WORLDWIDE wwPDB PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Sep 13, 2023 – 01:18 PM EDT

PDB ID	:	4QRN
Title	:	HIGH-RESOLUTION CRYSTAL STRUCTURE of 5-CARBOXYVANILLATE DECARBOXYLASE (TARGET EFI-505250) FROM NOVOSPHINGOBIUM AROMATICIVORANS DSM 12444 COMPLEXED WITH MANGANESE AND 4-HYDROXY-3-METHOXY-5-NITROBENZOIC ACID
Authors	:	Patskovsky, Y.; Vladimirova, A.; Toro, R.; Bhosle, R.; Gerlt, J.A.; Raushel, F.M.; Almo, S.C.
Deposited on	:	2014-07-01
Resolution	:	1.07 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:

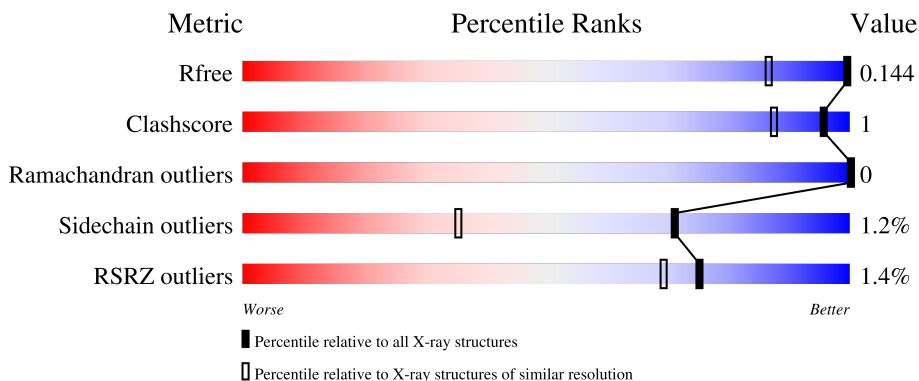|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)

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 1.07 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	Percentile Ranks	Value
Rfree		0.144
Clashscore		1
Ramachandran outliers		0
Sidechain outliers		1.2%
RSRZ outliers		1.4%

Worse ... *Better*

▌ Percentile relative to all X-ray structures

◨ Percentile relative to X-ray structures of similar resolution

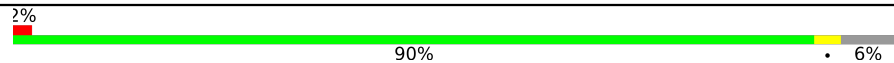| Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	1386 (1.12-1.04)
Clashscore	141614	1021 (1.10-1.06)
Ramachandran outliers	138981	1381 (1.12-1.04)
Sidechain outliers	138945	1379 (1.12-1.04)
RSRZ outliers	127900	1359 (1.12-1.04)

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 <=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	373	2% / 90% 5% 6%
1	B	373	% / 91% · 7%
1	C	373	% / 90% · 7%

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Ideal geometry (DNA, RNA)   :   Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) :   2.35.1

WORLDWIDE **wwPDB** PROTEIN DATA BANK

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Mol	Chain	Length	Quality of chain
1	D	373	

