



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 10:04 PM GMT

PDB ID : 1RSC  
Title : STRUCTURE OF AN EFFECTOR INDUCED INACTIVATED STATE OF  
RIBULOSE BISPHTHOSPHATE CARBOXYLASE(SLASH)OXYGENASE  
: THE BINARY COMPLEX BETWEEN ENZYME AND XYLULOSE BIS-  
PHOSPHATE  
Authors : Newman, J.; Gutteridge, S.  
Deposited on : 1994-03-29  
Resolution : 2.30 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](mailto: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.

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

MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	<b>NOT EXECUTED</b>
EDS	:	<b>NOT EXECUTED</b>
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

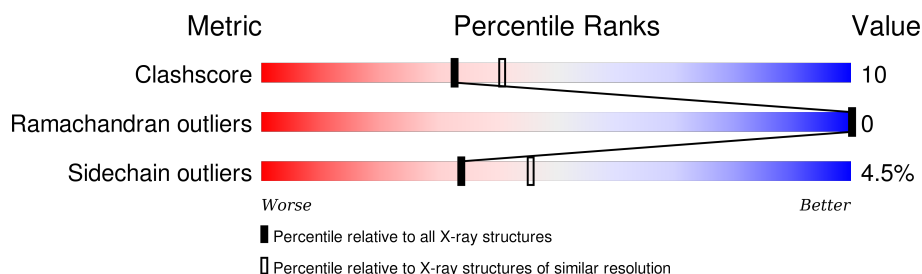
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)










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  $\geq 3$ , 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	472	
1	B	472	
1	C	472	
1	D	472	
1	E	472	
1	F	472	
1	G	472	

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Mol	Chain	Length	Quality of chain
1	H	472	 73%23%...
2	I	111	 77%22%.
2	J	111	 76%23%.
2	K	111	 79%19%.
2	L	111	 77%22%.
2	M	111	 74%24%.
2	N	111	 79%19%.
2	O	111	 74%24%.
2	P	111	 75%23%.

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 36846 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 BISPHTHOSPHATE CARBOXYLASE/OXYGENASE (LARGE CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	467	Total	C	N	O	S	72	0	0
			3653	2324	638	673	18			
1	B	467	Total	C	N	O	S	72	0	0
			3653	2324	638	673	18			
1	C	467	Total	C	N	O	S	72	0	0
			3653	2324	638	673	18			
1	D	467	Total	C	N	O	S	72	0	0
			3653	2324	638	673	18			
1	E	467	Total	C	N	O	S	72	0	0
			3653	2324	638	673	18			
1	F	467	Total	C	N	O	S	72	0	0
			3653	2324	638	673	18			
1	G	467	Total	C	N	O	S	72	0	0
			3653	2324	638	673	18			
1	H	467	Total	C	N	O	S	72	0	0
			3653	2324	638	673	18			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	109	Total	C	N	O	S	58	0	0
			909	583	154	165	7			
2	I	109	Total	C	N	O	S	58	0	0
			909	583	154	165	7			
2	N	109	Total	C	N	O	S	58	0	0
			909	583	154	165	7			
2	J	109	Total	C	N	O	S	58	0	0
			909	583	154	165	7			
2	O	109	Total	C	N	O	S	58	0	0
			909	583	154	165	7			

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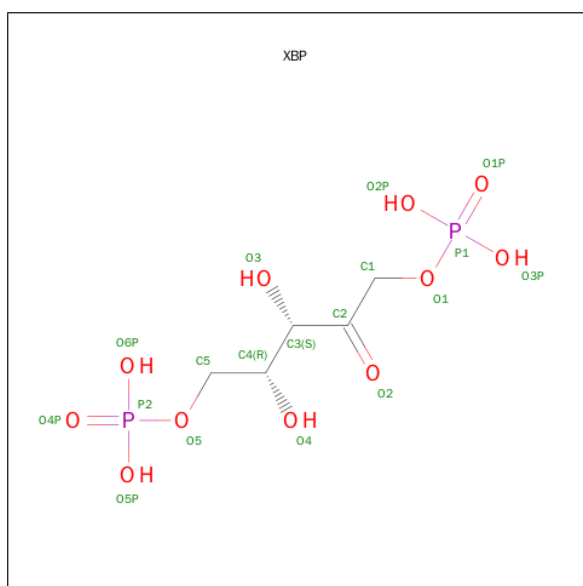
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	K	109	Total	C	N	O	S	58	0	0
			909	583	154	165	7			
2	P	109	Total	C	N	O	S	58	0	0
			909	583	154	165	7			
2	L	109	Total	C	N	O	S	58	0	0
			909	583	154	165	7			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	109	GLU	GLN	CONFLICT	UNP P04716
I	109	GLU	GLN	CONFLICT	UNP P04716
N	109	GLU	GLN	CONFLICT	UNP P04716
J	109	GLU	GLN	CONFLICT	UNP P04716
O	109	GLU	GLN	CONFLICT	UNP P04716
K	109	GLU	GLN	CONFLICT	UNP P04716
P	109	GLU	GLN	CONFLICT	UNP P04716
L	109	GLU	GLN	CONFLICT	UNP P04716

