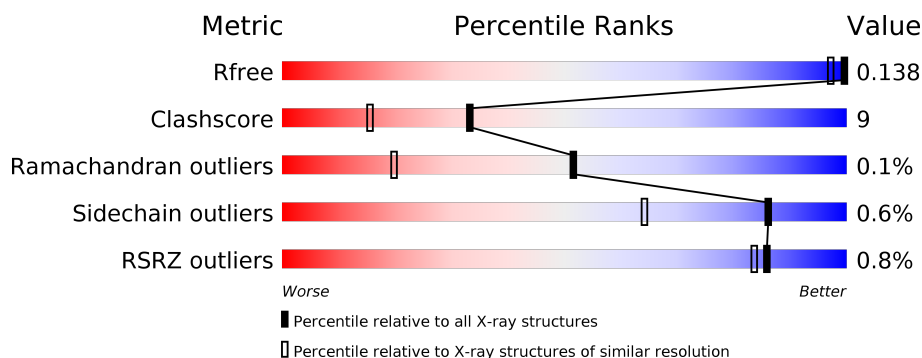
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.27 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}	130704	1850 (1.30-1.26)
Clashscore	141614	1926 (1.30-1.26)
Ramachandran outliers	138981	1860 (1.30-1.26)
Sidechain outliers	138945	1859 (1.30-1.26)
RSRZ outliers	127900	1807 (1.30-1.26)

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 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	692	<div> <div>%</div> <div> <div></div> <div>86%</div> <div>9%</div> <div>• •</div> </div> </div>
1	B	692	<div> <div>%</div> <div> <div></div> <div>86%</div> <div>9%</div> <div>• •</div> </div> </div>
1	C	692	<div> <div>%</div> <div> <div></div> <div>85%</div> <div>11%</div> <div>•</div> </div> </div>
1	D	692	<div> <div>%</div> <div> <div></div> <div>87%</div> <div>7%</div> <div>• 5%</div> </div> </div>
1	E	692	<div> <div></div> <div> <div>88%</div> <div>7%</div> <div>• 5%</div> </div> </div>
1	F	692	<div> <div>%</div> <div> <div></div> <div>86%</div> <div>10%</div> <div>• •</div> </div> </div>

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	GOL	A	807	-	X	X	-
3	GOL	A	810	-	-	X	-
3	GOL	A	811	-	X	-	-
3	GOL	B	805[A]	-	-	X	-
3	GOL	B	805[B]	-	-	X	-
3	GOL	B	806	-	-	X	-
3	GOL	B	807	-	-	X	-
3	GOL	C	802	-	X	-	-
3	GOL	C	809	-	-	X	-
3	GOL	D	805	-	X	X	-
3	GOL	D	806	-	-	X	-
3	GOL	E	806	-	-	X	-
3	GOL	F	803	-	-	X	-
3	GOL	F	808	-	-	X	-
4	PO4	C	804	-	X	-	-
4	PO4	F	806	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 38975 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 Peroxisomal primary amine oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	666	Total	C	N	O	S	0	38	0
			5423	3465	912	1014	32			
1	B	664	Total	C	N	O	S	0	37	0
			5441	3467	926	1017	31			
1	C	666	Total	C	N	O	S	0	34	0
			5427	3467	921	1005	34			
1	D	657	Total	C	N	O	S	0	31	0
			5368	3427	916	996	29			
1	E	656	Total	C	N	O	S	3	31	0
			5355	3423	912	991	29			
1	F	665	Total	C	N	O	S	0	34	0
			5426	3469	915	1008	34			

- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Co	0	0
			1	1		
2	E	1	Total	Co	0	0
			1	1		
2	B	1	Total	Co	0	0
			1	1		
2	C	1	Total	Co	0	0
			1	1		
2	A	1	Total	Co	0	0
			1	1		
2	F	1	Total	Co	0	0
			1	1		

