



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 9, 2023 – 05:06 pm GMT

PDB ID : 1E5V  
Title : OXIDIZED DMSO REDUCTASE EXPOSED TO HEPES BUFFER  
Authors : Bailey, S.; Bennett, B.; Adams, B.; Smith, A.T.; Bray, R.C.  
Deposited on : 2000-08-03  
Resolution : 2.40 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](mailto: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>.

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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 : 1.8.4, CSD as541be (2020)  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

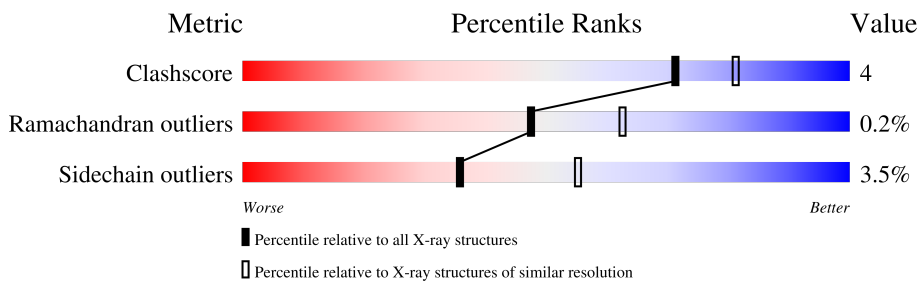
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

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  $\geq 3$ , 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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	823	
1	C	823	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 12440 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 Dimethyl sulfoxide/trimethylamine N-oxide reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	766	5884	3741	996	1120	27	0	0	0
1	C	766	5884	3741	996	1120	27	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

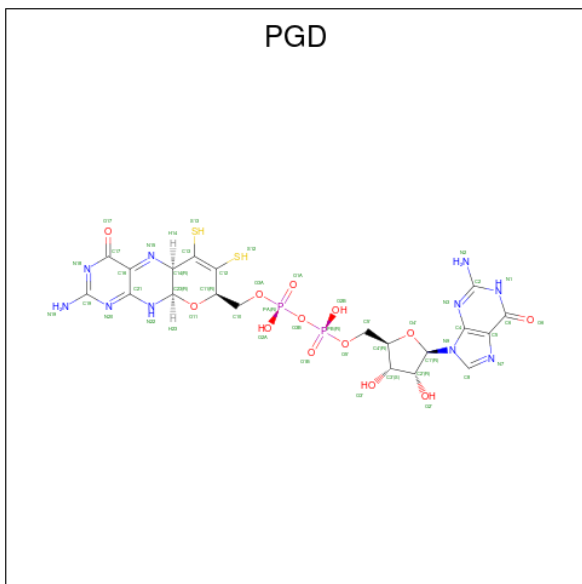
Chain	Residue	Modelled	Actual	Comment	Reference
A	39	SER	THR	conflict	UNP Q52675
A	43	ALA	GLU	conflict	UNP Q52675
A	107	GLU	GLN	conflict	UNP Q52675
A	234	GLU	ASP	conflict	UNP Q52675
A	236	ILE	VAL	conflict	UNP Q52675
A	280	ASP	MET	conflict	UNP Q52675
A	294	GLU	SER	conflict	UNP Q52675
A	295	GLY	ASP	conflict	UNP Q52675
A	312	GLU	ILE	conflict	UNP Q52675
A	374	ALA	SER	conflict	UNP Q52675
A	456	VAL	ILE	conflict	UNP Q52675
A	526	ALA	LYS	conflict	UNP Q52675
A	552	ALA	GLY	conflict	UNP Q52675
A	555	GLN	GLU	conflict	UNP Q52675
C	39	SER	THR	conflict	UNP Q52675
C	43	ALA	GLU	conflict	UNP Q52675
C	107	GLU	GLN	conflict	UNP Q52675
C	234	GLU	ASP	conflict	UNP Q52675
C	236	ILE	VAL	conflict	UNP Q52675
C	280	ASP	MET	conflict	UNP Q52675
C	294	GLU	SER	conflict	UNP Q52675
C	295	GLY	ASP	conflict	UNP Q52675
C	312	GLU	ILE	conflict	UNP Q52675
C	374	ALA	SER	conflict	UNP Q52675
C	456	VAL	ILE	conflict	UNP Q52675

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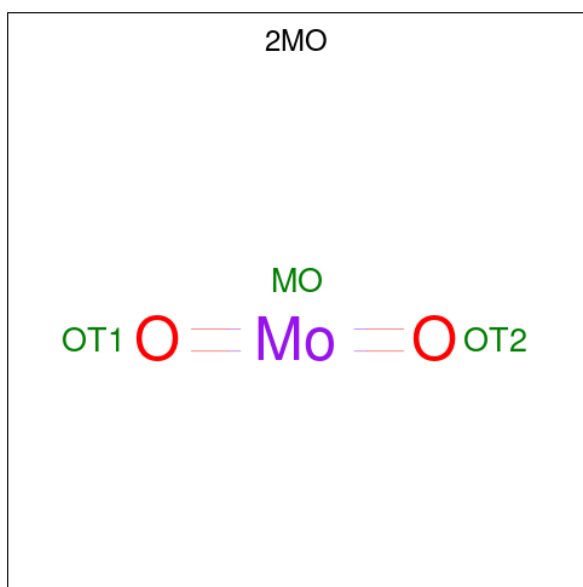
Chain	Residue	Modelled	Actual	Comment	Reference
C	526	ALA	LYS	conflict	UNP Q52675
C	552	ALA	GLY	conflict	UNP Q52675
C	555	GLN	GLU	conflict	UNP Q52675

- Molecule 2 is 2-AMINO-5,6-DIMERCAPTO-7-METHYL-3,7,8A,9-TETRAHYDRO-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-4-ONE GUANOSINE DINUCLEOTIDE (three-letter code: PGD) (formula: C<sub>20</sub>H<sub>24</sub>N<sub>10</sub>O<sub>13</sub>P<sub>2</sub>S<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			S
2	A	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
2	A	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
2	C	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
2	C	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		

- Molecule 3 is MOLYBDENUM (IV)OXIDE (three-letter code: 2MO) (formula: MoO<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Mo	O		
3	A	1	3	1	2	0	0
3	C	1	3	1	2	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
4	A	1	5	4	1	0	0
4	C	1	5	4	1	0	0

- Molecule 5 is water.