- Molecule 3 is SUGAR (XYLULOSE-1,5-BISPHOSPHATE) (three-letter code: XBP) (formula: C<sub>5</sub>H<sub>12</sub>O<sub>11</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			18	5	11	2		
3	B	1	Total	C	O	P	0	0
			18	5	11	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total	C	O	P	0	0
			18	5	11	2		
3	D	1	Total	C	O	P	0	0
			18	5	11	2		
3	E	1	Total	C	O	P	0	0
			18	5	11	2		
3	F	1	Total	C	O	P	0	0
			18	5	11	2		
3	G	1	Total	C	O	P	0	0
			18	5	11	2		
3	H	1	Total	C	O	P	0	0
			18	5	11	2		

- Molecule 4 is water.

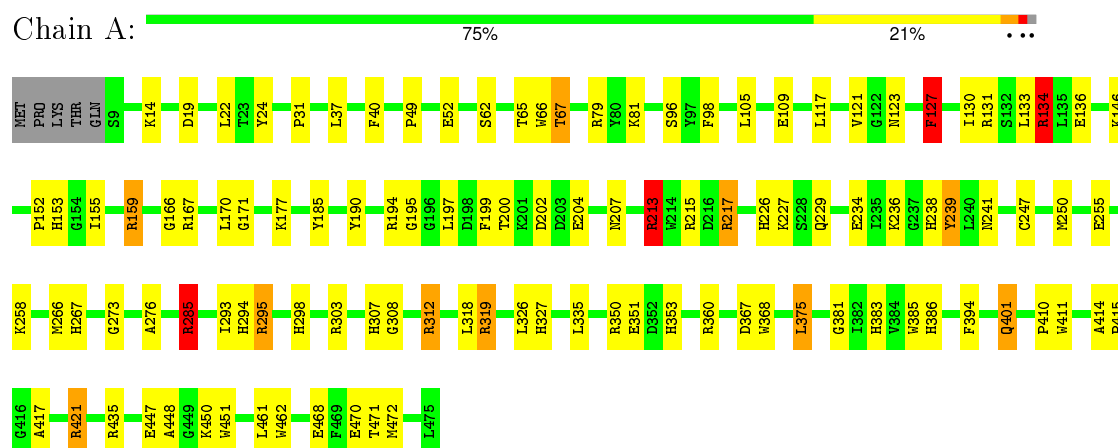
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	148	Total	O	0	0
			148	148		
4	B	9	Total	O	0	0
			9	9		
4	C	8	Total	O	0	0
			8	8		
4	D	4	Total	O	0	0
			4	4		
4	G	1	Total	O	0	0
			1	1		
4	J	1	Total	O	0	0
			1	1		
4	M	35	Total	O	0	0
			35	35		