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	1
			12	6	6		
3	A	1	Total	C	O	0	1
			12	6	6		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	1
			12	6	6		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	1
			12	6	6		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	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		
3	C	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		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	1
			12	6	6		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	E	1	Total	C	O	0	0
			6	3	3		
3	F	1	Total	C	O	0	0
			6	3	3		
3	F	1	Total	C	O	0	0
			6	3	3		
3	F	1	Total	C	O	0	1
			12	6	6		
3	F	1	Total	C	O	0	0
			6	3	3		
3	F	1	Total	C	O	0	0
			6	3	3		
3	F	1	Total	C	O	0	0
			6	3	3		
3	F	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	O	P	0	0
			5	4	1		
4	F	1	Total	O	P	0	0
			5	4	1		

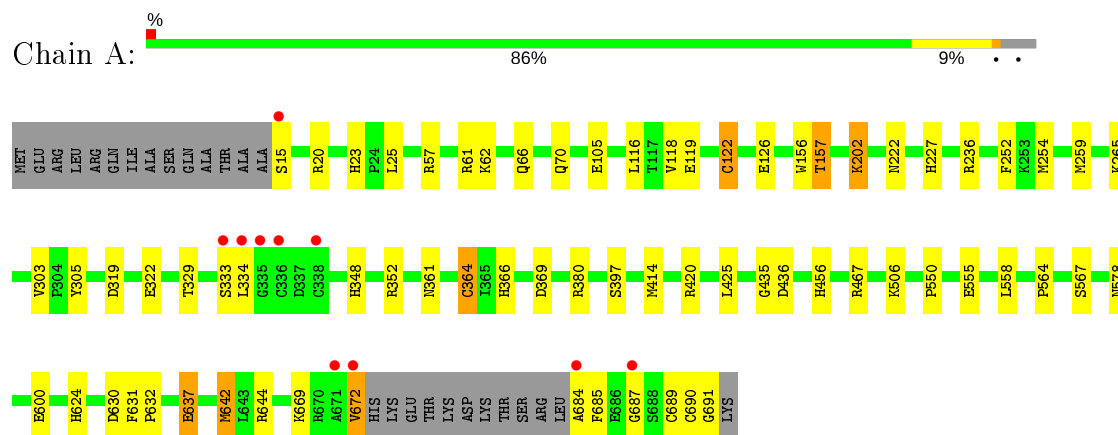
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1035	Total 1035	O 1035	0	0
5	B	1038	Total 1038	O 1038	0	0
5	C	1037	Total 1037	O 1037	0	0
5	D	1044	Total 1044	O 1044	0	0
5	E	1033	Total 1033	O 1033	0	0
5	F	1038	Total 1038	O 1038	0	0

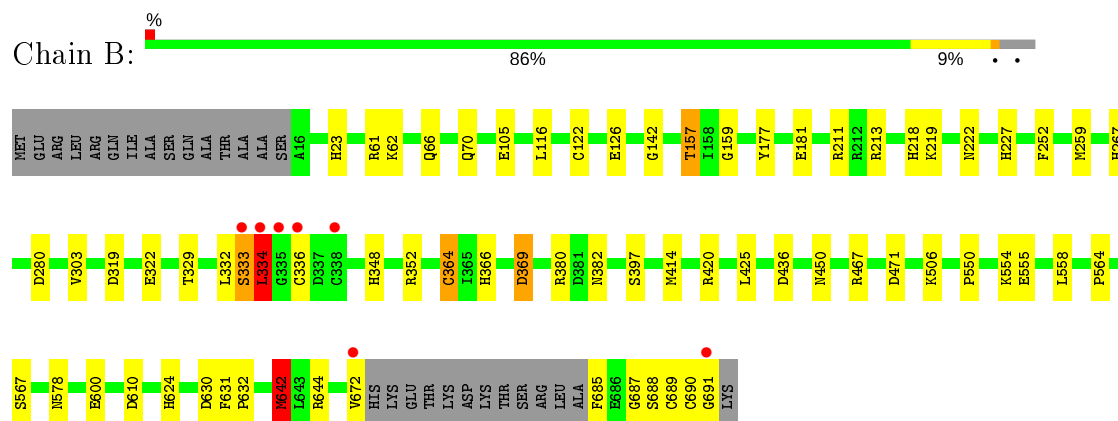
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