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	261	Total 261	O 261	0	0
5	C	207	Total 207	O 207	0	0

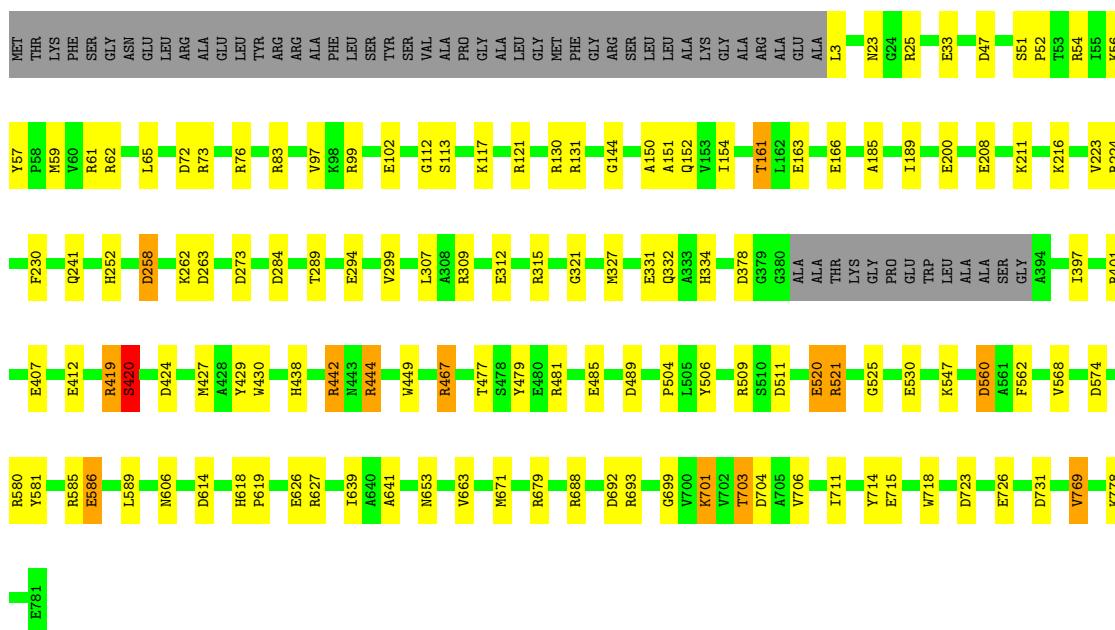
### 3 Residue-property plots

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. 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. 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.

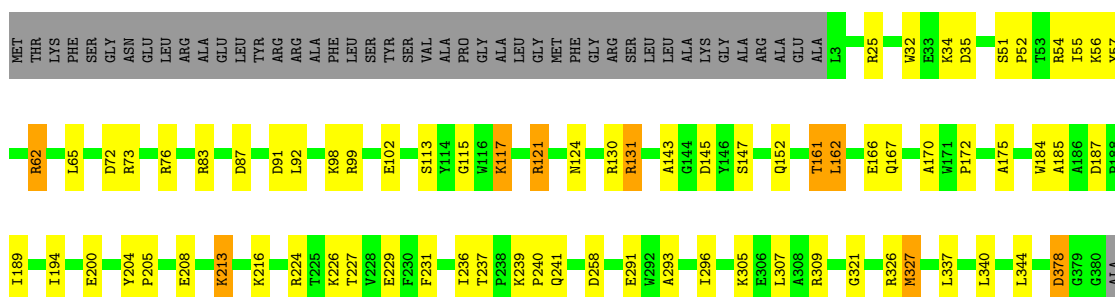
- Molecule 1: Dimethyl sulfoxide/trimethylamine N-oxide reductase

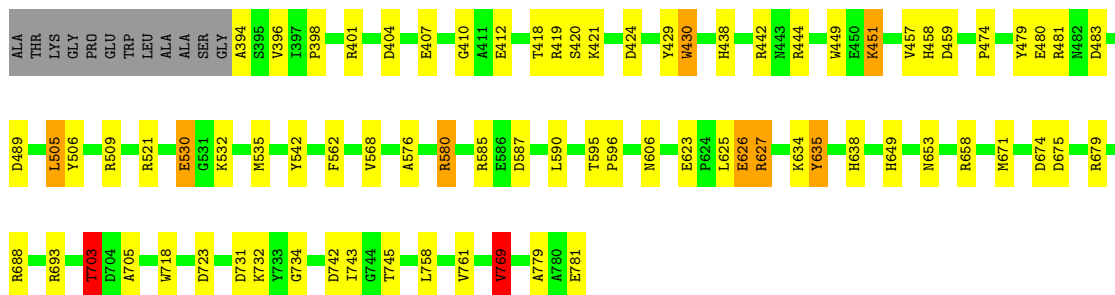
Chain A: 



- Molecule 1: Dimethyl sulfoxide/trimethylamine N-oxide reductase

Chain C: 







## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.35Å 117.18Å 233.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.40	Depositor
% Data completeness (in resolution range)	80.4 (20.00-2.40)	Depositor
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.171 , 0.223	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	12440	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

## 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: SO4, 2MO, PGD

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	0.65	0/6041	1.59	91/8221 (1.1%)
1	C	0.66	1/6041 (0.0%)	1.64	100/8221 (1.2%)
All	All	0.66	1/12082 (0.0%)	1.62	191/16442 (1.2%)

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	C	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	147	SER	CB-OG	-5.62	1.34	1.42

