



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 03:42 am GMT

PDB ID : 4RUB
Title : A CRYSTAL FORM OF RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE(SLASH)OXYGENASE FROM NICOTIANA TABACUM IN THE ACTIVATED STATE
Authors : Schreuder, H.; Cascio, D.; Curmi, P.M.G.; Eisenberg, D.
Deposited on : 1990-05-25
Resolution : 2.70 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

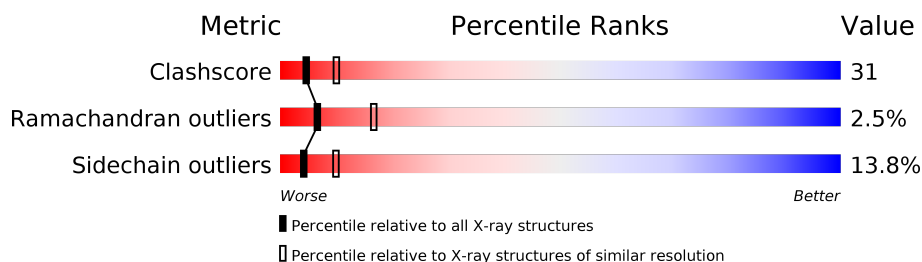
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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))
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	477	
1	B	477	
1	C	477	
1	D	477	
2	S	123	
2	T	123	
2	U	123	

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Mol	Chain	Length	Quality of chain
2	V	123	<div><div></div><div>27%</div><div>41%</div><div>25%</div><div>7%</div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 18708 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 RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE (FORM IV).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	465	Total	C	N	O	S	0	0	1
			3628	2307	641	664	16			
1	B	465	Total	C	N	O	S	0	0	1
			3628	2307	641	664	16			
1	C	465	Total	C	N	O	S	0	0	1
			3628	2307	641	664	16			
1	D	465	Total	C	N	O	S	0	0	1
			3628	2307	641	664	16			

- Molecule 2 is a protein called RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE (FORM IV).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	S	123	Total	C	N	O	S	0	0	0
			1024	669	163	186	6			
2	T	123	Total	C	N	O	S	0	0	0
			1024	669	163	186	6			
2	U	123	Total	C	N	O	S	0	0	0
			1024	669	163	186	6			
2	V	123	Total	C	N	O	S	0	0	0
			1024	669	163	186	6			

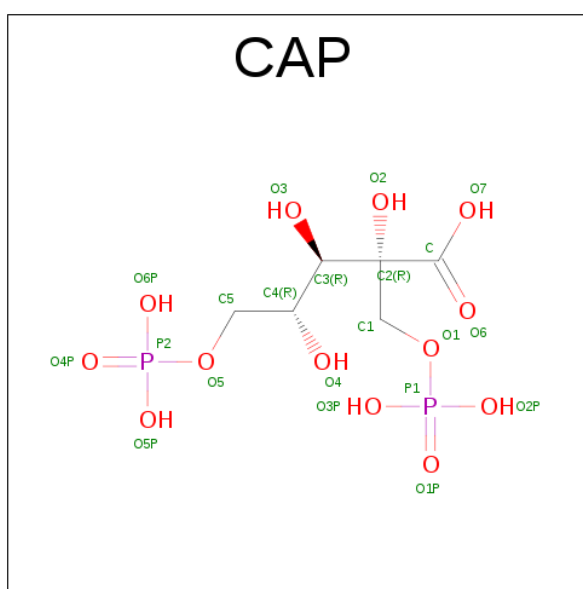
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	88	GLY	GLU	CONFLICT	UNP P69249
T	88	GLY	GLU	CONFLICT	UNP P69249
U	88	GLY	GLU	CONFLICT	UNP P69249
V	88	GLY	GLU	CONFLICT	UNP P69249

