



wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2024 – 12:54 PM EDT

PDB ID : 1RLD
Title : SOLID-STATE PHASE TRANSITION IN THE CRYSTAL STRUCTURE OF RIBULOSE 1,5-BIPHOSPHATE CARBOXYLASE(SLASH)OXYGENASE
Authors : Zhang, K.Y.J.; Eisenberg, D.
Deposited on : 1993-12-10
Resolution : 2.50 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 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
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
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)	:	2.36.2

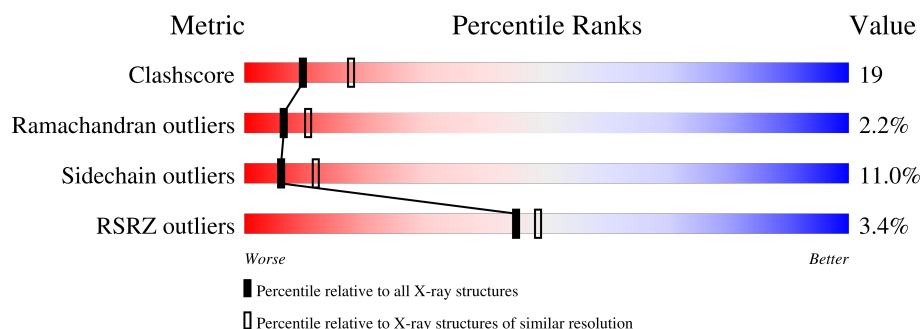
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	446	<div> <div>3%</div> <div> <div></div> <div>51%</div> <div>36%</div> <div>10%</div> <div>..</div> </div> </div>
1	B	446	<div> <div>4%</div> <div> <div></div> <div>50%</div> <div>37%</div> <div>10%</div> <div>..</div> </div> </div>
2	S	123	<div> <div>%</div> <div> <div></div> <div>49%</div> <div>35%</div> <div>13%</div> <div>.</div> </div> </div>
2	T	123	<div> <div>2%</div> <div> <div></div> <div>49%</div> <div>37%</div> <div>11%</div> <div>.</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8970 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 (LARGE CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	441	Total	C	N	O	S	0	0	0
			3456	2194	611	635	16			
1	B	441	Total	C	N	O	S	0	0	0
			3456	2194	611	635	16			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	229	GLU	GLN	conflict	UNP P00876
A	377	VAL	GLU	conflict	UNP P00876
B	229	GLU	GLN	conflict	UNP P00876
B	377	VAL	GLU	conflict	UNP P00876

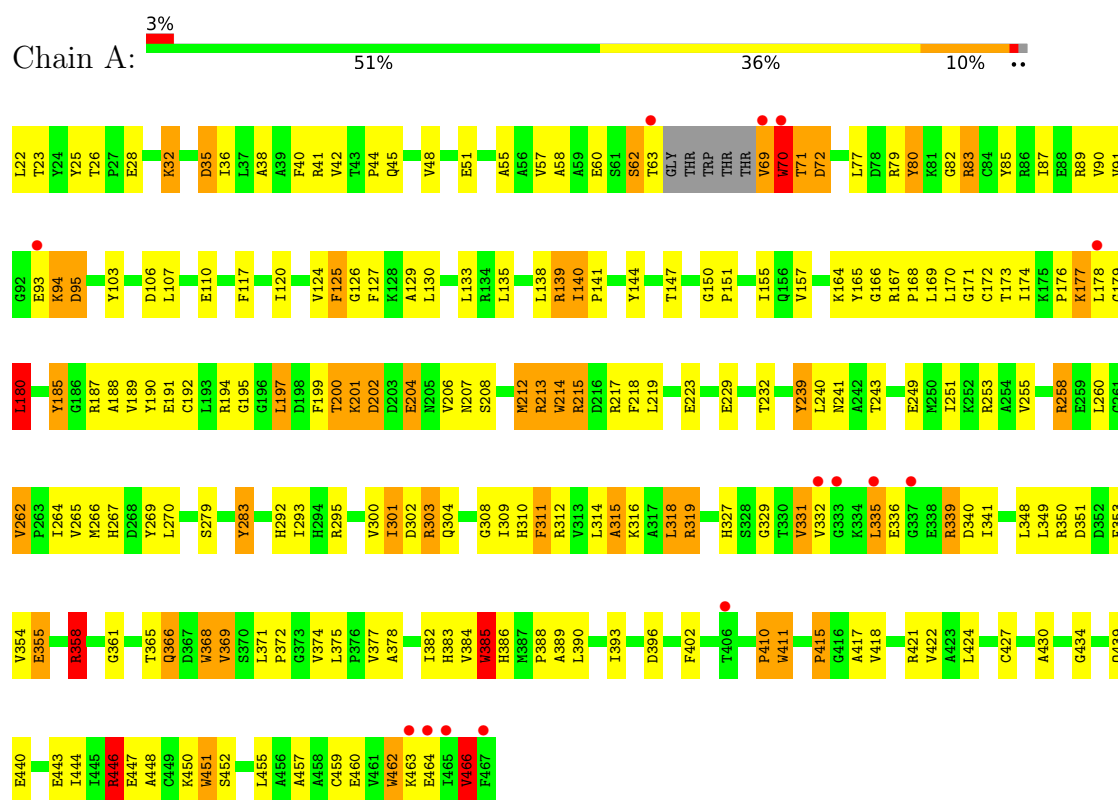
- Molecule 2 is a protein called RIBULOSE 1,5 BISPHOSPHATE CARBOXYLASE/OXYGENASE (SMALL CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	S	123	Total	C	N	O	S	0	0	0
			1029	672	163	188	6			
2	T	123	Total	C	N	O	S	0	0	0
			1029	672	163	188	6			