All (191) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	121	ARG	CD-NE-CZ	25.09	158.72	123.60
1	C	442	ARG	NE-CZ-NH2	-17.94	111.33	120.30
1	C	62	ARG	NE-CZ-NH2	17.25	128.93	120.30
1	C	326	ARG	NE-CZ-NH2	-16.13	112.24	120.30
1	C	627	ARG	NE-CZ-NH2	-14.53	113.03	120.30
1	A	62	ARG	NE-CZ-NH1	13.70	127.15	120.30
1	A	54	ARG	NE-CZ-NH2	-13.50	113.55	120.30
1	C	309	ARG	NE-CZ-NH2	-13.29	113.66	120.30
1	C	442	ARG	NE-CZ-NH1	12.95	126.78	120.30
1	A	509	ARG	NE-CZ-NH2	-12.57	114.01	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	99	ARG	CD-NE-CZ	12.32	140.85	123.60
1	A	61	ARG	NE-CZ-NH2	-12.19	114.21	120.30
1	C	326	ARG	NE-CZ-NH1	12.11	126.35	120.30
1	C	688	ARG	NE-CZ-NH2	-11.76	114.42	120.30
1	A	585	ARG	NE-CZ-NH2	-11.72	114.44	120.30
1	C	99	ARG	NE-CZ-NH1	11.66	126.13	120.30
1	A	585	ARG	NE-CZ-NH1	11.34	125.97	120.30
1	A	312	GLU	OE1-CD-OE2	-11.29	109.75	123.30
1	A	401	ARG	NE-CZ-NH2	10.95	125.77	120.30
1	A	25	ARG	NE-CZ-NH1	10.75	125.68	120.30
1	C	145	ASP	CB-CG-OD1	10.74	127.97	118.30
1	A	424	ASP	CB-CG-OD1	10.71	127.94	118.30
1	A	693	ARG	CD-NE-CZ	10.66	138.53	123.60
1	A	692	ASP	CB-CG-OD1	10.62	127.86	118.30
1	A	224	ARG	NE-CZ-NH1	10.62	125.61	120.30
1	A	444	ARG	NE-CZ-NH1	-10.50	115.05	120.30
1	C	693	ARG	NE-CZ-NH1	10.37	125.48	120.30
1	A	76	ARG	NE-CZ-NH1	-10.28	115.16	120.30
1	A	401	ARG	NE-CZ-NH1	-10.20	115.20	120.30
1	C	679	ARG	NE-CZ-NH2	-10.07	115.27	120.30
1	A	309	ARG	NE-CZ-NH1	-9.90	115.35	120.30
1	A	467	ARG	NE-CZ-NH2	9.78	125.19	120.30
1	A	580	ARG	NE-CZ-NH2	-9.75	115.42	120.30
1	C	459	ASP	CB-CG-OD1	9.73	127.06	118.30
1	C	688	ARG	NE-CZ-NH1	9.64	125.12	120.30
1	A	47	ASP	CB-CG-OD2	9.59	126.93	118.30
1	C	723	ASP	CB-CG-OD1	9.41	126.77	118.30
1	C	72	ASP	CB-CG-OD1	9.30	126.67	118.30
1	C	585	ARG	NE-CZ-NH1	8.97	124.78	120.30
1	A	489	ASP	CB-CG-OD2	8.68	126.11	118.30
1	C	25	ARG	NE-CZ-NH1	8.63	124.62	120.30
1	C	35	ASP	CB-CG-OD2	-8.58	110.58	118.30
1	A	121	ARG	NE-CZ-NH1	8.48	124.54	120.30
1	C	521	ARG	NE-CZ-NH2	-8.47	116.07	120.30
1	A	62	ARG	CD-NE-CZ	8.38	135.33	123.60
1	A	131	ARG	NE-CZ-NH2	-8.34	116.13	120.30
1	A	284	ASP	CB-CG-OD1	8.18	125.66	118.30
1	C	327	MET	CG-SD-CE	8.12	113.20	100.20
1	A	688	ARG	NE-CZ-NH1	7.98	124.29	120.30
1	C	25	ARG	NE-CZ-NH2	-7.98	116.31	120.30
1	C	25	ARG	CD-NE-CZ	7.94	134.72	123.60
1	C	479	TYR	CB-CG-CD1	-7.94	116.24	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	781	GLU	CA-CB-CG	7.91	130.80	113.40
1	C	121	ARG	NE-CZ-NH1	7.88	124.24	120.30
1	C	76	ARG	NE-CZ-NH2	-7.88	116.36	120.30
1	A	130	ARG	NE-CZ-NH1	-7.85	116.37	120.30
1	A	258	ASP	CB-CG-OD2	7.83	125.34	118.30
1	C	489	ASP	CB-CG-OD2	-7.82	111.26	118.30
1	C	585	ARG	CD-NE-CZ	7.69	134.37	123.60
1	A	614	ASP	CB-CG-OD1	7.64	125.18	118.30
1	A	57	TYR	CB-CG-CD1	-7.57	116.46	121.00
1	C	57	TYR	CB-CG-CD1	-7.50	116.50	121.00
1	A	688	ARG	CD-NE-CZ	7.38	133.94	123.60
1	A	509	ARG	NE-CZ-NH1	7.33	123.96	120.30
1	A	442	ARG	NE-CZ-NH2	-7.30	116.65	120.30
1	C	580	ARG	NE-CZ-NH2	-7.30	116.65	120.30
1	A	701	LYS	N-CA-CB	7.30	123.73	110.60
1	C	688	ARG	CD-NE-CZ	7.26	133.77	123.60
1	A	723	ASP	CB-CG-OD1	7.20	124.78	118.30
1	A	586	GLU	OE1-CD-OE2	7.16	131.89	123.30
1	C	585	ARG	NE-CZ-NH2	-7.14	116.73	120.30
1	C	675	ASP	CB-CG-OD2	7.13	124.72	118.30
1	C	57	TYR	CB-CG-CD2	7.12	125.27	121.00
1	A	723	ASP	CB-CG-OD2	-7.11	111.90	118.30
1	C	693	ARG	CD-NE-CZ	7.11	133.55	123.60
1	A	73	ARG	NE-CZ-NH2	-7.07	116.76	120.30
1	C	83	ARG	CD-NE-CZ	7.05	133.47	123.60
1	C	703	THR	CB-CA-C	-7.02	92.65	111.60
1	C	509	ARG	NE-CZ-NH1	6.95	123.78	120.30
1	C	131	ARG	NE-CZ-NH1	-6.89	116.86	120.30
1	C	404	ASP	CB-CG-OD2	6.84	124.46	118.30
1	A	693	ARG	NE-CZ-NH2	-6.81	116.89	120.30
1	C	481	ARG	NE-CZ-NH2	6.80	123.70	120.30
1	A	520	GLU	OE1-CD-OE2	-6.77	115.17	123.30
1	A	315	ARG	NE-CZ-NH1	6.76	123.68	120.30
1	C	87	ASP	CB-CG-OD1	6.72	124.35	118.30
1	C	674	ASP	CB-CG-OD2	-6.66	112.30	118.30
1	A	99	ARG	NE-CZ-NH1	6.65	123.62	120.30
1	A	467	ARG	NE-CZ-NH1	-6.62	116.99	120.30
1	A	72	ASP	CB-CG-OD1	6.57	124.21	118.30
1	C	258	ASP	CB-CG-OD1	6.52	124.17	118.30
1	A	560	ASP	CB-CG-OD1	-6.52	112.43	118.30
1	A	224	ARG	NE-CZ-NH2	-6.47	117.06	120.30
1	C	394	ALA	N-CA-CB	6.47	119.16	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	521	ARG	NE-CZ-NH1	6.46	123.53	120.30
1	C	481	ARG	NE-CZ-NH1	-6.44	117.08	120.30