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

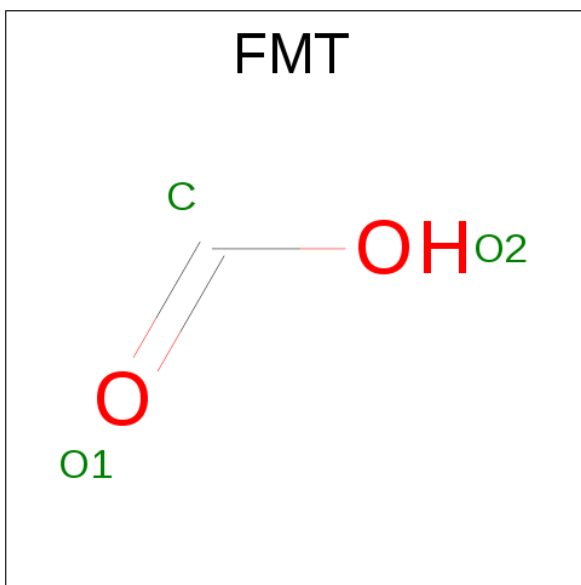
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0
3	A	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0

- Molecule 4 is 2-CARBOXYARABINITOL-1,5-DIPHOSPHATE (three-letter code: CAP) (formula: $C_6H_{14}O_{13}P_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O P 21 6 13 2	0	0
4	B	1	Total C O P 21 6 13 2	0	0
4	C	1	Total C O P 21 6 13 2	0	0
4	D	1	Total C O P 21 6 13 2	0	0

- Molecule 5 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2).



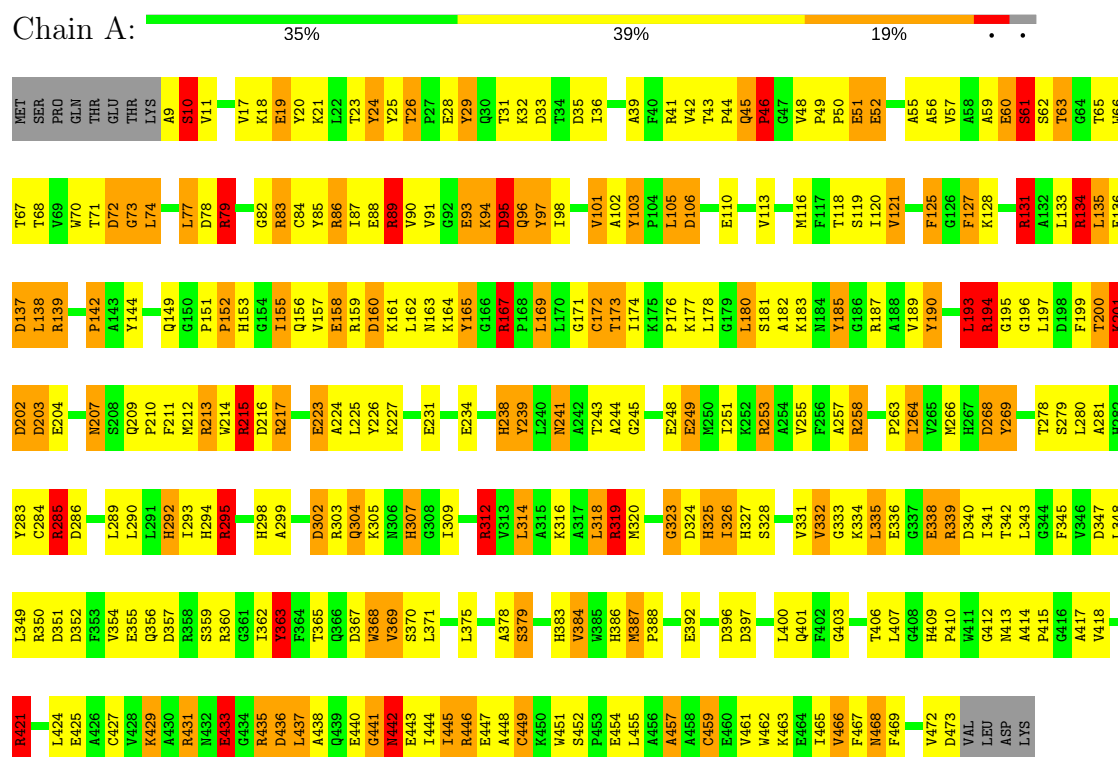
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			3	1	2		
5	B	1	Total	C	O	0	0
			3	1	2		
5	C	1	Total	C	O	0	0
			3	1	2		
5	D	1	Total	C	O	0	0
			3	1	2		