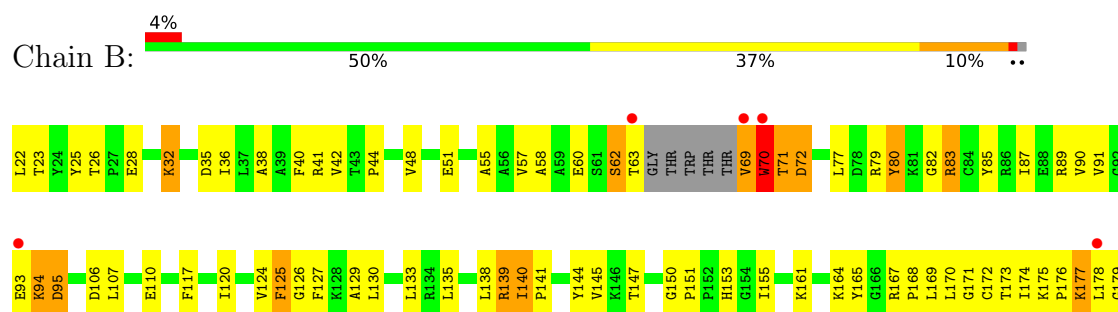
3 Residue-property plots [i](#)

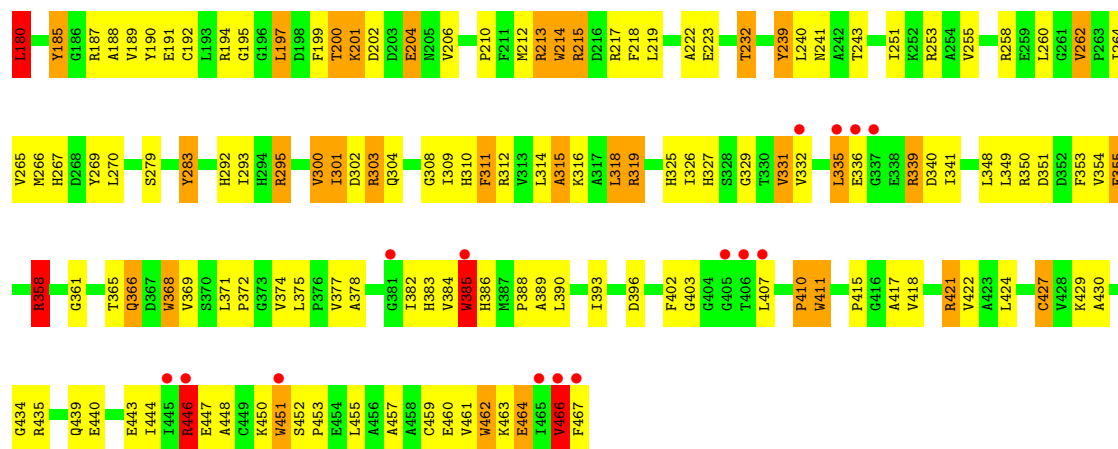
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: RIBULOSE 1,5 BISPHTHOSPHATE CARBOXYLASE/OXYGENASE (LARGE CHAIN)

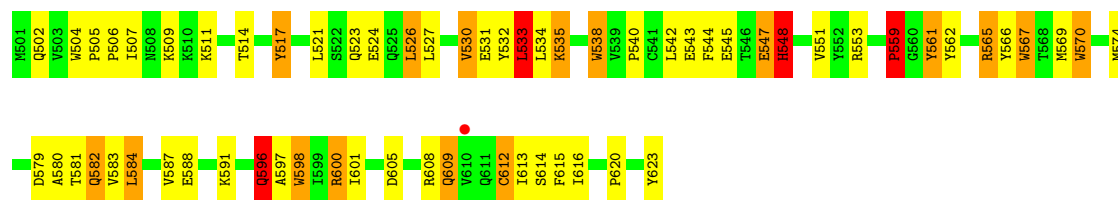


- Molecule 1: RIBULOSE 1,5 BISPHTHOSPHATE CARBOXYLASE/OXYGENASE (LARGE CHAIN)