1	C	73	ARG	NE-CZ-NH2	-6.42	117.09	120.30
1	C	224	ARG	NE-CZ-NH2	-6.41	117.09	120.30
1	A	315	ARG	CD-NE-CZ	6.38	132.53	123.60
1	A	378	ASP	CB-CG-OD1	-6.33	112.60	118.30
1	A	284	ASP	CB-CG-OD2	-6.33	112.60	118.30
1	C	587	ASP	CB-CG-OD1	6.30	123.97	118.30
1	A	62	ARG	NE-CZ-NH2	-6.26	117.17	120.30
1	C	742	ASP	CB-CG-OD1	6.26	123.93	118.30
1	C	731	ASP	CB-CG-OD1	6.25	123.93	118.30
1	C	623	GLU	OE1-CD-OE2	-6.20	115.86	123.30
1	A	574	ASP	CB-CG-OD1	6.16	123.84	118.30
1	C	779	ALA	N-CA-CB	6.15	118.71	110.10
1	A	626	GLU	OE1-CD-OE2	-6.13	115.94	123.30
1	C	626	GLU	OE1-CD-OE2	-6.13	115.94	123.30
1	C	229	GLU	OE1-CD-OE2	6.12	130.65	123.30
1	C	458	HIS	N-CA-CB	6.12	121.61	110.60
1	C	121	ARG	NH1-CZ-NH2	-6.12	112.67	119.40
1	C	326	ARG	CD-NE-CZ	6.11	132.15	123.60
1	A	671	MET	CA-CB-CG	6.09	123.65	113.30
1	C	418	THR	N-CA-CB	6.09	121.87	110.30
1	A	726	GLU	OE1-CD-OE2	-6.06	116.03	123.30
1	A	485	GLU	OE1-CD-OE2	6.04	130.55	123.30
1	A	703	THR	CB-CA-C	-6.03	95.31	111.60
1	C	530	GLU	OE1-CD-OE2	6.03	130.54	123.30
1	C	378	ASP	CB-CG-OD2	-6.02	112.88	118.30
1	A	263	ASP	CB-CG-OD2	-6.00	112.90	118.30
1	A	704	ASP	CB-CG-OD1	5.97	123.67	118.30
1	C	769	VAL	CA-CB-CG1	5.96	119.84	110.90
1	C	83	ARG	NE-CZ-NH1	-5.95	117.32	120.30
1	A	424	ASP	CB-CG-OD2	-5.90	112.99	118.30
1	A	83	ARG	NE-CZ-NH1	5.90	123.25	120.30
1	A	57	TYR	CB-CG-CD2	5.86	124.52	121.00
1	A	769	VAL	N-CA-CB	-5.85	98.63	111.50
1	C	635	TYR	CB-CG-CD1	-5.85	117.49	121.00
1	A	25	ARG	NE-CZ-NH2	-5.84	117.38	120.30
1	A	679	ARG	NE-CZ-NH2	-5.84	117.38	120.30
1	A	641	ALA	N-CA-CB	-5.83	101.93	110.10
1	C	62	ARG	NH1-CZ-NH2	-5.82	112.99	119.40
1	A	714	TYR	CB-CG-CD1	5.82	124.49	121.00
1	A	99	ARG	NE-CZ-NH2	-5.81	117.39	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	723	ASP	CB-CG-OD2	-5.81	113.07	118.30
1	C	91	ASP	CB-CG-OD2	-5.78	113.09	118.30
1	C	521	ARG	CD-NE-CZ	5.73	131.62	123.60
1	C	542	TYR	CB-CG-CD2	-5.73	117.56	121.00
1	A	581	TYR	CB-CG-CD1	-5.69	117.58	121.00
1	C	521	ARG	NE-CZ-NH1	5.69	123.14	120.30
1	A	420	SER	N-CA-CB	5.68	119.03	110.50
1	C	458	HIS	CA-CB-CG	5.65	123.21	113.60
1	A	419	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	C	83	ARG	NE-CZ-NH2	5.61	123.10	120.30
1	C	769	VAL	N-CA-CB	-5.59	99.20	111.50
1	C	113	SER	N-CA-CB	-5.59	102.12	110.50
1	C	121	ARG	NE-CZ-NH2	5.57	123.09	120.30
1	C	693	ARG	NE-CZ-NH2	-5.49	117.56	120.30
1	C	489	ASP	CB-CG-OD1	5.46	123.22	118.30
1	C	674	ASP	CB-CG-OD1	5.46	123.21	118.30
1	C	479	TYR	CB-CG-CD2	5.41	124.25	121.00
1	A	521	ARG	NE-CZ-NH2	-5.41	117.60	120.30
1	C	576	ALA	N-CA-CB	5.40	117.66	110.10
1	A	3	LEU	CA-C-O	5.39	131.43	120.10
1	C	162	LEU	CB-CG-CD2	-5.39	101.83	111.00
1	C	167	GLN	CA-CB-CG	5.39	125.25	113.40
1	A	481	ARG	NE-CZ-NH2	5.37	122.98	120.30
1	A	334	HIS	CA-CB-CG	-5.36	104.49	113.60
1	C	535	MET	CA-CB-CG	5.35	122.40	113.30
1	A	530	GLU	OE1-CD-OE2	5.35	129.72	123.30
1	A	692	ASP	CB-CG-OD2	-5.35	113.49	118.30
1	A	273	ASP	CB-CG-OD2	-5.34	113.49	118.30
1	A	59	MET	CA-CB-CG	5.34	122.38	113.30
1	A	614	ASP	CB-CG-OD2	-5.26	113.57	118.30
1	C	130	ARG	NE-CZ-NH2	-5.24	117.68	120.30
1	A	312	GLU	CG-CD-OE2	5.22	128.75	118.30
1	C	438	HIS	CA-CB-CG	5.21	122.46	113.60
1	A	83	ARG	NE-CZ-NH2	-5.20	117.70	120.30
1	C	658	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	C	627	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	A	442	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	C	483	ASP	CB-CG-OD2	-5.16	113.65	118.30
1	A	23	ASN	N-CA-CB	-5.15	101.32	110.60
1	C	187	ASP	CB-CG-OD2	-5.15	113.67	118.30
1	C	419	ARG	NE-CZ-NH1	-5.14	117.73	120.30
1	C	480	GLU	OE1-CD-OE2	-5.14	117.13	123.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	92	LEU	CB-CA-C	5.14	119.97	110.20
1	A	511	ASP	CB-CG-OD1	5.12	122.91	118.30
1	C	568	VAL	CB-CA-C	-5.12	101.68	111.40
1	A	627	ARG	NE-CZ-NH2	-5.11	117.75	120.30
1	A	731	ASP	CB-CG-OD1	5.10	122.89	118.30
1	A	208	GLU	OE1-CD-OE2	-5.10	117.18	123.30
1	C	293	ALA	CB-CA-C	5.09	117.74	110.10
1	A	102	GLU	CG-CD-OE2	-5.08	108.14	118.30
1	C	76	ARG	NE-CZ-NH1	5.06	122.83	120.30
1	C	606	ASN	N-CA-CB	-5.05	101.50	110.60
1	A	131	ARG	NE-CZ-NH1	5.01	122.81	120.30
1	C	505	LEU	CB-CG-CD1	-5.01	102.48	111.00
1	A	163	GLU	OE1-CD-OE2	-5.00	117.30	123.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	231	PHE	Mainchain