2 Entry composition ⓘ

There are 7 unique types of molecules in this entry. The entry contains 25095 atoms, of which 11402 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 5-Carboxyvanillate Decarboxylase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	352	Total	C	H	N	O	S	0	19	0
			5828	1860	2898	498	549	23			
1	B	348	Total	C	H	N	O	S	0	13	0
			5683	1823	2822	483	534	21			
1	C	348	Total	C	H	N	O	S	0	12	0
			5648	1815	2804	478	530	21			
1	D	350	Total	C	H	N	O	S	0	15	0
			5756	1839	2858	496	542	21			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	expression tag	UNP Q2GA79
A	-20	HIS	-	expression tag	UNP Q2GA79
A	-19	HIS	-	expression tag	UNP Q2GA79
A	-18	HIS	-	expression tag	UNP Q2GA79
A	-17	HIS	-	expression tag	UNP Q2GA79
A	-16	HIS	-	expression tag	UNP Q2GA79
A	-15	HIS	-	expression tag	UNP Q2GA79
A	-14	SER	-	expression tag	UNP Q2GA79
A	-13	SER	-	expression tag	UNP Q2GA79
A	-12	GLY	-	expression tag	UNP Q2GA79
A	-11	VAL	-	expression tag	UNP Q2GA79
A	-10	ASP	-	expression tag	UNP Q2GA79
A	-9	LEU	-	expression tag	UNP Q2GA79
A	-8	GLY	-	expression tag	UNP Q2GA79
A	-7	THR	-	expression tag	UNP Q2GA79
A	-6	GLU	-	expression tag	UNP Q2GA79
A	-5	ASN	-	expression tag	UNP Q2GA79
A	-4	LEU	-	expression tag	UNP Q2GA79
A	-3	TYR	-	expression tag	UNP Q2GA79
A	-2	PHE	-	expression tag	UNP Q2GA79
A	-1	GLN	-	expression tag	UNP Q2GA79

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| Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP Q2GA79
B	-21	MET	-	expression tag	UNP Q2GA79
B	-20	HIS	-	expression tag	UNP Q2GA79
B	-19	HIS	-	expression tag	UNP Q2GA79
B	-18	HIS	-	expression tag	UNP Q2GA79
B	-17	HIS	-	expression tag	UNP Q2GA79
B	-16	HIS	-	expression tag	UNP Q2GA79
B	-15	HIS	-	expression tag	UNP Q2GA79
B	-14	SER	-	expression tag	UNP Q2GA79
B	-13	SER	-	expression tag	UNP Q2GA79
B	-12	GLY	-	expression tag	UNP Q2GA79
B	-11	VAL	-	expression tag	UNP Q2GA79
B	-10	ASP	-	expression tag	UNP Q2GA79
B	-9	LEU	-	expression tag	UNP Q2GA79
B	-8	GLY	-	expression tag	UNP Q2GA79
B	-7	THR	-	expression tag	UNP Q2GA79
B	-6	GLU	-	expression tag	UNP Q2GA79
B	-5	ASN	-	expression tag	UNP Q2GA79
B	-4	LEU	-	expression tag	UNP Q2GA79
B	-3	TYR	-	expression tag	UNP Q2GA79
B	-2	PHE	-	expression tag	UNP Q2GA79
B	-1	GLN	-	expression tag	UNP Q2GA79
B	0	SER	-	expression tag	UNP Q2GA79
C	-21	MET	-	expression tag	UNP Q2GA79
C	-20	HIS	-	expression tag	UNP Q2GA79
C	-19	HIS	-	expression tag	UNP Q2GA79
C	-18	HIS	-	expression tag	UNP Q2GA79
C	-17	HIS	-	expression tag	UNP Q2GA79
C	-16	HIS	-	expression tag	UNP Q2GA79
C	-15	HIS	-	expression tag	UNP Q2GA79
C	-14	SER	-	expression tag	UNP Q2GA79
C	-13	SER	-	expression tag	UNP Q2GA79
C	-12	GLY	-	expression tag	UNP Q2GA79
C	-11	VAL	-	expression tag	UNP Q2GA79
C	-10	ASP	-	expression tag	UNP Q2GA79
C	-9	LEU	-	expression tag	UNP Q2GA79
C	-8	GLY	-	expression tag	UNP Q2GA79
C	-7	THR	-	expression tag	UNP Q2GA79
C	-6	GLU	-	expression tag	UNP Q2GA79
C	-5	ASN	-	expression tag	UNP Q2GA79
C	-4	LEU	-	expression tag	UNP Q2GA79
C	-3	TYR	-	expression tag	UNP Q2GA79