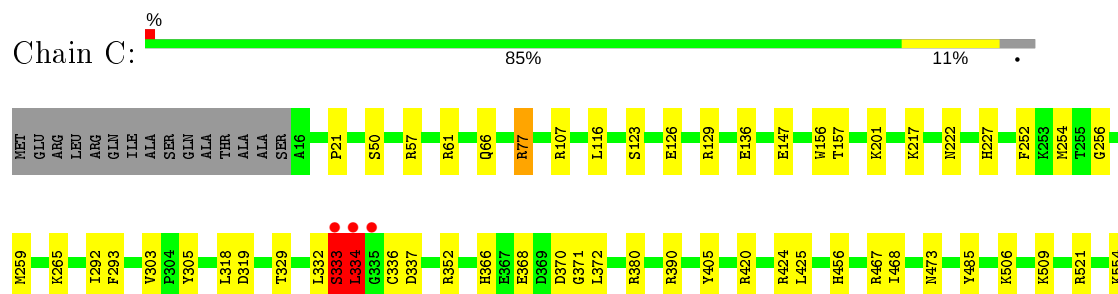
- Molecule 1: Peroxisomal primary amine oxidase



- Molecule 1: Peroxisomal primary amine oxidase

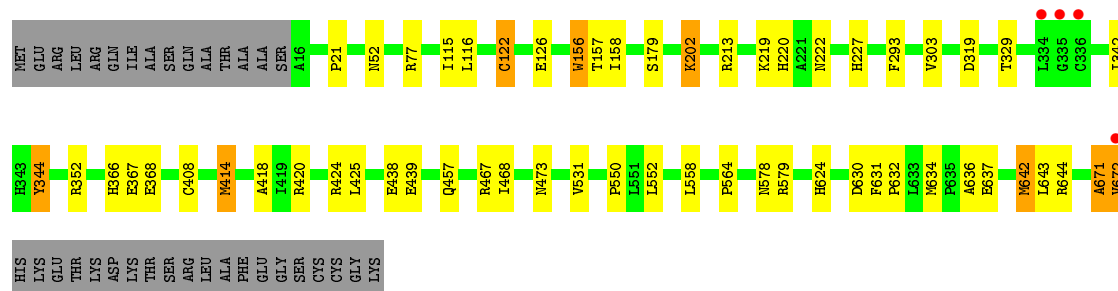
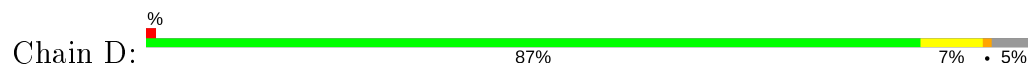


- Molecule 1: Peroxisomal primary amine oxidase

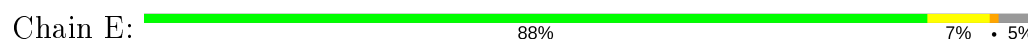




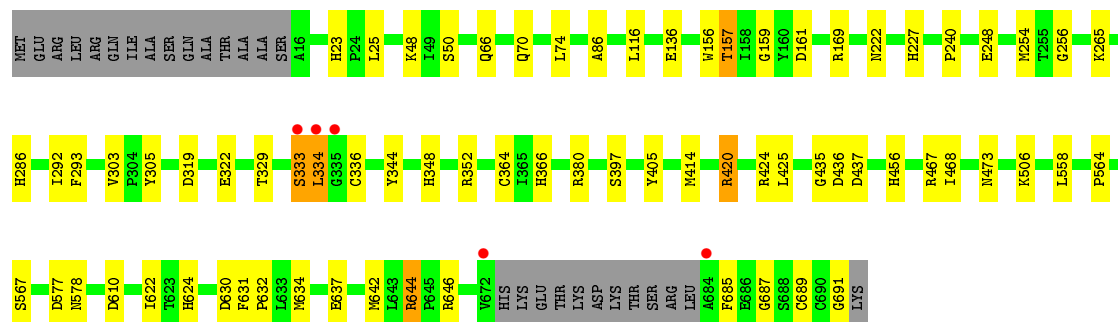
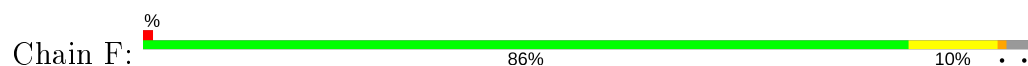
- Molecule 1: Peroxisomal primary amine oxidase