### 3 Residue-property plots

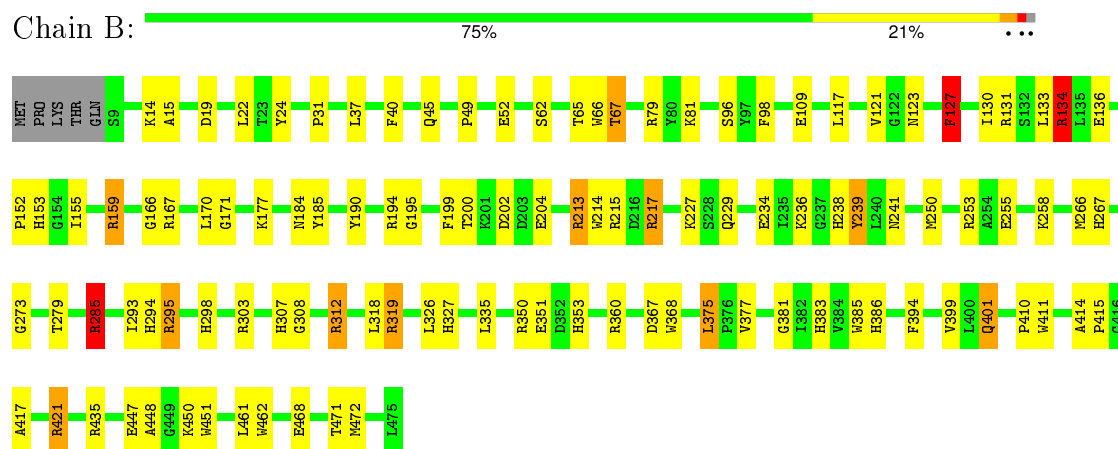
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 BISPHTHOSPHATE CARBOXYLASE/OXYGENASE (LARGE CHAIN)



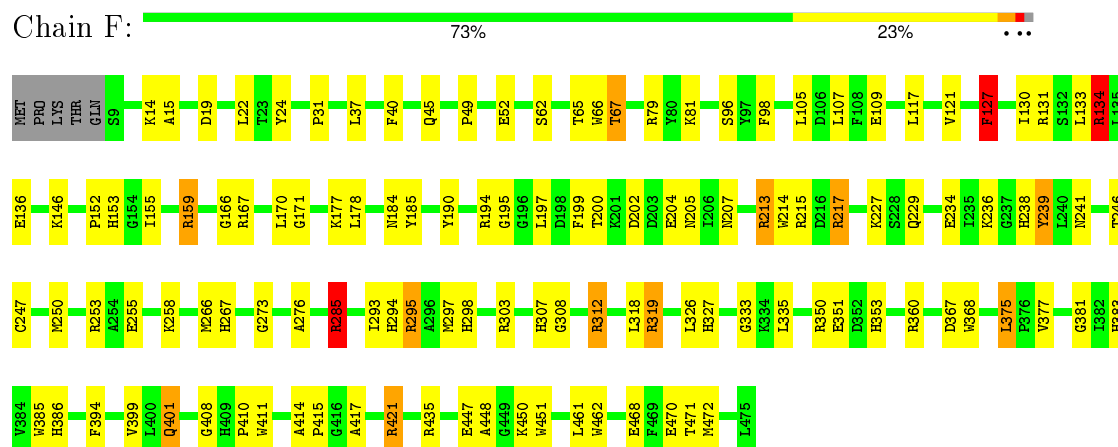
- Molecule 1: RIBULOSE 1,5 BISPHTHOSPHATE CARBOXYLASE/OXYGENASE (LARGE CHAIN)



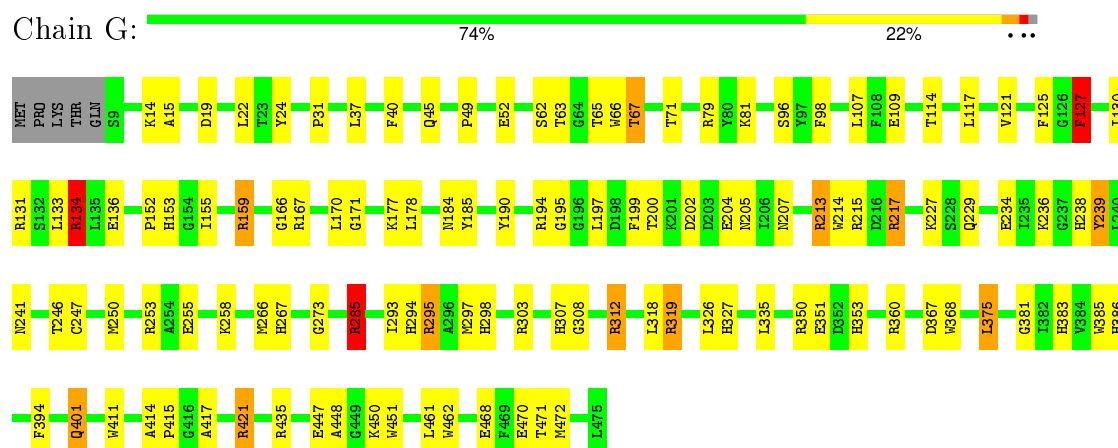
- Molecule 1: RIBULOSE 1,5 BISPHTHOSPHATE CARBOXYLASE/OXYGENASE (LARGE CHAIN)