## 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	5884	0	5690	31	0
1	C	5884	0	5690	52	0
2	A	94	0	40	0	0
2	C	94	0	40	2	0
3	A	3	0	0	0	0
3	C	3	0	0	0	0
4	A	5	0	0	0	0
4	C	5	0	0	0	0
5	A	261	0	0	2	0
5	C	207	0	0	1	0
All	All	12440	0	11460	83	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 4.

All (83) 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:54:ARG:NH1	1:C:505:LEU:HD12	2.09	0.68
1:A:223:VAL:HG22	1:A:706:VAL:HG12	1.75	0.67
1:C:732:LYS:HD2	1:C:769:VAL:HG13	1.77	0.65
1:C:627:ARG:HD2	5:C:2152:HOH:O	1.98	0.64
1:C:131:ARG:HB2	1:C:378:ASP:HA	1.79	0.63
1:C:410:GLY:O	1:C:421:LYS:HG2	1.97	0.63
1:C:703:THR:HG22	1:C:705:ALA:H	1.63	0.63
1:C:671:MET:HE1	1:C:761:VAL:HG11	1.82	0.61
1:C:152:GLN:HB2	1:C:162:LEU:HD11	1.85	0.59
1:A:520:GLU:OE1	1:A:525:GLY:HA3	2.02	0.58
1:C:161:THR:HB	1:C:166:GLU:OE2	2.04	0.58
1:A:653:ASN:ND2	1:A:718:TRP:H	2.01	0.58
1:C:412:GLU:HA	1:C:420:SER:O	2.04	0.57
1:C:56:LYS:HG2	1:C:506:TYR:CD2	2.40	0.57
1:C:398:PRO:HG2	1:C:401:ARG:HG3	1.87	0.56
1:C:653:ASN:ND2	1:C:718:TRP:H	2.04	0.55
1:A:639:ILE:HG12	1:A:711:ILE:HD11	1.88	0.55
1:A:294:GLU:HG3	1:A:299:VAL:O	2.09	0.53
1:C:625:LEU:HD23	1:C:626:GLU:HG2	1.91	0.53
1:C:170:ALA:HB1	1:C:172:PRO:HD2	1.92	0.51
1:A:618:HIS:HB2	1:A:619:PRO:HD2	1.92	0.51
1:C:32:TRP:CE2	1:C:34:LYS:HB2	2.45	0.51
1:A:701:LYS:HG2	5:A:2220:HOH:O	2.10	0.51
1:C:291:GLU:OE2	1:C:305:LYS:NZ	2.43	0.50
1:A:397:ILE:HG13	1:A:397:ILE:O	2.12	0.49
1:C:703:THR:CG2	1:C:705:ALA:H	2.24	0.49
1:C:671:MET:CE	1:C:761:VAL:HG11	2.42	0.49
1:C:595:THR:HB	1:C:596:PRO:CD	2.44	0.48
1:C:185:ALA:O	1:C:321:GLY:HA3	2.14	0.48
1:C:649:HIS:CG	2:C:801:PGD:H102	2.48	0.48
1:C:98:LYS:HE3	1:C:102:GLU:OE2	2.14	0.48
1:A:521:ARG:HH11	1:A:521:ARG:HG3	1.78	0.48
1:C:189:ILE:HD12	1:C:227:THR:HA	1.96	0.48
1:A:407:GLU:OE1	1:A:444:ARG:NH2	2.29	0.47
1:A:161:THR:HB	1:A:166:GLU:OE2	2.15	0.47
1:C:241:GLN:HG2	1:C:327:MET:SD	2.55	0.47
1:C:530:GLU:HG3	1:C:532:LYS:HE3	1.96	0.47
1:A:112:GLY:O	1:A:113:SER:C	2.53	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:407:GLU:OE1	1:C:444:ARG:NH2	2.42	0.46
1:C:595:THR:HB	1:C:596:PRO:HD2	1.98	0.46
1:C:743:ILE:O	1:C:743:ILE:HG13	2.15	0.46
1:A:332:GLN:OE1	1:A:619:PRO:HA	2.16	0.46
1:A:562:PHE:CD1	1:A:568:VAL:HG23	2.51	0.46
1:C:184:TRP:O	1:C:185:ALA:HB3	2.16	0.45
1:C:638:HIS:HA	1:C:758:LEU:HD23	1.99	0.45
1:A:189:ILE:HD12	1:A:230:PHE:HB2	1.97	0.45
1:A:252:HIS:CE1	1:A:289:THR:HG22	2.52	0.45
1:A:185:ALA:O	1:A:321:GLY:HA3	2.17	0.45
1:C:204:TYR:HB2	1:C:205:PRO:HD3	1.97	0.45
1:A:241:GLN:HG2	1:A:327:MET:SD	2.56	0.45
1:C:115:GLY:HA2	2:C:801:PGD:O2A	2.17	0.45
1:A:562:PHE:HD1	1:A:568:VAL:HG23	1.82	0.44
1:A:477:THR:HG1	1:A:479:TYR:HD2	1.61	0.44
1:A:663:VAL:HB	1:A:699:GLY:HA3	1.99	0.44
1:C:143:ALA:HB2	1:C:396:VAL:CG1	2.47	0.44
1:C:240:PRO:O	1:C:241:GLN:HB2	2.16	0.44
1:C:327:MET:O	1:C:745:THR:HG22	2.17	0.44
1:A:51:SER:HB2	1:A:52:PRO:HD2	2.00	0.44
1:A:144:GLY:HA2	1:A:152:GLN:OE1	2.17	0.43
1:A:97:VAL:HG22	1:A:427:MET:CE	2.48	0.43
1:C:239:LYS:O	1:C:240:PRO:C	2.57	0.43
1:C:55:ILE:HG22	1:C:474:PRO:HB3	2.01	0.42
1:C:194:ILE:C	1:C:194:ILE:HD12	2.39	0.42
1:A:151:ALA:HA	1:A:154:ILE:HG22	2.00	0.42
1:C:51:SER:HB2	1:C:52:PRO:HD2	2.01	0.42
1:C:430:TRP:O	1:C:457:VAL:HA	2.19	0.42
1:A:56:LYS:HG2	1:A:506:TYR:CD2	2.54	0.42
1:A:467:ARG:HD3	5:A:2150:HOH:O	2.18	0.42
1:C:732:LYS:CD	1:C:769:VAL:HG13	2.47	0.42
1:C:237:THR:O	1:C:237:THR:OG1	2.36	0.42
1:A:258:ASP:OD1	1:A:262:LYS:NZ	2.34	0.42
1:C:634:LYS:HG2	1:C:635:TYR:CE2	2.54	0.42
1:C:152:GLN:HB2	1:C:162:LEU:CD1	2.49	0.42
1:A:412:GLU:HA	1:A:420:SER:O	2.20	0.42
1:C:424:ASP:OD1	1:C:451:LYS:NZ	2.50	0.41
1:A:150:ALA:HB1	1:A:331:GLU:HG3	2.02	0.41
1:C:98:LYS:HA	1:C:98:LYS:HD2	1.80	0.41
1:C:62:ARG:NH1	1:C:62:ARG:HG3	2.35	0.41
1:C:175:ALA:O	1:C:213:LYS:HD2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:117:LYS:HE2	1:C:124:ASN:OD1	2.21	0.41
1:A:211:LYS:HE3	1:A:230:PHE:O	2.21	0.40
1:C:340:LEU:O	1:C:344:LEU:HG	2.21	0.40
1:C:204:TYR:O	1:C:208:GLU:HG3	2.22	0.40

There are no symmetry-related clashes.

## 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	762/823 (93%)	736 (97%)	25 (3%)	1 (0%)	51 68
1	C	762/823 (93%)	736 (97%)	24 (3%)	2 (0%)	41 55
All	All	1524/1646 (93%)	1472 (97%)	49 (3%)	3 (0%)	47 62

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	117	LYS
1	A	117	LYS
1	C	734	GLY

### 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	610/648 (94%)	587 (96%)	23 (4%)	33	51
1	C	610/648 (94%)	590 (97%)	20 (3%)	38	57
All	All	1220/1296 (94%)	1177 (96%)	43 (4%)	36	55

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	GLU
1	A	65	LEU
1	A	161	THR
1	A	200	GLU
1	A	216	LYS
1	A	307	LEU
1	A	419	ARG
1	A	420	SER
1	A	429	TYR
1	A	430	TRP
1	A	438	HIS
1	A	442	ARG
1	A	449	TRP
1	A	504	PRO
1	A	547	LYS
1	A	560	ASP
1	A	586	GLU
1	A	589	LEU
1	A	606	ASN
1	A	703	THR
1	A	715	GLU
1	A	769	VAL
1	A	778	LYS
1	C	65	LEU
1	C	121	ARG
1	C	161	THR
1	C	200	GLU
1	C	213	LYS
1	C	216	LYS
1	C	226	LYS
1	C	236	ILE
1	C	296	ILE
1	C	307	LEU
1	C	337	LEU
1	C	429	TYR