- Molecule 1: Peroxisomal primary amine oxidase



- Molecule 1: Peroxisomal primary amine oxidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	103.89Å 223.36Å 103.97Å 90.00° 95.61° 90.00°	Depositor
Resolution (Å)	31.70 – 1.27 31.70 – 1.27	Depositor EDS
% Data completeness (in resolution range)	94.9 (31.70-1.27) 94.6 (31.70-1.27)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.08 (at 1.27Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.108 , 0.138 0.107 , 0.138	Depositor DCC
R_{free} test set	58671 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	7.8	Xtriage
Anisotropy	0.242	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.477 for l,-k,h	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	38975	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.81% 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: GOL, PO4, CO

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	0.91	9/5672 (0.2%)	0.94	11/7715 (0.1%)
1	B	0.90	10/5675 (0.2%)	0.94	17/7715 (0.2%)
1	C	0.87	3/5664 (0.1%)	0.94	15/7701 (0.2%)
1	D	0.87	2/5595 (0.0%)	0.92	11/7609 (0.1%)
1	E	0.90	4/5592 (0.1%)	0.90	9/7604 (0.1%)
1	F	0.86	5/5675 (0.1%)	0.93	18/7717 (0.2%)
All	All	0.88	33/33873 (0.1%)	0.93	81/46061 (0.2%)

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
1	B	0	2
1	C	0	4
1	D	0	3
1	F	0	1
All	All	0	12

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	364[A]	CYS	CB-SG	-9.00	1.67	1.82
1	B	364[B]	CYS	CB-SG	-9.00	1.67	1.82
1	E	122[A]	CYS	CB-SG	8.52	1.96	1.82
1	E	122[B]	CYS	CB-SG	8.52	1.96	1.82
1	A	364[A]	CYS	CB-SG	-8.46	1.67	1.82

The worst 5 of 81 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	414[A]	MET	CG-SD-CE	-11.74	81.41	100.20
1	D	414[B]	MET	CG-SD-CE	-11.74	81.41	100.20
1	F	157[A]	THR	N-CA-CB	11.39	131.94	110.30
1	F	157[B]	THR	N-CA-CB	11.39	131.94	110.30
1	B	157[A]	THR	N-CA-CB	10.61	130.46	110.30

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	156	TRP	Peptide
1	A	684	ALA	Peptide
1	B	333	SER	Peptide
1	B	334	LEU	Peptide
1	C	156	TRP	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	5423	0	5319	104	0
1	B	5441	0	5319	99	0
1	C	5427	0	5331	99	0
1	D	5368	0	5278	91	0
1	E	5355	0	5280	76	0
1	F	5426	0	5334	95	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	72	0	94	30	0
3	B	60	0	79	29	0
3	C	48	0	63	9	0
3	D	36	0	48	14	0
3	E	30	0	40	9	0
3	F	48	0	63	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	5	0	0	0	0
4	F	5	0	0	0	0
5	A	1035	0	0	51	0
5	B	1038	0	0	47	1
5	C	1037	0	0	38	0
5	D	1044	0	0	22	1
5	E	1033	0	0	42	0
5	F	1038	0	0	40	0
All	All	38975	0	32248	556	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 9.

The worst 5 of 556 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:C:292:ILE:HG22	1:C:293[B]:PHE:CD2	1.59	1.37
1:F:292:ILE:HG22	1:F:293[B]:PHE:CD2	1.59	1.37
1:B:425[B]:LEU:HD21	5:B:1629:HOH:O	1.24	1.35
1:A:685:PHE:CZ	5:B:1745:HOH:O	1.79	1.33
1:B:157[B]:THR:CG2	5:B:1655:HOH:O	1.76	1.32

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)
5:B:1586:HOH:O	5:D:1105:HOH:O[1_556]	2.14	0.06

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	696/692 (101%)	673 (97%)	23 (3%)	0	100	100
1	B	695/692 (100%)	675 (97%)	19 (3%)	1 (0%)	51	20
1	C	694/692 (100%)	670 (96%)	22 (3%)	2 (0%)	41	16
1	D	685/692 (99%)	665 (97%)	20 (3%)	0	100	100
1	E	684/692 (99%)	667 (98%)	17 (2%)	0	100	100
1	F	695/692 (100%)	672 (97%)	23 (3%)	0	100	100
All	All	4149/4152 (100%)	4022 (97%)	124 (3%)	3 (0%)	51	20