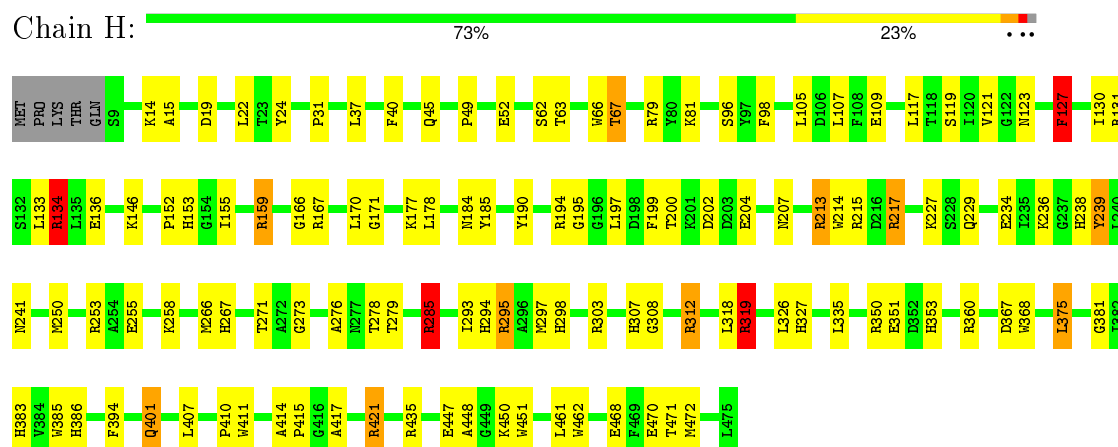




- Molecule 1: RIBULOSE 1,5 BISPHTHOSPHATE CARBOXYLASE/OXYGENASE (LARGE CHAIN)



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



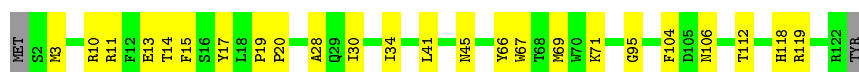
- Molecule 2: RIBULOSE 1,5 BISPHTHOSPHATE CARBOXYLASE/OXYGENASE (SMALL CHAIN)

Chain M:  74% 24%




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

Chain I:  77% 22%



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

Chain N:  79% 19%



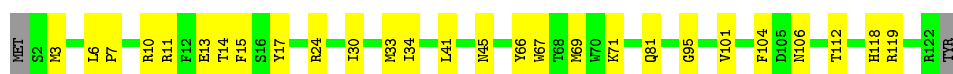
- Molecule 2: RIBULOSE 1,5 BISPHOSPHATE CARBOXYLASE/OXYGENASE (SMALL CHAIN)

Chain J:  76% 23%




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

Chain O:  74% 24%



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

Chain K:  79% 19%



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

Chain P:  75% 23%



● Molecule 2: RIBULOSE 1,5 BISPHOSPHATE CARBOXYLASE/OXYGENASE (SMALL CHAIN)



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	224.40Å 112.60Å 200.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.30	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.30)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.255 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	36846	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	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: XBP

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	0.32	1/3745 (0.0%)	0.51	1/5071 (0.0%)
1	B	0.32	1/3745 (0.0%)	0.51	1/5071 (0.0%)
1	C	0.32	1/3745 (0.0%)	0.52	1/5071 (0.0%)
1	D	0.32	1/3745 (0.0%)	0.51	1/5071 (0.0%)
1	E	0.32	1/3745 (0.0%)	0.52	1/5071 (0.0%)
1	F	0.32	1/3745 (0.0%)	0.52	1/5071 (0.0%)
1	G	0.32	1/3745 (0.0%)	0.52	1/5071 (0.0%)
1	H	0.32	1/3745 (0.0%)	0.51	1/5071 (0.0%)
2	I	0.30	0/936	0.46	0/1267
2	J	0.30	0/936	0.46	0/1267
2	K	0.30	0/936	0.46	0/1267
2	L	0.30	0/936	0.46	0/1267
2	M	0.30	0/936	0.46	0/1267
2	N	0.30	0/936	0.46	0/1267
2	O	0.30	0/936	0.47	0/1267
2	P	0.31	0/936	0.47	0/1267
All	All	0.32	8/37448 (0.0%)	0.51	8/50704 (0.0%)