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	PHE	-	expression tag	UNP Q2GA79
C	-1	GLN	-	expression tag	UNP Q2GA79
C	0	SER	-	expression tag	UNP Q2GA79
D	-21	MET	-	expression tag	UNP Q2GA79
D	-20	HIS	-	expression tag	UNP Q2GA79
D	-19	HIS	-	expression tag	UNP Q2GA79
D	-18	HIS	-	expression tag	UNP Q2GA79
D	-17	HIS	-	expression tag	UNP Q2GA79
D	-16	HIS	-	expression tag	UNP Q2GA79
D	-15	HIS	-	expression tag	UNP Q2GA79
D	-14	SER	-	expression tag	UNP Q2GA79
D	-13	SER	-	expression tag	UNP Q2GA79
D	-12	GLY	-	expression tag	UNP Q2GA79
D	-11	VAL	-	expression tag	UNP Q2GA79
D	-10	ASP	-	expression tag	UNP Q2GA79
D	-9	LEU	-	expression tag	UNP Q2GA79
D	-8	GLY	-	expression tag	UNP Q2GA79
D	-7	THR	-	expression tag	UNP Q2GA79
D	-6	GLU	-	expression tag	UNP Q2GA79
D	-5	ASN	-	expression tag	UNP Q2GA79
D	-4	LEU	-	expression tag	UNP Q2GA79
D	-3	TYR	-	expression tag	UNP Q2GA79
D	-2	PHE	-	expression tag	UNP Q2GA79
D	-1	GLN	-	expression tag	UNP Q2GA79
D	0	SER	-	expression tag	UNP Q2GA79

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Mn 1	0	0
2	B	1	Total 1	Mn 1	0	0
2	C	1	Total 1	Mn 1	0	0
2	D	1	Total 1	Mn 1	0	0

- Molecule 3 is 4-hydroxy-3-methoxy-5-nitrobenzoic acid (three-letter code: 1DF) (formula: $C_8H_7NO_6$).
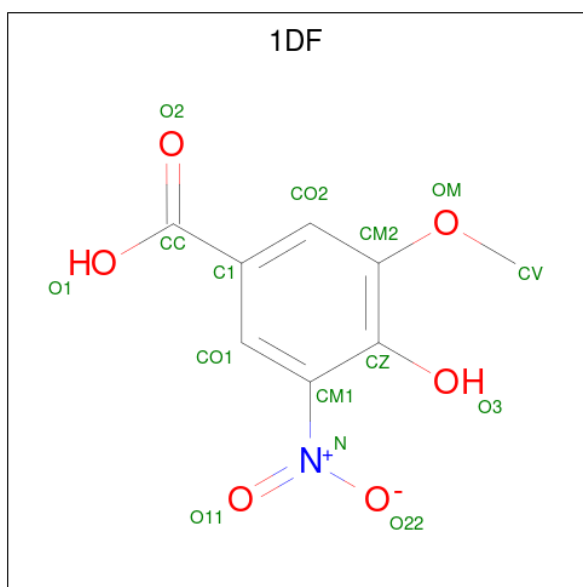
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	0
			20	8	5	1	6		
3	B	1	Total	C	H	N	O	0	0
			20	8	5	1	6		
3	C	1	Total	C	H	N	O	0	0
			20	8	5	1	6		
3	D	1	Total	C	H	N	O	0	0
			20	8	5	1	6		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

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

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total 3	Cl 3	0	0
5	B	1	Total 1	Cl 1	0	0
5	C	2	Total 2	Cl 2	0	0
5	D	2	Total 2	Cl 2	0	0

- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).
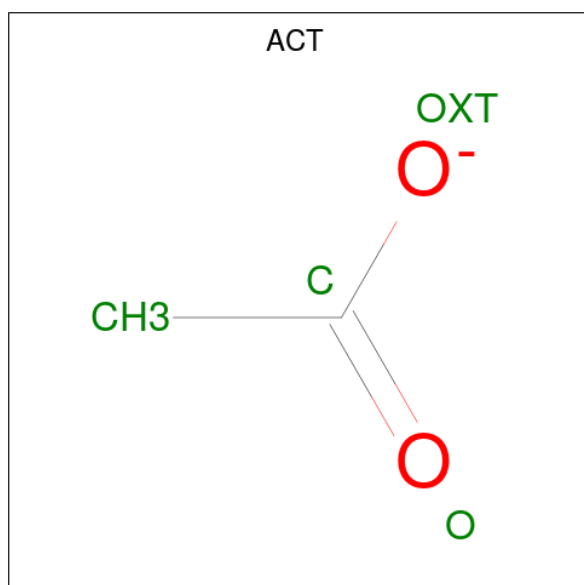
| Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total 4	C 2	O 2	0	0

- Molecule 7 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	558	Total 567	O 567	0	9
7	B	474	Total 480	O 480	0	5
7	C	517	Total 523	O 523	0	6
7	D	456	Total 460	O 460	0	4

3 Residue-property plots ⓘ

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.
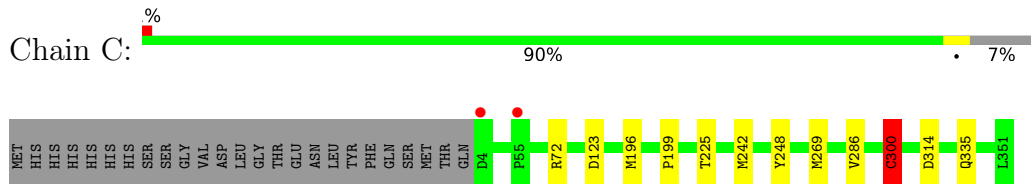
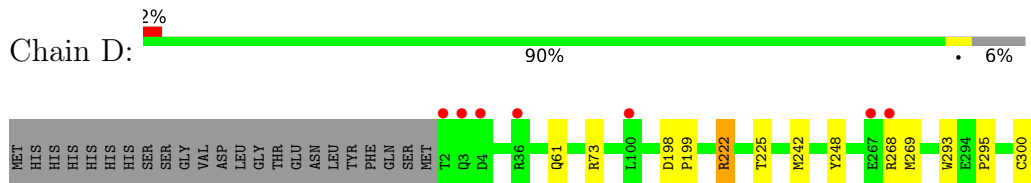- Molecule 1: 5-Carboxyvanillate Decarboxylase
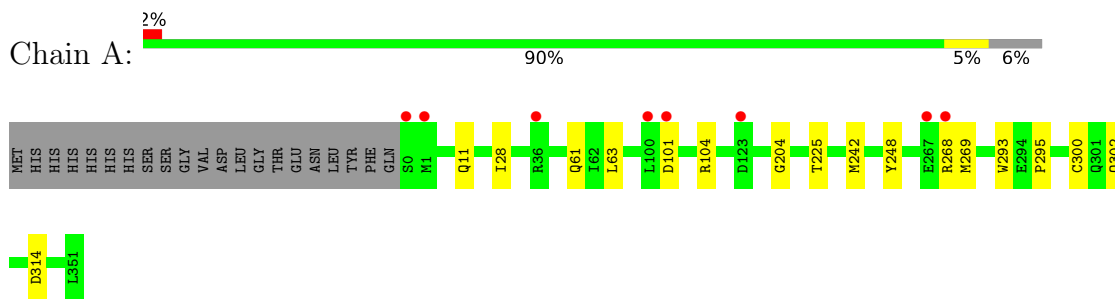
- Molecule 1: 5-Carboxyvanillate Decarboxylase
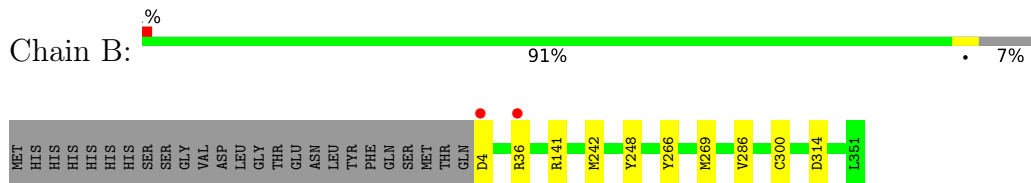
- Molecule 1: 5-Carboxyvanillate Decarboxylase