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	334	LEU
1	C	333	SER
1	C	334	LEU

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	605/594 (102%)	599 (99%)	6 (1%)	76	46
1	B	605/594 (102%)	601 (99%)	4 (1%)	84	60
1	C	603/594 (102%)	602 (100%)	1 (0%)	93	79
1	D	596/594 (100%)	591 (99%)	5 (1%)	81	56
1	E	595/594 (100%)	591 (99%)	4 (1%)	84	60
1	F	605/594 (102%)	601 (99%)	4 (1%)	84	60
All	All	3609/3564 (101%)	3585 (99%)	24 (1%)	86	60

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	329	THR
1	D	202	LYS

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Mol	Chain	Res	Type
1	F	333	SER
1	D	122[A]	CYS
1	D	122[B]	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	70	GLN
1	D	473	ASN
1	F	348	HIS
1	D	288	ASN
1	E	23	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 57 ligands modelled in this entry, 6 are monoatomic - leaving 51 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	$\# Z > 2$
3	GOL	E	804	-	5,5,5	0.30	0	5,5,5	0.83	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	F	804[B]	-	5,5,5	0.49	0	5,5,5	0.75	0
3	GOL	D	804	-	5,5,5	0.34	0	5,5,5	0.51	0
3	GOL	F	803	-	5,5,5	0.96	0	5,5,5	1.27	1 (20%)
3	GOL	B	808	-	5,5,5	0.62	0	5,5,5	1.51	2 (40%)
3	GOL	A	803[A]	-	5,5,5	0.51	0	5,5,5	0.65	0
3	GOL	A	803[B]	-	5,5,5	0.48	0	5,5,5	0.47	0
3	GOL	A	811	-	5,5,5	0.84	0	5,5,5	1.88	2 (40%)
3	GOL	C	807	-	5,5,5	0.54	0	5,5,5	0.53	0
3	GOL	D	805	-	5,5,5	1.02	0	5,5,5	3.75	4 (80%)
3	GOL	F	808	-	5,5,5	1.68	1 (20%)	5,5,5	0.93	0
3	GOL	C	803	-	5,5,5	0.31	0	5,5,5	0.89	0
3	GOL	D	803[A]	-	5,5,5	0.50	0	5,5,5	0.67	0
3	GOL	F	804[A]	-	5,5,5	0.46	0	5,5,5	0.52	0
3	GOL	E	803	-	5,5,5	0.64	0	5,5,5	1.32	1 (20%)
3	GOL	D	803[B]	-	5,5,5	0.38	0	5,5,5	0.50	0
3	GOL	B	805[A]	-	5,5,5	0.73	0	5,5,5	1.29	1 (20%)
3	GOL	B	803	-	5,5,5	0.65	0	5,5,5	0.63	0
3	GOL	C	805	-	5,5,5	0.34	0	5,5,5	0.76	0
3	GOL	C	808	-	5,5,5	0.61	0	5,5,5	0.91	0
3	GOL	C	806	-	5,5,5	0.36	0	5,5,5	0.95	0
3	GOL	B	806	-	5,5,5	0.64	0	5,5,5	1.03	0
3	GOL	B	805[B]	-	5,5,5	0.37	0	5,5,5	1.45	2 (40%)
3	GOL	F	809	-	5,5,5	0.71	0	5,5,5	0.80	0
3	GOL	A	804	-	5,5,5	0.53	0	5,5,5	0.80	0
4	PO4	C	804	-	4,4,4	1.17	0	6,6,6	2.40	4 (66%)
3	GOL	B	804	-	5,5,5	0.44	0	5,5,5	0.66	0
3	GOL	F	807	-	5,5,5	0.41	0	5,5,5	0.35	0
3	GOL	D	806	-	5,5,5	0.80	0	5,5,5	2.92	2 (40%)
3	GOL	E	805	-	5,5,5	0.29	0	5,5,5	0.51	0
3	GOL	A	806	-	5,5,5	0.30	0	5,5,5	0.85	0