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Mol	Chain	Res	Type
1	C	430	TRP
1	C	449	TRP
1	C	451	LYS
1	C	562	PHE
1	C	580	ARG
1	C	590	LEU
1	C	703	THR
1	C	769	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	241	GLN
1	A	653	ASN
1	C	37	HIS
1	C	241	GLN
1	C	653	ASN

### 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](#)

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
2	PGD	C	801	3	40,52,52	2.69	19 (47%)	38,81,81	2.04	11 (28%)
2	PGD	A	801	3	40,52,52	2.63	15 (37%)	38,81,81	2.11	12 (31%)
4	SO4	A	901	-	4,4,4	0.36	0	6,6,6	0.48	0
3	2MO	C	803	2,1	0,2,2	-	-	-	-	-
2	PGD	C	802	3	40,52,52	2.75	13 (32%)	38,81,81	2.04	8 (21%)
3	2MO	A	803	2,1	0,2,2	-	-	-	-	-
4	SO4	C	901	-	4,4,4	0.53	0	6,6,6	0.56	0
2	PGD	A	802	3	40,52,52	2.67	14 (35%)	38,81,81	1.76	9 (23%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PGD	A	801	3	-	5/18/82/82	0/6/6/6
2	PGD	A	802	3	-	2/18/82/82	0/6/6/6
2	PGD	C	801	3	-	5/18/82/82	0/6/6/6
2	PGD	C	802	3	-	0/18/82/82	0/6/6/6

All (61) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	802	PGD	C21-N22	7.82	1.44	1.35
2	C	802	PGD	C16-N15	7.45	1.45	1.28
2	A	802	PGD	C21-N22	7.41	1.43	1.35
2	A	801	PGD	C21-N22	7.24	1.43	1.35
2	C	801	PGD	C16-N15	6.85	1.44	1.28
2	C	801	PGD	C21-N22	6.73	1.42	1.35
2	A	802	PGD	C16-N15	6.48	1.43	1.28
2	C	802	PGD	PA-O1A	6.04	1.72	1.50
2	A	802	PGD	PA-O1A	5.96	1.72	1.50
2	A	801	PGD	C16-N15	5.88	1.42	1.28
2	A	802	PGD	PB-O1B	5.66	1.71	1.50
2	A	801	PGD	PA-O1A	5.46	1.70	1.50
2	A	801	PGD	PB-O1B	5.40	1.70	1.50
2	C	801	PGD	PB-O1B	5.23	1.69	1.50
2	C	801	PGD	PA-O1A	5.02	1.68	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	802	PGD	PB-O1B	5.02	1.68	1.50
2	C	801	PGD	C5-C6	-4.57	1.38	1.47
2	A	801	PGD	C5-C6	-4.28	1.38	1.47
2	A	801	PGD	PB-O5'	4.17	1.76	1.59
2	C	801	PGD	O11-C11	-4.11	1.38	1.43
2	C	802	PGD	C5-C6	-3.97	1.39	1.47
2	A	802	PGD	O11-C11	-3.91	1.38	1.43
2	C	802	PGD	PB-O5'	3.79	1.74	1.59
2	C	801	PGD	PB-O2B	3.59	1.72	1.55
2	C	802	PGD	C14-N15	3.58	1.50	1.46
2	A	802	PGD	C5-C4	-3.49	1.34	1.43
2	C	802	PGD	PA-O3A	3.49	1.73	1.59
2	C	802	PGD	C5-C4	-3.42	1.34	1.43
2	A	802	PGD	PB-O2B	3.37	1.71	1.55
2	C	801	PGD	PA-O3A	3.37	1.72	1.59
2	A	801	PGD	PA-O3A	3.32	1.72	1.59
2	A	802	PGD	PA-O3A	3.20	1.72	1.59
2	A	802	PGD	C19-N19	3.15	1.43	1.34
2	A	802	PGD	PA-O2A	3.06	1.69	1.55
2	A	801	PGD	C5-C4	-3.03	1.35	1.43
2	C	801	PGD	PA-O2A	3.02	1.69	1.55
2	C	802	PGD	PB-O2B	2.96	1.69	1.55
2	A	801	PGD	C10-C11	2.95	1.56	1.52
2	C	802	PGD	C19-N19	2.89	1.42	1.34
2	A	802	PGD	PB-O5'	2.83	1.70	1.59
2	A	801	PGD	C2-N2	2.81	1.40	1.34
2	C	802	PGD	PA-O2A	2.80	1.68	1.55
2	A	802	PGD	C5-C6	-2.79	1.41	1.47
2	C	801	PGD	C23-N22	2.70	1.49	1.45
2	A	802	PGD	C2-N2	2.68	1.40	1.34
2	C	801	PGD	C5-C4	-2.66	1.36	1.43
2	C	801	PGD	O4'-C4'	-2.61	1.39	1.45
2	C	801	PGD	C19-N19	2.59	1.41	1.34
2	C	801	PGD	C21-N20	2.56	1.37	1.32
2	C	801	PGD	PB-O5'	2.56	1.69	1.59
2	A	801	PGD	PA-O2A	2.54	1.67	1.55
2	C	802	PGD	C2-N2	2.52	1.40	1.34
2	A	801	PGD	C19-N19	2.38	1.41	1.34
2	A	801	PGD	PB-O2B	2.37	1.66	1.55
2	A	802	PGD	O4'-C4'	-2.34	1.39	1.45
2	C	801	PGD	O3A-C10	-2.31	1.35	1.44
2	A	801	PGD	O11-C23	-2.23	1.40	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	801	PGD	C10-C11	2.16	1.54	1.52
2	A	801	PGD	C21-N20	2.07	1.36	1.32
2	C	801	PGD	O2'-C2'	-2.04	1.38	1.43
2	C	801	PGD	C2-N2	2.04	1.39	1.34