- Molecule 1: 5-Carboxyvanillate Decarboxylase

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	92.72Å 60.75Å 130.52Å 90.00° 103.33° 90.00°	Depositor
Resolution (Å)	28.14 – 1.07 30.44 – 1.07	Depositor EDS
% Data completeness (in resolution range)	98.7 (28.14-1.07) 90.9 (30.44-1.07)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$<I/\sigma(I)>$ [1]	1.53 (at 1.07Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.135 , 0.155 0.127 , 0.144	Depositor DCC
R_{free} test set	12448 reflections (2.03%)	wwPDB-VP
Wilson B-factor (Å^2)	7.8	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.50 , 59.7	EDS
L-test for twinning[2]	$<|L|>=0.50$, $<L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.98	EDS
Total number of atoms	25095	wwPDB-VP
Average B, all atoms (Å^2)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.68 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.4254e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $<|L|>$, $<L^2>$ 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: CL, 1DF, GOL, ACT, MN

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	0.49	0/3031	0.74	0/4090
1	B	0.56	4/2952 (0.1%)	0.75	0/3988
1	C	0.53	3/2938 (0.1%)	0.77	3/3970 (0.1%)
1	D	0.45	0/2985	0.75	5/4029 (0.1%)
All	All	0.51	7/11906 (0.1%)	0.76	8/16077 (0.0%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	286[A]	VAL	N-CA	7.11	1.60	1.46
1	B	286[B]	VAL	N-CA	7.11	1.60	1.46
1	C	123	ASP	CB-CG	6.92	1.66	1.51
1	C	300[A]	CYS	CB-SG	-6.13	1.71	1.82
1	C	300[B]	CYS	CB-SG	-6.13	1.71	1.82
1	B	286[A]	VAL	CA-C	5.25	1.66	1.52
1	B	286[B]	VAL	CA-C	5.25	1.66	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	123	ASP	CB-CG-OD1	11.84	128.96	118.30
1	D	222[A]	ARG	NE-CZ-NH1	7.98	124.29	120.30
1	D	222[B]	ARG	NE-CZ-NH1	7.98	124.29	120.30
1	C	123	ASP	CB-CG-OD2	-6.90	112.09	118.30
1	D	222[A]	ARG	NE-CZ-NH2	-6.78	116.91	120.30
1	D	222[B]	ARG	NE-CZ-NH2	-6.78	116.91	120.30
1	C	196	MET	CG-SD-CE	-5.95	90.68	100.20
1	D	73	ARG	NE-CZ-NH2	-5.40	117.60	120.30

There are no chirality outliers.

There are no planarity outliers.

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	2930	2898	2912	11	0
1	B	2861	2822	2824	5	0
1	C	2844	2804	2811	6	0
1	D	2898	2858	2856	8	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
3	A	15	5	5	0	0
3	B	15	5	5	0	0
3	C	15	5	5	0	0
3	D	15	5	5	0	0
4	A	18	0	24	0	0
4	B	6	0	8	0	0
4	C	18	0	24	0	0
4	D	12	0	16	0	0
5	A	3	0	0	1	0
5	B	1	0	0	0	0
5	C	2	0	0	0	0
5	D	2	0	0	0	0
6	A	4	0	3	0	0
7	A	567	0	0	4	2
7	B	480	0	0	2	2
7	C	523	0	0	1	1
7	D	460	0	0	2	1
All	All	13693	11402	11498	25	3

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 1.