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	9
1	B	0	9
1	C	0	9
1	D	0	9
1	E	0	9
1	F	0	9
1	G	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	H	0	9
2	I	0	1
2	J	0	1
2	K	0	1
2	L	0	1
2	M	0	1
2	N	0	1
2	O	0	1
2	P	0	1
All	All	0	80

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	127	PHE	CA-CB	-6.84	1.39	1.53
1	H	127	PHE	CA-CB	-6.76	1.39	1.53
1	C	127	PHE	CA-CB	-6.76	1.39	1.53
1	A	127	PHE	CA-CB	-6.75	1.39	1.53
1	B	127	PHE	CA-CB	-6.75	1.39	1.53

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	217	ARG	NE-CZ-NH2	-5.57	117.51	120.30
1	B	217	ARG	NE-CZ-NH2	-5.57	117.52	120.30
1	D	217	ARG	NE-CZ-NH2	-5.54	117.53	120.30
1	E	217	ARG	NE-CZ-NH2	-5.53	117.53	120.30
1	H	217	ARG	NE-CZ-NH2	-5.52	117.54	120.30

There are no chirality outliers.

5 of 80 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	134	ARG	Sidechain
1	A	159	ARG	Sidechain
1	A	194	ARG	Sidechain
1	A	213	ARG	Sidechain
1	A	217	ARG	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	3653	0	3568	93	0
1	B	3653	0	3568	90	0
1	C	3653	0	3568	88	1
1	D	3653	0	3568	82	0
1	E	3653	0	3568	102	0
1	F	3653	0	3568	105	0
1	G	3653	0	3568	113	0
1	H	3653	0	3568	117	0
2	I	909	0	860	14	1
2	J	909	0	860	15	1
2	K	909	0	860	11	30
2	L	909	0	860	14	0
2	M	909	0	860	16	1
2	N	909	0	860	13	0
2	O	909	0	860	16	30
2	P	909	0	860	16	0
3	A	18	0	8	2	0
3	B	18	0	8	2	0
3	C	18	0	8	2	0
3	D	18	0	8	2	0
3	E	18	0	8	2	0
3	F	18	0	8	1	0
3	G	18	0	8	1	0
3	H	18	0	8	2	0
4	A	148	0	0	3	0
4	B	9	0	0	0	0
4	C	8	0	0	0	0
4	D	4	0	0	0	0
4	G	1	0	0	0	0
4	J	1	0	0	0	0
4	M	35	0	0	1	0
All	All	36846	0	35488	721	32

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 10.

The worst 5 of 721 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:G:462:TRP:HE1	1:H:67:THR:HG21	1.07	1.17
1:E:462:TRP:HE1	1:F:67:THR:HG21	0.98	1.14
1:C:462:TRP:HE1	1:D:67:THR:HG21	1.12	1.14
1:G:67:THR:HG21	1:H:462:TRP:HE1	1.02	1.11
1:A:462:TRP:HE1	1:B:67:THR:HG21	1.01	1.09

The worst 5 of 32 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)
2:O:24:ARG:CZ	2:K:21:LEU:C[2_554]	0.17	2.03
2:O:81:GLN:NE2	2:K:24:ARG:NH1[2_554]	0.59	1.61
2:O:81:GLN:CG	2:K:24:ARG:NH2[2_554]	0.80	1.40
2:O:81:GLN:NE2	2:K:24:ARG:CZ[2_554]	1.03	1.17
2:O:24:ARG:NH1	2:K:21:LEU:CA[2_554]	1.05	1.15