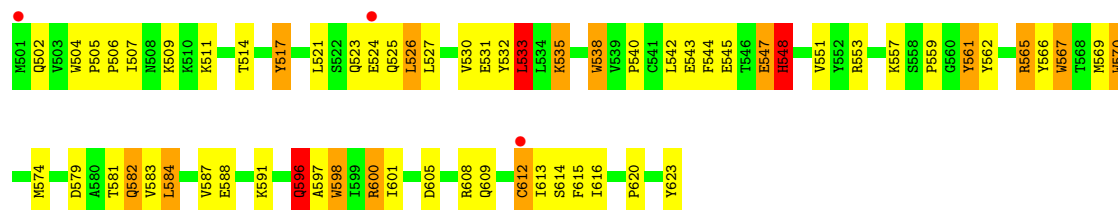




- Molecule 2: RIBULOSE 1,5 BISPHTHATE CARBOXYLASE/OXYGENASE (SMALL CHAIN)



- Molecule 2: RIBULOSE 1,5 BISPHTHATE CARBOXYLASE/OXYGENASE (SMALL CHAIN)



4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	153.01Å 153.01Å 113.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.50 19.53 – 2.48	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-2.50) 76.0 (19.53-2.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.90 (at 2.50Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.211 , (Not available) 0.231 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	32.3	Xtriage
Anisotropy	0.087	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 57.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.266 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8970	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% 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](#)

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	1.08	3/3539 (0.1%)	1.93	97/4796 (2.0%)
1	B	1.06	2/3539 (0.1%)	1.93	102/4796 (2.1%)
2	S	1.09	1/1062 (0.1%)	2.02	40/1442 (2.8%)
2	T	1.06	2/1062 (0.2%)	2.04	40/1442 (2.8%)
All	All	1.07	8/9202 (0.1%)	1.95	279/12476 (2.2%)

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
All	All	0	4

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	70	TRP	CB-CG	5.58	1.60	1.50
1	A	70	TRP	CB-CG	5.54	1.60	1.50
1	B	368	TRP	CD1-NE1	-5.53	1.28	1.38
2	T	538	TRP	CG-CD2	-5.51	1.34	1.43
1	A	229	GLU	CD-OE1	-5.34	1.19	1.25

The worst 5 of 279 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	S	565	ARG	NE-CZ-NH1	16.15	128.38	120.30
1	B	319	ARG	NE-CZ-NH1	16.05	128.33	120.30
1	A	215	ARG	NE-CZ-NH1	15.58	128.09	120.30
2	T	565	ARG	NE-CZ-NH1	15.26	127.93	120.30
1	B	215	ARG	NE-CZ-NH1	15.12	127.86	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	239	TYR	Sidechain
1	A	283	TYR	Sidechain
1	B	239	TYR	Sidechain
1	B	283	TYR	Sidechain

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	3456	0	3387	143	0
1	B	3456	0	3387	145	0
2	S	1029	0	991	39	0
2	T	1029	0	991	38	0
All	All	8970	0	8756	344	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 19.

The worst 5 of 344 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:B:463:LYS:HG2	1:B:466:VAL:HB	1.53	0.90
1:A:463:LYS:HG2	1:A:466:VAL:HB	1.51	0.90
2:T:521:LEU:HB2	2:T:526:LEU:HD12	1.51	0.90
1:B:151:PRO:HD2	1:B:372:PRO:HG2	1.54	0.89
2:S:521:LEU:HB2	2:S:526:LEU:HD12	1.53	0.87

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	439/446 (98%)	393 (90%)	36 (8%)	10 (2%)	6	10
1	B	439/446 (98%)	393 (90%)	35 (8%)	11 (2%)	5	8
2	S	121/123 (98%)	106 (88%)	13 (11%)	2 (2%)	9	16
2	T	121/123 (98%)	108 (89%)	11 (9%)	2 (2%)	9	16
All	All	1120/1138 (98%)	1000 (89%)	95 (8%)	25 (2%)	6	10

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	70	TRP
1	A	72	ASP
1	A	94	LYS
1	A	466	VAL
2	S	548	HIS

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	357/361 (99%)	320 (90%)	37 (10%)	7	13
1	B	357/361 (99%)	320 (90%)	37 (10%)	7	13
2	S	110/110 (100%)	95 (86%)	15 (14%)	3	7
2	T	110/110 (100%)	96 (87%)	14 (13%)	4	8
All	All	934/942 (99%)	831 (89%)	103 (11%)	6	12

5 of 103 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	63	THR
1	B	232	THR
2	T	596	GLN
1	B	71	THR
1	B	192	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	366	GLN
1	B	420	ASN
2	T	536	ASN
1	A	420	ASN
1	A	366	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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](#)

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	441/446 (98%)	0.03	14 (3%) 47 51	11, 25, 72, 101	0
1	B	441/446 (98%)	-0.07	20 (4%) 33 36	11, 25, 72, 101	0
2	S	123/123 (100%)	-0.02	1 (0%) 86 87	14, 38, 69, 84	0
2	T	123/123 (100%)	0.08	3 (2%) 59 62	14, 38, 69, 84	0
All	All	1128/1138 (99%)	-0.01	38 (3%) 45 48	11, 28, 71, 101	0

The worst 5 of 38 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	332	VAL	11.9
1	A	467	PHE	11.4
1	A	63	THR	7.9
1	A	465	ILE	7.0
1	B	467	PHE	6.9

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 monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.