All (25) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101[A]:ASP:OD1	1:A:104:ARG:NH2	2.35	0.60
1:C:286[A]:VAL:HG21	1:C:300[A]:CYS:SG	2.41	0.60
1:C:248:TYR:OH	1:D:300[B]:CYS:SG	2.62	0.57
1:A:11[A]:GLN:H	1:A:11[A]:GLN:CD	2.09	0.55
1:A:269[A]:MET:HG2	7:A:1054:HOH:O	2.08	0.54
5:A:406:CL:CL	7:A:768:HOH:O	2.56	0.54
1:A:302:GLN:NE2	7:A:1000:HOH:O	2.42	0.52
1:C:335[B]:GLN:NE2	7:C:736:HOH:O	2.46	0.49
1:C:300[B]:CYS:SG	1:D:248:TYR:OH	2.72	0.48
1:B:36[B]:ARG:NH1	7:B:830:HOH:O	2.47	0.47
1:A:300[B]:CYS:SG	1:B:248:TYR:OH	2.69	0.47
1:A:61:GLN:HG2	7:A:991:HOH:O	2.15	0.46
1:D:269[B]:MET:HG2	7:D:956:HOH:O	2.16	0.46
1:A:248:TYR:OH	1:B:300[B]:CYS:SG	2.74	0.46
1:D:61:GLN:HG2	7:D:799:HOH:O	2.16	0.45
1:D:225:THR:HB	1:D:269[B]:MET:SD	2.57	0.44
1:A:28[B]:ILE:HD13	1:A:63:LEU:HD11	2.00	0.44
1:B:269[A]:MET:HB2	7:B:921[A]:HOH:O	2.17	0.44
1:A:225:THR:HB	1:A:269[A]:MET:SD	2.59	0.42
1:C:199:PRO:O	1:D:222[B]:ARG:NH1	2.52	0.42
1:A:293:TRP:CD1	1:A:295:PRO:HD2	2.55	0.42
1:C:225:THR:HB	1:C:269[B]:MET:SD	2.60	0.42
1:D:293:TRP:CD1	1:D:295:PRO:HD2	2.55	0.42
1:D:198:ASP:HB2	1:D:199:PRO:HD3	2.03	0.40
1:A:204:GLY:HA2	1:B:266:TYR:CE1	2.57	0.40

All (3) 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)
7:A:1009:HOH:O	7:B:933:HOH:O[2_647]	1.98	0.22
7:C:917:HOH:O	7:D:774:HOH:O[2_546]	2.10	0.10
7:A:969:HOH:O	7:B:872:HOH:O[2_757]	2.14	0.06

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	369/373 (99%)	361 (98%)	8 (2%)	0	100	100
1	B	359/373 (96%)	351 (98%)	8 (2%)	0	100	100
1	C	358/373 (96%)	348 (97%)	10 (3%)	0	100	100
1	D	363/373 (97%)	355 (98%)	8 (2%)	0	100	100
All	All	1449/1492 (97%)	1415 (98%)	34 (2%)	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	312/312 (100%)	307 (98%)	5 (2%)	62	24
1	B	302/312 (97%)	297 (98%)	5 (2%)	60	22
1	C	300/312 (96%)	294 (98%)	6 (2%)	55	17
1	D	305/312 (98%)	300 (98%)	5 (2%)	62	24
All	All	1219/1248 (98%)	1198 (98%)	21 (2%)	71	22

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	242	MET
1	A	268[A]	ARG
1	A	268[B]	ARG
1	A	314[A]	ASP
1	A	314[B]	ASP
1	B	4	ASP
1	B	141	ARG
1	B	242	MET
1	B	314[A]	ASP
1	B	314[B]	ASP

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Mol	Chain	Res	Type
1	C	72	ARG
1	C	242	MET
1	C	300[A]	CYS
1	C	300[B]	CYS
1	C	314[A]	ASP
1	C	314[B]	ASP
1	D	242	MET
1	D	268[A]	ARG
1	D	268[B]	ARG
1	D	314[A]	ASP
1	D	314[B]	ASP