3 Residue-property plots

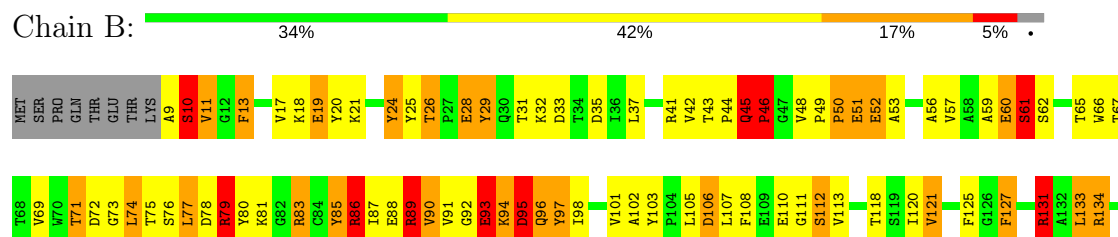
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

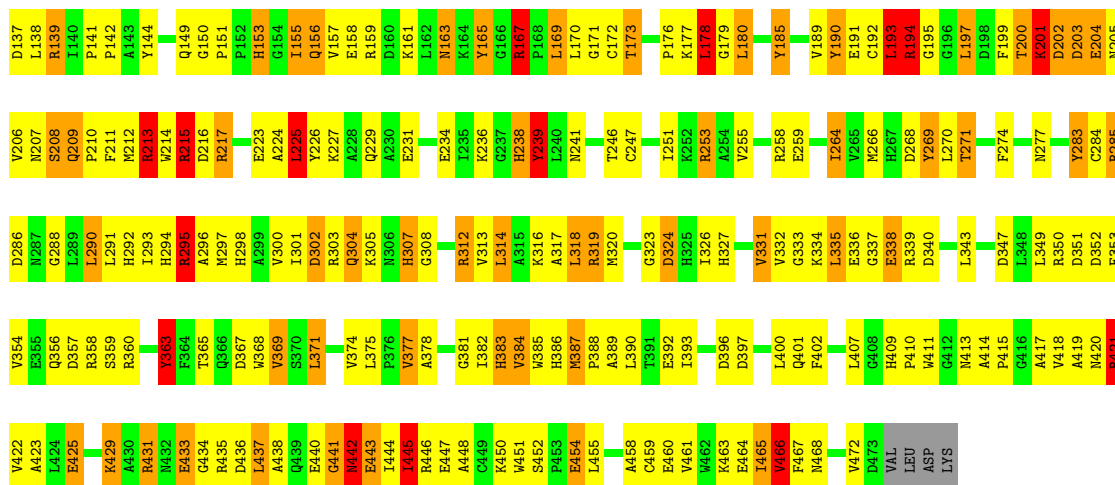
Note EDS was not executed.