3	GOL	B	802[B]	-	5,5,5	0.24	0	5,5,5	0.99	0
3	GOL	C	802	-	5,5,5	0.98	0	5,5,5	4.58	4 (80%)
3	GOL	B	802[A]	-	5,5,5	0.37	0	5,5,5	1.17	0
3	GOL	A	802[A]	-	5,5,5	0.82	0	5,5,5	1.02	0
3	GOL	A	802[B]	-	5,5,5	0.77	0	5,5,5	0.68	0
3	GOL	F	805	-	5,5,5	0.41	0	5,5,5	0.78	0
3	GOL	C	810	-	5,5,5	0.39	0	5,5,5	0.97	0
3	GOL	A	810	-	5,5,5	1.26	1 (20%)	5,5,5	0.57	0
3	GOL	B	807	-	5,5,5	1.39	1 (20%)	5,5,5	0.78	0
3	GOL	F	802	-	5,5,5	0.35	0	5,5,5	0.70	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	A	805	-	5,5,5	0.54	0	5,5,5	0.33	0
3	GOL	E	802	-	5,5,5	0.46	0	5,5,5	0.85	0
4	PO4	F	806	-	4,4,4	1.82	1 (25%)	6,6,6	2.71	3 (50%)
3	GOL	D	802	-	5,5,5	0.38	0	5,5,5	0.98	1 (20%)
3	GOL	E	806	-	5,5,5	0.60	0	5,5,5	2.93	2 (40%)
3	GOL	C	809	-	5,5,5	1.89	1 (20%)	5,5,5	1.21	0
3	GOL	B	809	-	5,5,5	0.85	0	5,5,5	1.11	0
3	GOL	A	807	-	5,5,5	1.32	1 (20%)	5,5,5	3.06	3 (60%)
3	GOL	A	808	-	5,5,5	0.43	0	5,5,5	0.50	0
3	GOL	A	809	-	5,5,5	0.52	0	5,5,5	1.04	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
3	GOL	E	804	-	-	0/4/4/4	-
3	GOL	F	804[B]	-	-	0/4/4/4	-
3	GOL	D	804	-	-	2/4/4/4	-
3	GOL	F	803	-	-	2/4/4/4	-
3	GOL	A	803[A]	-	-	2/4/4/4	-
3	GOL	A	803[B]	-	-	0/4/4/4	-
3	GOL	A	811	-	-	4/4/4/4	-
3	GOL	C	807	-	-	0/4/4/4	-
3	GOL	D	805	-	-	3/4/4/4	-
3	GOL	E	803	-	-	3/4/4/4	-
3	GOL	C	803	-	-	1/4/4/4	-
3	GOL	D	803[A]	-	-	2/4/4/4	-
3	GOL	F	804[A]	-	-	2/4/4/4	-
3	GOL	F	808	-	-	0/4/4/4	-
3	GOL	D	803[B]	-	-	2/4/4/4	-
3	GOL	B	805[A]	-	-	2/4/4/4	-
3	GOL	B	803	-	-	0/4/4/4	-
3	GOL	C	805	-	-	2/4/4/4	-
3	GOL	C	808	-	-	0/4/4/4	-
3	GOL	C	806	-	-	0/4/4/4	-
3	GOL	B	806	-	-	1/4/4/4	-
3	GOL	B	805[B]	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	F	809	-	-	0/4/4/4	-
3	GOL	A	804	-	-	0/4/4/4	-
3	GOL	B	808	-	-	2/4/4/4	-
3	GOL	B	804	-	-	2/4/4/4	-
3	GOL	F	807	-	-	2/4/4/4	-
3	GOL	D	806	-	-	2/4/4/4	-
3	GOL	E	805	-	-	2/4/4/4	-
3	GOL	A	806	-	-	0/4/4/4	-
3	GOL	B	802[B]	-	-	2/4/4/4	-
3	GOL	C	802	-	-	3/4/4/4	-
3	GOL	B	802[A]	-	-	2/4/4/4	-
3	GOL	A	802[A]	-	-	1/4/4/4	-
3	GOL	A	802[B]	-	-	4/4/4/4	-
3	GOL	F	805	-	-	2/4/4/4	-
3	GOL	C	810	-	-	2/4/4/4	-
3	GOL	A	810	-	-	0/4/4/4	-
3	GOL	B	807	-	-	0/4/4/4	-
3	GOL	F	802	-	-	0/4/4/4	-
3	GOL	A	805	-	-	0/4/4/4	-
3	GOL	E	802	-	-	1/4/4/4	-
3	GOL	D	802	-	-	0/4/4/4	-
3	GOL	E	806	-	-	2/4/4/4	-
3	GOL	C	809	-	-	0/4/4/4	-
3	GOL	B	809	-	-	0/4/4/4	-
3	GOL	A	807	-	-	2/4/4/4	-
3	GOL	A	808	-	-	0/4/4/4	-
3	GOL	A	809	-	-	2/4/4/4	-