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

Mol	Chain	Res	Type
1	B	302	GLN
1	C	258	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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 26 ligands modelled in this entry, 12 are monoatomic - leaving 14 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
4	GOL	A	403[A]	-	5,5,5	0.30	0	5,5,5	0.27	0
4	GOL	C	404	-	5,5,5	0.56	0	5,5,5	0.34	0
3	1DF	B	402	2	14,15,15	1.38	2 (14%)	16,21,21	1.13	1 (6%)
4	GOL	B	403	-	5,5,5	0.42	0	5,5,5	0.34	0
4	GOL	D	403[A]	-	5,5,5	0.36	0	5,5,5	0.18	0
3	1DF	A	402	2	14,15,15	1.46	3 (21%)	16,21,21	1.09	1 (6%)
3	1DF	D	402	2	14,15,15	1.51	3 (21%)	16,21,21	0.98	1 (6%)
3	1DF	C	402	2	14,15,15	1.45	3 (21%)	16,21,21	1.52	3 (18%)
4	GOL	C	403[A]	-	5,5,5	0.34	0	5,5,5	0.19	0
4	GOL	A	403[B]	-	5,5,5	0.30	0	5,5,5	0.32	0
6	ACT	A	408	-	3,3,3	0.71	0	3,3,3	1.20	0
4	GOL	A	404	-	5,5,5	0.42	0	5,5,5	0.53	0
4	GOL	D	403[B]	-	5,5,5	0.34	0	5,5,5	0.41	0
4	GOL	C	403[B]	-	5,5,5	0.38	0	5,5,5	0.23	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	A	403[A]	-	-	0/4/4/4	-
4	GOL	C	404	-	-	0/4/4/4	-
3	1DF	B	402	2	-	4/8/10/10	0/1/1/1
4	GOL	B	403	-	-	0/4/4/4	-
4	GOL	D	403[A]	-	-	0/4/4/4	-
3	1DF	A	402	2	-	4/8/10/10	0/1/1/1
3	1DF	D	402	2	-	4/8/10/10	0/1/1/1
3	1DF	C	402	2	-	4/8/10/10	0/1/1/1
4	GOL	C	403[A]	-	-	0/4/4/4	-
4	GOL	A	403[B]	-	-	0/4/4/4	-
4	GOL	A	404	-	-	0/4/4/4	-
4	GOL	D	403[B]	-	-	0/4/4/4	-
4	GOL	C	403[B]	-	-	0/4/4/4	-

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	402	1DF	CM1-N	2.80	1.50	1.45
3	A	402	1DF	CM1-N	2.79	1.50	1.45
3	A	402	1DF	O3-CZ	-2.76	1.30	1.37
3	C	402	1DF	CM1-N	2.75	1.50	1.45
3	D	402	1DF	O2-CC	2.66	1.30	1.22
3	B	402	1DF	CM1-N	2.65	1.50	1.45
3	D	402	1DF	O3-CZ	-2.55	1.31	1.37
3	C	402	1DF	CM2-CZ	-2.46	1.37	1.40
3	A	402	1DF	CO1-CM1	2.46	1.44	1.39
3	B	402	1DF	O2-CC	2.25	1.29	1.22
3	C	402	1DF	C1-CC	-2.00	1.45	1.49

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	402	1DF	O11-N-CM1	4.30	126.39	119.03
3	B	402	1DF	O11-N-CM1	2.86	123.92	119.03
3	C	402	1DF	OM-CM2-CZ	2.73	117.30	114.54
3	D	402	1DF	O11-N-CM1	2.21	122.81	119.03
3	C	402	1DF	O1-CC-C1	2.10	120.31	114.85
3	A	402	1DF	C1-CO1-CM1	-2.10	116.29	118.88

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	402	1DF	CO2-C1-CC-O1
3	A	402	1DF	CO1-C1-CC-O1
3	C	402	1DF	CO1-C1-CC-O1
3	D	402	1DF	CO1-C1-CC-O2
3	A	402	1DF	CO1-C1-CC-O2
3	B	402	1DF	CO2-C1-CC-O2
3	D	402	1DF	CO2-C1-CC-O2
3	B	402	1DF	CO1-C1-CC-O2
3	D	402	1DF	CO1-C1-CC-O1
3	A	402	1DF	CO2-C1-CC-O1
3	D	402	1DF	CO2-C1-CC-O1
3	B	402	1DF	CO2-C1-CC-O1
3	C	402	1DF	CO2-C1-CC-O2
3	B	402	1DF	CO1-C1-CC-O1
3	A	402	1DF	CO2-C1-CC-O2
3	C	402	1DF	CO1-C1-CC-O2

There are no ring outliers.