- Molecule 1: RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE (FORM IV)



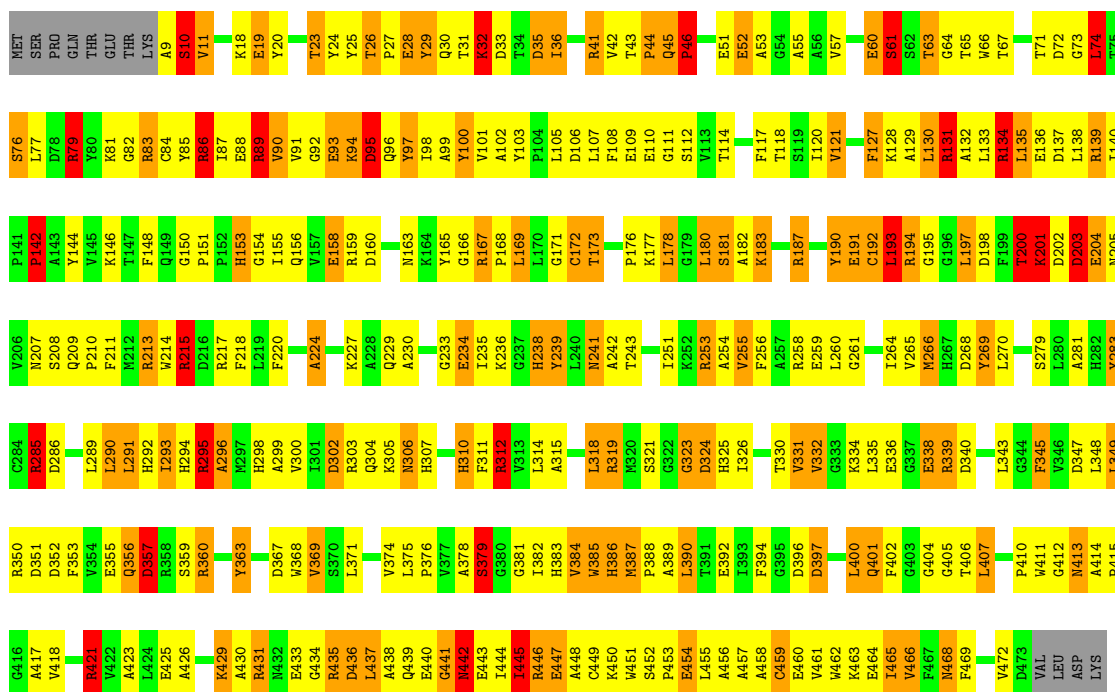
- Molecule 1: RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE (FORM IV)





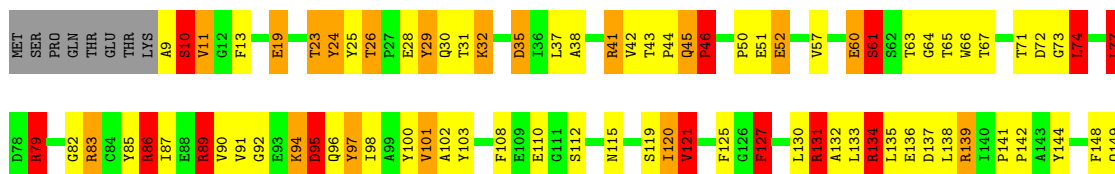
• Molecule 1: RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE (FORM IV)