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	809	GOL	O3-C3	-3.19	1.29	1.42
3	F	808	GOL	O1-C1	-3.00	1.29	1.42
3	A	807	GOL	O1-C1	-2.81	1.30	1.42
3	B	807	GOL	O1-C1	-2.35	1.32	1.42
3	A	810	GOL	O3-C3	-2.24	1.33	1.42

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	802	GOL	O2-C2-C1	-7.26	77.16	109.12
3	D	805	GOL	O2-C2-C3	-7.05	78.06	109.12
3	A	807	GOL	O1-C1-C2	-5.29	84.81	110.20
3	D	806	GOL	O2-C2-C3	-4.89	87.56	109.12
3	C	802	GOL	C3-C2-C1	-4.86	92.81	111.70

There are no chirality outliers.

5 of 63 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	804	GOL	C1-C2-C3-O3
3	A	811	GOL	C1-C2-C3-O3
3	D	805	GOL	O1-C1-C2-O2
3	D	805	GOL	C1-C2-C3-O3
3	F	804[A]	GOL	C1-C2-C3-O3

There are no ring outliers.

27 monomers are involved in 107 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	803	GOL	5	0
3	B	808	GOL	2	0
3	D	805	GOL	6	0
3	F	808	GOL	7	0
3	F	804[A]	GOL	1	0
3	D	803[B]	GOL	3	0
3	B	805[A]	GOL	4	0
3	C	808	GOL	1	0
3	C	806	GOL	1	0
3	B	806	GOL	5	0
3	B	805[B]	GOL	4	0
3	F	809	GOL	1	0
3	A	804	GOL	3	0
3	D	806	GOL	5	0
3	B	802[B]	GOL	2	0
3	C	802	GOL	1	0
3	A	802[A]	GOL	2	0
3	A	802[B]	GOL	3	0
3	A	810	GOL	8	0
3	B	807	GOL	10	0
3	F	802	GOL	2	0
3	E	802	GOL	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	806	GOL	7	0
3	C	809	GOL	6	0
3	B	809	GOL	2	0
3	A	807	GOL	11	0
3	A	809	GOL	3	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	666/692 (96%)	-0.77	10 (1%) 73 71	5, 8, 21, 44	8 (1%)
1	B	664/692 (95%)	-0.77	7 (1%) 80 78	5, 8, 20, 46	7 (1%)
1	C	666/692 (96%)	-0.77	5 (0%) 86 83	5, 8, 23, 49	11 (1%)
1	D	657/692 (94%)	-0.81	4 (0%) 89 87	5, 8, 20, 52	1 (0%)
1	E	656/692 (94%)	-0.83	2 (0%) 94 92	5, 8, 19, 38	2 (0%)
1	F	665/692 (96%)	-0.77	5 (0%) 86 83	5, 8, 23, 51	8 (1%)
All	All	3974/4152 (95%)	-0.79	33 (0%) 86 83	5, 8, 21, 52	37 (0%)

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	334	LEU	8.9
1	B	334	LEU	7.4
1	B	335	GLY	5.4
1	F	333	SER	5.3
1	F	672	VAL	4.8