No monomer is involved in short contacts.

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(Å²)	Q<0.9
1	A	352/373 (94%)	-0.07	8 (2%)	60	54	6, 10, 20, 62	1 (0%)
1	B	348/373 (93%)	-0.13	2 (0%)	89	86	6, 10, 17, 58	0
1	C	348/373 (93%)	-0.09	2 (0%)	89	86	7, 11, 19, 63	0
1	D	350/373 (93%)	0.02	7 (2%)	65	58	7, 12, 24, 69	3 (0%)
All	All	1398/1492 (93%)	-0.07	19 (1%)	75	69	6, 10, 22, 69	4 (0%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	2	THR	4.8
1	B	4	ASP	4.1
1	D	4	ASP	4.1
1	C	4	ASP	3.9
1	A	1[A]	MET	3.7
1	D	36[A]	ARG	3.2
1	A	36[A]	ARG	3.0
1	D	100	LEU	2.9
1	D	268[A]	ARG	2.7
1	A	0	SER	2.7
1	C	55	PRO	2.6
1	A	267[A]	GLU	2.6
1	D	3	GLN	2.4
1	A	123[A]	ASP	2.3
1	D	267[A]	GLU	2.3
1	B	36[A]	ARG	2.2
1	A	101[A]	ASP	2.2
1	A	100	LEU	2.1
1	A	268[A]	ARG	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 monosaccharides 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
6	ACT	A	408	4/4	0.75	0.21	37,37,38,38	0
4	GOL	A	403[B]	6/6	0.96	0.13	8,12,13,13	6
4	GOL	A	403[A]	6/6	0.96	0.13	12,16,18,18	6
4	GOL	C	403[A]	6/6	0.97	0.13	11,14,16,16	6
4	GOL	C	403[B]	6/6	0.97	0.13	10,15,16,17	6
4	GOL	D	403[A]	6/6	0.97	0.12	14,18,19,19	6
4	GOL	D	403[B]	6/6	0.97	0.12	12,16,18,19	6
4	GOL	B	403	6/6	0.97	0.13	9,14,17,21	0
4	GOL	C	404	6/6	0.98	0.10	12,14,15,15	0
5	CL	C	406	1/1	0.98	0.06	30,30,30,30	0
4	GOL	A	404	6/6	0.98	0.11	12,13,14,14	0
3	1DF	D	402	15/15	0.99	0.10	8,9,13,13	0
3	1DF	A	402	15/15	0.99	0.09	6,8,12,12	0
5	CL	A	405	1/1	0.99	0.06	19,19,19,19	1
5	CL	A	406	1/1	0.99	0.09	27,27,27,27	0
5	CL	A	407	1/1	0.99	0.08	22,22,22,22	0
5	CL	B	404	1/1	0.99	0.04	21,21,21,21	1
5	CL	C	405	1/1	0.99	0.08	30,30,30,30	0
3	1DF	B	402	15/15	0.99	0.10	7,8,13,13	0
5	CL	D	404	1/1	0.99	0.09	25,25,25,25	0
5	CL	D	405	1/1	0.99	0.07	24,24,24,24	0
3	1DF	C	402	15/15	0.99	0.09	8,9,13,14	0
2	MN	C	401	1/1	1.00	0.07	8,8,8,8	1
2	MN	D	401	1/1	1.00	0.06	8,8,8,8	1
2	MN	A	401	1/1	1.00	0.07	7,7,7,7	1
2	MN	B	401	1/1	1.00	0.07	7,7,7,7	1

6.5 Other polymers ⓘ

There are no such residues in this entry.