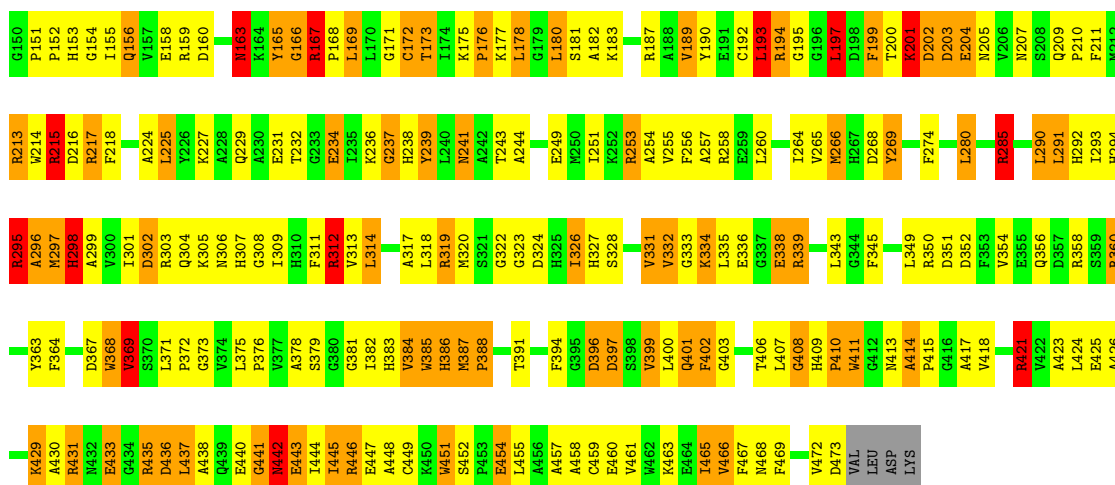
Chain C: 31% 41% 21% 5%



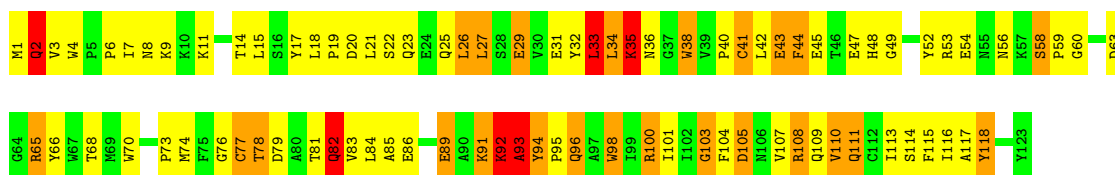
• Molecule 1: RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE (FORM IV)

Chain D: 36% 38% 18% 5%

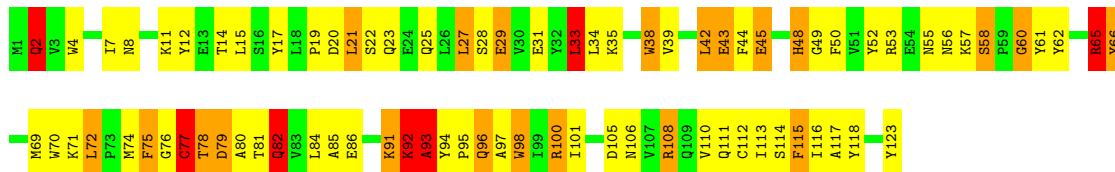




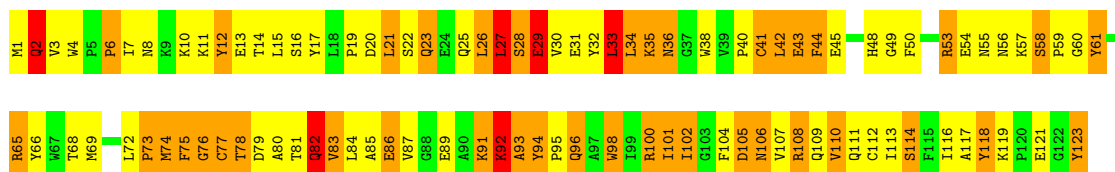
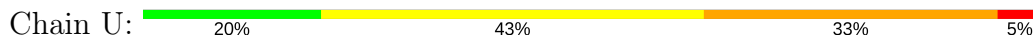
- Molecule 2: RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE (FORM IV)



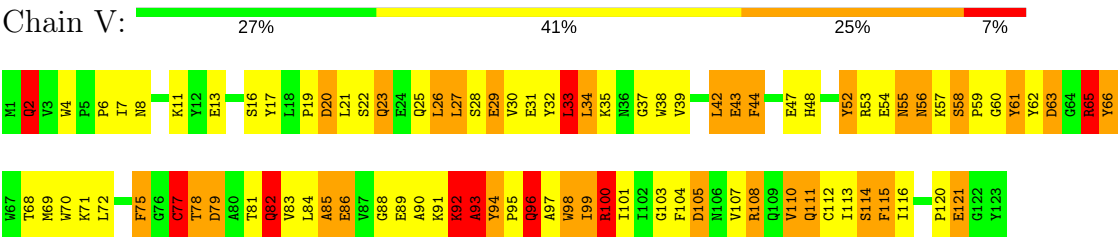
- Molecule 2: RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE (FORM IV)