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	PGD	O6-C6-N1	-6.16	113.38	120.65
2	C	802	PGD	C17-C16-N15	5.75	124.37	118.06
2	C	802	PGD	O6-C6-N1	-5.65	113.97	120.65
2	C	801	PGD	C17-C16-N15	5.43	124.02	118.06
2	C	801	PGD	O6-C6-N1	-4.97	114.78	120.65
2	C	801	PGD	O4'-C1'-C2'	-4.42	100.47	106.93
2	A	801	PGD	C17-C16-N15	4.28	122.76	118.06
2	A	802	PGD	N20-C19-N18	-4.27	119.50	126.43
2	A	801	PGD	PA-O3B-PB	4.00	146.57	132.83
2	A	802	PGD	C17-C16-N15	4.00	122.46	118.06
2	A	802	PGD	O4'-C1'-C2'	-3.86	101.28	106.93
2	C	802	PGD	N20-C19-N18	-3.69	120.43	126.43
2	A	801	PGD	O4'-C1'-C2'	-3.33	102.06	106.93
2	A	801	PGD	C23-C14-N15	3.17	115.96	111.33
2	C	802	PGD	O17-C17-N18	-3.10	114.96	120.23
2	C	801	PGD	PA-O3B-PB	3.08	143.40	132.83
2	C	801	PGD	C5-C6-N1	3.07	119.37	113.95
2	A	801	PGD	N20-C19-N18	-3.05	121.48	126.43
2	C	802	PGD	N19-C19-N18	3.04	121.84	117.06
2	A	801	PGD	C5-C6-N1	2.96	119.17	113.95
2	A	801	PGD	N19-C19-N18	2.92	121.66	117.06
2	C	802	PGD	C16-C21-N22	2.86	123.57	116.62
2	A	802	PGD	N19-C19-N18	2.81	121.48	117.06
2	C	801	PGD	N20-C19-N18	-2.73	122.00	126.43
2	C	801	PGD	O17-C17-N18	-2.67	115.68	120.23
2	A	802	PGD	PA-O3B-PB	2.64	141.90	132.83
2	C	801	PGD	C16-C21-N22	2.48	122.63	116.62
2	A	801	PGD	C17-C16-C21	2.46	120.22	117.40
2	C	802	PGD	O6-C6-C5	2.40	129.06	124.37
2	A	802	PGD	O11-C23-N22	-2.38	106.12	108.57
2	C	801	PGD	C17-C16-C21	2.37	120.13	117.40
2	A	801	PGD	C16-C21-N22	2.33	122.27	116.62
2	A	801	PGD	N1-C2-N3	-2.31	119.00	123.32
2	A	802	PGD	O6-C6-N1	-2.28	117.95	120.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	802	PGD	C16-C21-N22	2.23	122.04	116.62
2	A	801	PGD	C5'-C4'-C3'	-2.20	106.94	115.18
2	A	802	PGD	PA-O3A-C10	-2.15	109.08	121.68
2	C	802	PGD	PA-O3B-PB	2.14	140.16	132.83
2	C	801	PGD	C2-N1-C6	-2.13	121.17	125.10
2	C	801	PGD	N19-C19-N20	2.12	120.01	116.57

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	PGD	PA-O3B-PB-O5'
2	A	801	PGD	C5'-O5'-PB-O2B
2	C	801	PGD	C5'-O5'-PB-O1B
2	C	801	PGD	C5'-O5'-PB-O2B
2	A	802	PGD	PA-O3B-PB-O5'
2	C	801	PGD	PA-O3B-PB-O5'
2	A	801	PGD	C5'-O5'-PB-O3B
2	A	801	PGD	C5'-O5'-PB-O1B
2	A	801	PGD	O4'-C4'-C5'-O5'
2	C	801	PGD	C5'-O5'-PB-O3B
2	A	802	PGD	C5'-O5'-PB-O1B
2	C	801	PGD	O4'-C4'-C5'-O5'

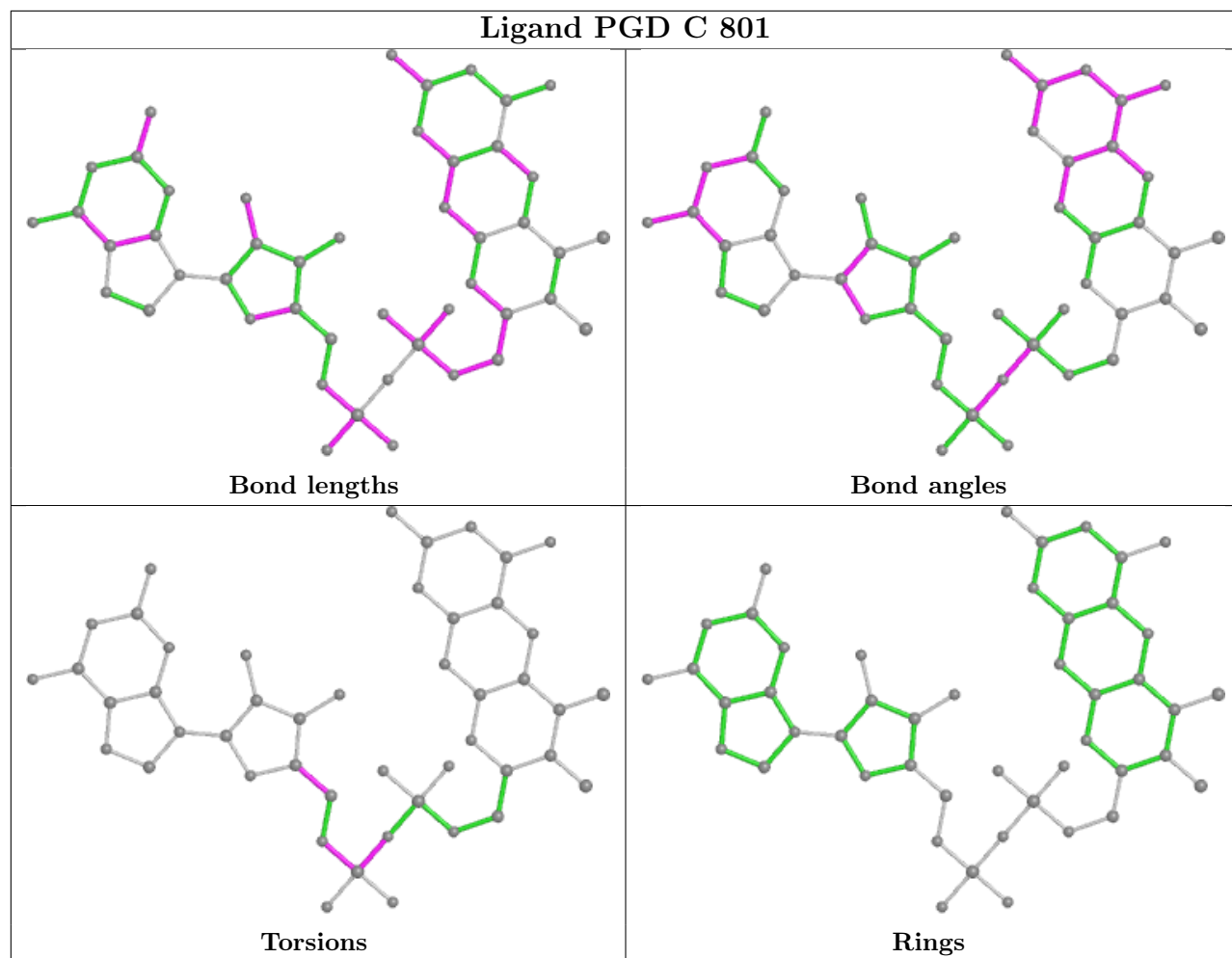
There are no ring outliers.