## 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	465/472 (98%)	451 (97%)	14 (3%)	0	100	100
1	B	465/472 (98%)	451 (97%)	14 (3%)	0	100	100
1	C	465/472 (98%)	451 (97%)	14 (3%)	0	100	100
1	D	465/472 (98%)	451 (97%)	14 (3%)	0	100	100
1	E	465/472 (98%)	451 (97%)	14 (3%)	0	100	100
1	F	465/472 (98%)	451 (97%)	14 (3%)	0	100	100
1	G	465/472 (98%)	451 (97%)	14 (3%)	0	100	100
1	H	465/472 (98%)	451 (97%)	14 (3%)	0	100	100
2	I	107/111 (96%)	98 (92%)	9 (8%)	0	100	100
2	J	107/111 (96%)	98 (92%)	9 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	K	107/111 (96%)	98 (92%)	9 (8%)	0	100	100
2	L	107/111 (96%)	98 (92%)	9 (8%)	0	100	100
2	M	107/111 (96%)	98 (92%)	9 (8%)	0	100	100
2	N	107/111 (96%)	98 (92%)	9 (8%)	0	100	100
2	O	107/111 (96%)	98 (92%)	9 (8%)	0	100	100
2	P	107/111 (96%)	98 (92%)	9 (8%)	0	100	100
All	All	4576/4664 (98%)	4392 (96%)	184 (4%)	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	377/383 (98%)	357 (95%)	20 (5%)	28	37
1	B	377/383 (98%)	357 (95%)	20 (5%)	28	37
1	C	377/383 (98%)	357 (95%)	20 (5%)	28	37
1	D	377/383 (98%)	357 (95%)	20 (5%)	28	37
1	E	377/383 (98%)	356 (94%)	21 (6%)	26	35
1	F	377/383 (98%)	357 (95%)	20 (5%)	28	37
1	G	377/383 (98%)	357 (95%)	20 (5%)	28	37
1	H	377/383 (98%)	356 (94%)	21 (6%)	26	35
2	I	99/104 (95%)	98 (99%)	1 (1%)	82	91
2	J	99/104 (95%)	98 (99%)	1 (1%)	82	91
2	K	99/104 (95%)	98 (99%)	1 (1%)	82	91
2	L	99/104 (95%)	98 (99%)	1 (1%)	82	91
2	M	99/104 (95%)	98 (99%)	1 (1%)	82	91
2	N	99/104 (95%)	98 (99%)	1 (1%)	82	91
2	O	99/104 (95%)	98 (99%)	1 (1%)	82	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	P	99/104 (95%)	98 (99%)	1 (1%)	82	91
All	All	3808/3896 (98%)	3638 (96%)	170 (4%)	34	46

5 of 170 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	285	ARG
1	E	255	GLU
1	H	239	TYR
1	D	375	LEU
1	E	79	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 103 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	401	GLN
1	E	383	HIS
1	H	304	GLN
1	D	420	ASN
1	E	238	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](#)

8 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
3	XBP	A	476	-	17,17,17	2.11	5 (29%)	15,25,25	1.20	0
3	XBP	B	476	-	17,17,17	2.12	6 (35%)	15,25,25	1.20	0
3	XBP	C	476	-	17,17,17	2.12	5 (29%)	15,25,25	1.20	0
3	XBP	D	476	-	17,17,17	2.12	5 (29%)	15,25,25	1.19	0
3	XBP	E	476	-	17,17,17	2.12	5 (29%)	15,25,25	1.19	0
3	XBP	F	476	1	17,17,17	2.12	5 (29%)	15,25,25	1.20	0
3	XBP	G	476	1	17,17,17	2.11	5 (29%)	15,25,25	1.20	0
3	XBP	H	476	-	17,17,17	2.11	6 (35%)	15,25,25	1.20	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	XBP	A	476	-	-	0/20/20/20	0/0/0/0
3	XBP	B	476	-	-	0/20/20/20	0/0/0/0
3	XBP	C	476	-	-	0/20/20/20	0/0/0/0
3	XBP	D	476	-	-	0/20/20/20	0/0/0/0
3	XBP	E	476	-	-	0/20/20/20	0/0/0/0
3	XBP	F	476	1	-	0/20/20/20	0/0/0/0
3	XBP	G	476	1	-	0/20/20/20	0/0/0/0
3	XBP	H	476	-	-	0/20/20/20	0/0/0/0

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	476	XBP	P2-O5	-3.42	1.48	1.60
3	B	476	XBP	P2-O5	-3.39	1.48	1.60
3	H	476	XBP	P2-O5	-3.38	1.48	1.60
3	D	476	XBP	P2-O5	-3.38	1.48	1.60
3	F	476	XBP	P2-O5	-3.38	1.48	1.60

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	476	XBP	2	0
3	B	476	XBP	2	0
3	C	476	XBP	2	0
3	D	476	XBP	2	0
3	E	476	XBP	2	0
3	F	476	XBP	1	0
3	G	476	XBP	1	0
3	H	476	XBP	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 ⓘ

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.