- Molecule 2: RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE (FORM IV)



- Molecule 2: RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE (FORM IV)



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	204.60Å 204.60Å 117.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 2.70	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROFFT	Depositor
R, R_{free}	0.202 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	18708	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FMT, CAP, MG

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	1.69	30/3716 (0.8%)	2.59	253/5038 (5.0%)
1	B	1.66	24/3716 (0.6%)	2.57	227/5038 (4.5%)
1	C	1.75	46/3716 (1.2%)	2.66	253/5038 (5.0%)
1	D	1.69	39/3716 (1.0%)	2.60	235/5038 (4.7%)
2	S	1.57	8/1057 (0.8%)	2.51	71/1435 (4.9%)
2	T	1.48	3/1057 (0.3%)	2.25	56/1435 (3.9%)
2	U	1.79	13/1057 (1.2%)	2.53	70/1435 (4.9%)
2	V	1.70	14/1057 (1.3%)	2.50	80/1435 (5.6%)
All	All	1.68	177/19092 (0.9%)	2.57	1245/25892 (4.8%)

The worst 5 of 177 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	S	58	SER	CB-OG	-9.13	1.30	1.42
1	C	181	SER	CB-OG	8.99	1.53	1.42
1	C	323	GLY	N-CA	8.87	1.59	1.46
1	A	459	CYS	CB-SG	-8.49	1.67	1.82
1	A	134	ARG	CZ-NH1	8.02	1.43	1.33

The worst 5 of 1245 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	350	ARG	NE-CZ-NH2	-35.79	102.40	120.30
1	A	319	ARG	CD-NE-CZ	25.36	159.11	123.60
1	C	319	ARG	CD-NE-CZ	23.95	157.13	123.60
1	D	139	ARG	NE-CZ-NH1	-23.24	108.68	120.30
1	A	139	ARG	NE-CZ-NH2	23.20	131.90	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	3628	0	3559	200	0
1	B	3628	0	3558	225	1
1	C	3628	0	3556	246	1
1	D	3628	0	3557	242	0
2	S	1024	0	991	67	0
2	T	1024	0	991	85	0
2	U	1024	0	991	95	0
2	V	1024	0	991	93	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	21	0	6	2	0
4	B	21	0	5	0	0
4	C	21	0	6	1	0
4	D	21	0	6	3	0
5	A	3	0	0	1	0
5	B	3	0	0	0	0
5	C	3	0	0	1	0
5	D	3	0	0	1	0
All	All	18708	0	18217	1145	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 31.

The worst 5 of 1145 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:U:79:ASP:HB3	2:U:82:GLN:HE21	1.13	1.10
1:A:79:ARG:HG2	1:A:79:ARG:HH11	1.18	1.09
2:V:79:ASP:HB3	2:V:82:GLN:HE21	1.14	1.09
1:D:79:ARG:HH11	1:D:79:ARG:HG2	1.15	1.06
1:C:26:THR:HG22	1:C:29:TYR:HB2	1.37	1.05

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:446:ARG:NH2	1:C:30:GLN:NE2[3_654]	2.00	0.20

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	463/477 (97%)	402 (87%)	48 (10%)	13 (3%)	6	14
1	B	463/477 (97%)	399 (86%)	52 (11%)	12 (3%)	6	15
1	C	463/477 (97%)	388 (84%)	63 (14%)	12 (3%)	6	15
1	D	463/477 (97%)	400 (86%)	52 (11%)	11 (2%)	7	17
2	S	121/123 (98%)	104 (86%)	14 (12%)	3 (2%)	6	17
2	T	121/123 (98%)	102 (84%)	17 (14%)	2 (2%)	11	27
2	U	121/123 (98%)	99 (82%)	19 (16%)	3 (2%)	6	17
2	V	121/123 (98%)	100 (83%)	19 (16%)	2 (2%)	11	27
All	All	2336/2400 (97%)	1994 (85%)	284 (12%)	58 (2%)	6	17