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 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. 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
3	GOL	C	803	6/6	0.81	0.16	22,26,28,28	0
3	GOL	F	803	6/6	0.82	0.14	21,23,34,35	0
3	GOL	A	811	6/6	0.83	0.18	30,31,33,40	0
3	GOL	B	805[A]	6/6	0.85	0.24	11,22,25,29	6
3	GOL	B	805[B]	6/6	0.85	0.24	7,16,24,28	6
3	GOL	A	802[B]	6/6	0.85	0.15	17,20,24,26	6
3	GOL	A	802[A]	6/6	0.85	0.15	17,24,25,26	6
3	GOL	D	804	6/6	0.86	0.12	36,37,42,48	0
3	GOL	A	806	6/6	0.87	0.12	27,29,37,43	0
3	GOL	B	802[B]	6/6	0.87	0.15	17,20,23,23	6
3	GOL	B	802[A]	6/6	0.87	0.15	19,21,26,32	6
3	GOL	A	803[B]	6/6	0.87	0.13	13,19,22,25	6
3	GOL	A	803[A]	6/6	0.87	0.13	15,17,20,20	6
3	GOL	E	803	6/6	0.88	0.13	21,24,26,28	0
3	GOL	F	804[A]	6/6	0.89	0.15	12,18,20,24	6
3	GOL	F	804[B]	6/6	0.89	0.15	16,22,24,29	6
3	GOL	A	809	6/6	0.89	0.14	18,23,38,40	0
3	GOL	E	806	6/6	0.90	0.20	11,27,30,31	0
3	GOL	B	808	6/6	0.90	0.12	25,30,33,37	0
3	GOL	C	805	6/6	0.90	0.14	25,32,38,43	0
3	GOL	E	805	6/6	0.91	0.10	22,23,25,34	0
3	GOL	C	802	6/6	0.91	0.10	19,24,29,35	0
3	GOL	F	807	6/6	0.92	0.09	40,41,43,46	0
3	GOL	E	804	6/6	0.92	0.12	32,35,37,43	0
3	GOL	F	805	6/6	0.92	0.12	34,36,42,48	0
3	GOL	E	802	6/6	0.93	0.14	14,18,20,29	0
3	GOL	B	806	6/6	0.93	0.12	20,42,49,55	0
3	GOL	D	806	6/6	0.93	0.17	11,27,29,30	0
3	GOL	A	808	6/6	0.93	0.08	20,30,32,38	0
3	GOL	C	810	6/6	0.93	0.17	32,38,41,45	0
3	GOL	D	803[B]	6/6	0.94	0.12	13,25,26,35	6
3	GOL	D	802	6/6	0.94	0.11	14,19,21,28	0
3	GOL	A	804	6/6	0.94	0.13	20,32,40,40	0
3	GOL	C	809	6/6	0.94	0.13	10,16,20,21	0
3	GOL	D	803[A]	6/6	0.94	0.12	11,16,17,21	6
3	GOL	B	804	6/6	0.94	0.11	28,31,33,39	0
3	GOL	B	803	6/6	0.94	0.12	17,20,20,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	GOL	A	810	6/6	0.95	0.15	10,17,19,21	0
3	GOL	F	809	6/6	0.95	0.11	18,21,25,31	0
3	GOL	D	805	6/6	0.95	0.17	12,24,27,32	0
3	GOL	B	807	6/6	0.96	0.14	10,17,19,21	0
3	GOL	A	807	6/6	0.96	0.19	16,26,31,38	0
3	GOL	F	802	6/6	0.96	0.08	15,20,22,32	0
4	PO4	C	804	5/5	0.96	0.14	13,18,25,26	5
4	PO4	F	806	5/5	0.97	0.12	12,16,24,25	5
3	GOL	C	808	6/6	0.97	0.15	17,22,25,30	0
3	GOL	A	805	6/6	0.97	0.15	10,18,22,31	0
3	GOL	F	808	6/6	0.97	0.13	10,17,20,21	0
3	GOL	C	806	6/6	0.98	0.09	15,20,22,31	0
3	GOL	B	809	6/6	0.98	0.12	21,25,27,31	0
3	GOL	C	807	6/6	0.98	0.12	10,18,22,29	0
2	CO	A	801	1/1	1.00	0.03	8,8,8,8	1
2	CO	C	801	1/1	1.00	0.03	6,6,6,6	1
2	CO	F	801	1/1	1.00	0.04	6,6,6,6	1
2	CO	D	801	1/1	1.00	0.03	7,7,7,7	1
2	CO	E	801	1/1	1.00	0.02	7,7,7,7	1
2	CO	B	801	1/1	1.00	0.03	8,8,8,8	1

6.5 Other polymers ⓘ

There are no such residues in this entry.