5 of 58 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	46	PRO
1	A	95	ASP
1	A	167	ARG
2	S	93	ALA
1	B	46	PRO

5.3.2 Protein sidechains [i](#)

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	373/386 (97%)	326 (87%)	47 (13%)	5	12
1	B	373/386 (97%)	321 (86%)	52 (14%)	4	10
1	C	373/386 (97%)	322 (86%)	51 (14%)	4	10
1	D	373/386 (97%)	325 (87%)	48 (13%)	5	12
2	S	109/109 (100%)	94 (86%)	15 (14%)	4	10
2	T	109/109 (100%)	93 (85%)	16 (15%)	3	9
2	U	109/109 (100%)	91 (84%)	18 (16%)	2	7
2	V	109/109 (100%)	90 (83%)	19 (17%)	2	5
All	All	1928/1980 (97%)	1662 (86%)	266 (14%)	4	10

5 of 266 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	T	42	LEU
1	C	169	LEU
1	D	465	ILE
2	T	77	CYS
1	C	61	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
2	T	25	GLN
1	C	238	HIS
2	V	23	GLN
2	T	36	ASN
2	T	82	GLN

5.3.3 RNA ⓘ

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 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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	CAP	A	490	3	14,20,20	2.75	8 (57%)	17,31,31	4.28	9 (52%)
5	FMT	A	492	1,3	0,2,2	0.00	-	0,1,1	0.00	-
4	CAP	B	490	3	14,20,20	3.20	6 (42%)	17,31,31	4.65	9 (52%)
5	FMT	B	492	1,3	0,2,2	0.00	-	0,1,1	0.00	-
4	CAP	C	490	3	14,20,20	2.09	7 (50%)	17,31,31	5.12	10 (58%)
5	FMT	C	492	1,3	0,2,2	0.00	-	0,1,1	0.00	-
4	CAP	D	490	3	14,20,20	2.00	4 (28%)	17,31,31	4.89	8 (47%)
5	FMT	D	492	1,3	0,2,2	0.00	-	0,1,1	0.00	-

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	CAP	A	490	3	-	0/23/29/29	0/0/0/0
5	FMT	A	492	1,3	-	0/0/0/0	0/0/0/0
4	CAP	B	490	3	-	0/23/29/29	0/0/0/0
5	FMT	B	492	1,3	-	0/0/0/0	0/0/0/0
4	CAP	C	490	3	-	0/23/29/29	0/0/0/0
5	FMT	C	492	1,3	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	CAP	D	490	3	-	0/23/29/29	0/0/0/0
5	FMT	D	492	1,3	-	0/0/0/0	0/0/0/0

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	490	CAP	C5-C4	-6.84	1.41	1.51
4	B	490	CAP	O2-C2	-6.18	1.32	1.43
4	A	490	CAP	O2-C2	-5.59	1.33	1.43
4	D	490	CAP	O2-C2	-4.27	1.36	1.43
4	C	490	CAP	O2-C2	-3.71	1.37	1.43

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	490	CAP	C5-C4-C3	-14.64	81.95	112.05
4	D	490	CAP	C5-C4-C3	-13.06	85.20	112.05
4	B	490	CAP	C5-C4-C3	-11.72	87.95	112.05
4	A	490	CAP	C5-C4-C3	-11.46	88.49	112.05
4	B	490	CAP	P1-O1-C1	-4.83	104.98	118.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	490	CAP	2	0
5	A	492	FMT	1	0
4	C	490	CAP	1	0
5	C	492	FMT	1	0
4	D	490	CAP	3	0
5	D	492	FMT	1	0

5.7 Other polymers [i](#)

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 [i](#)

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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.