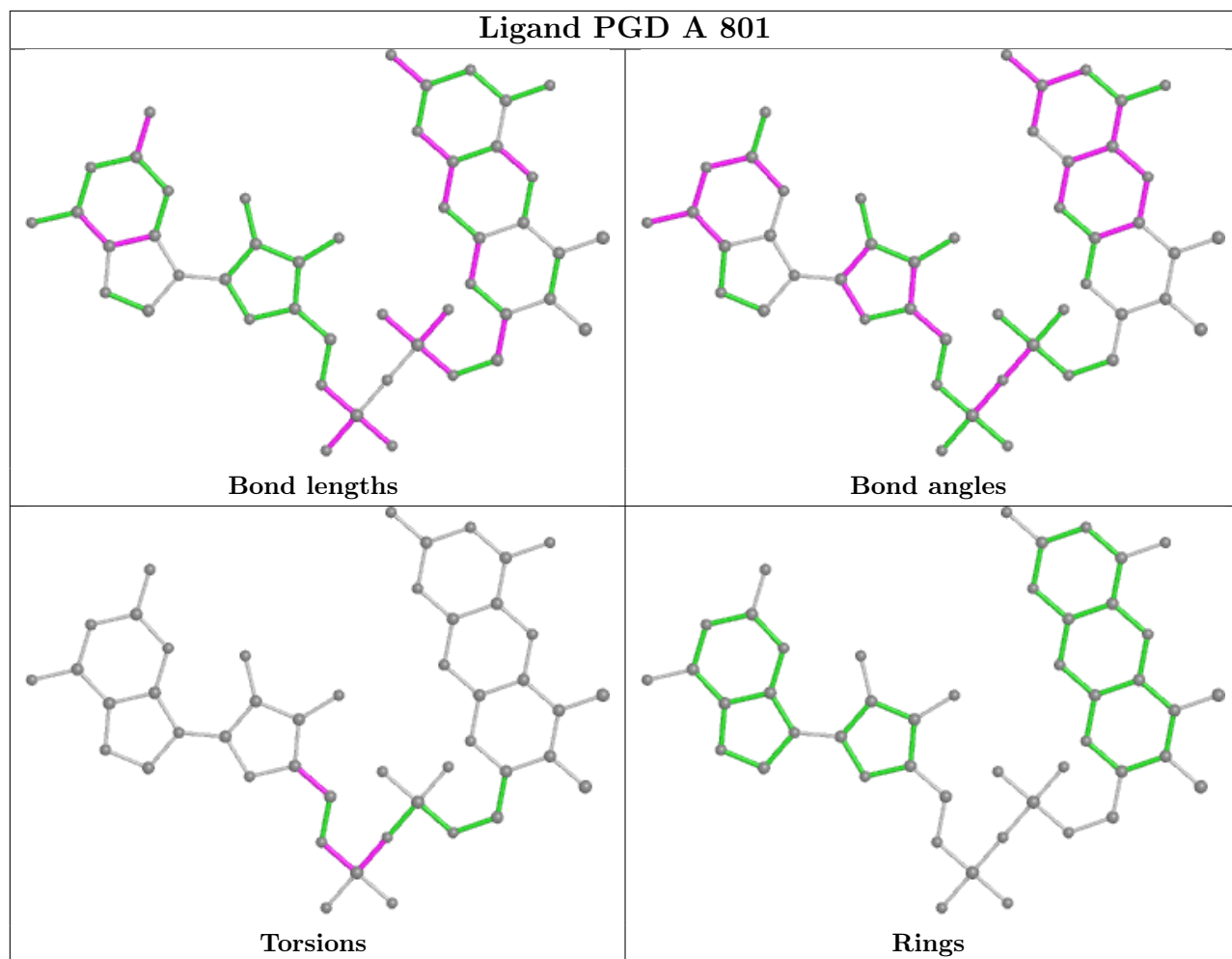
1 monomer is involved in 2 short contacts:

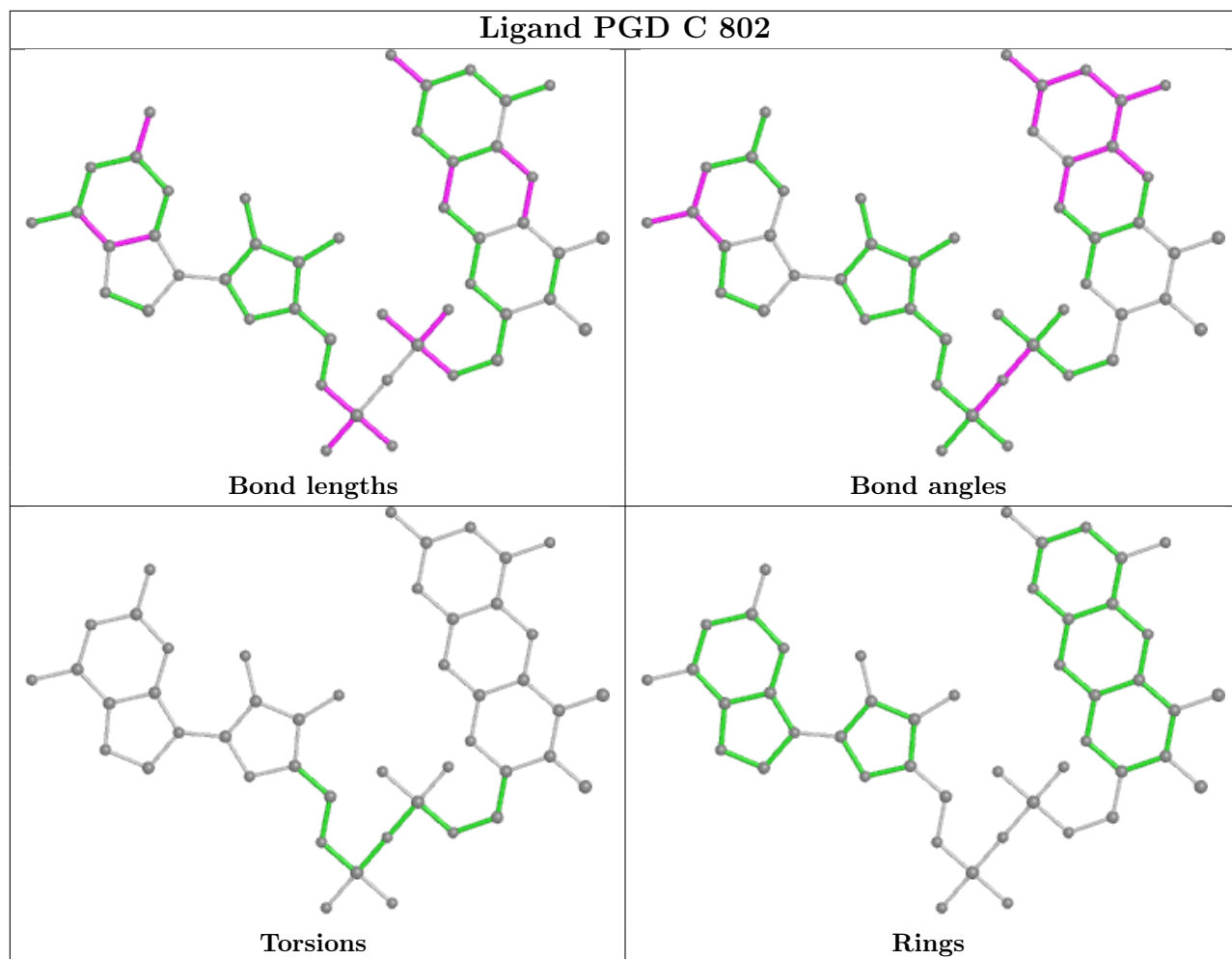
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	801	PGD	2	0

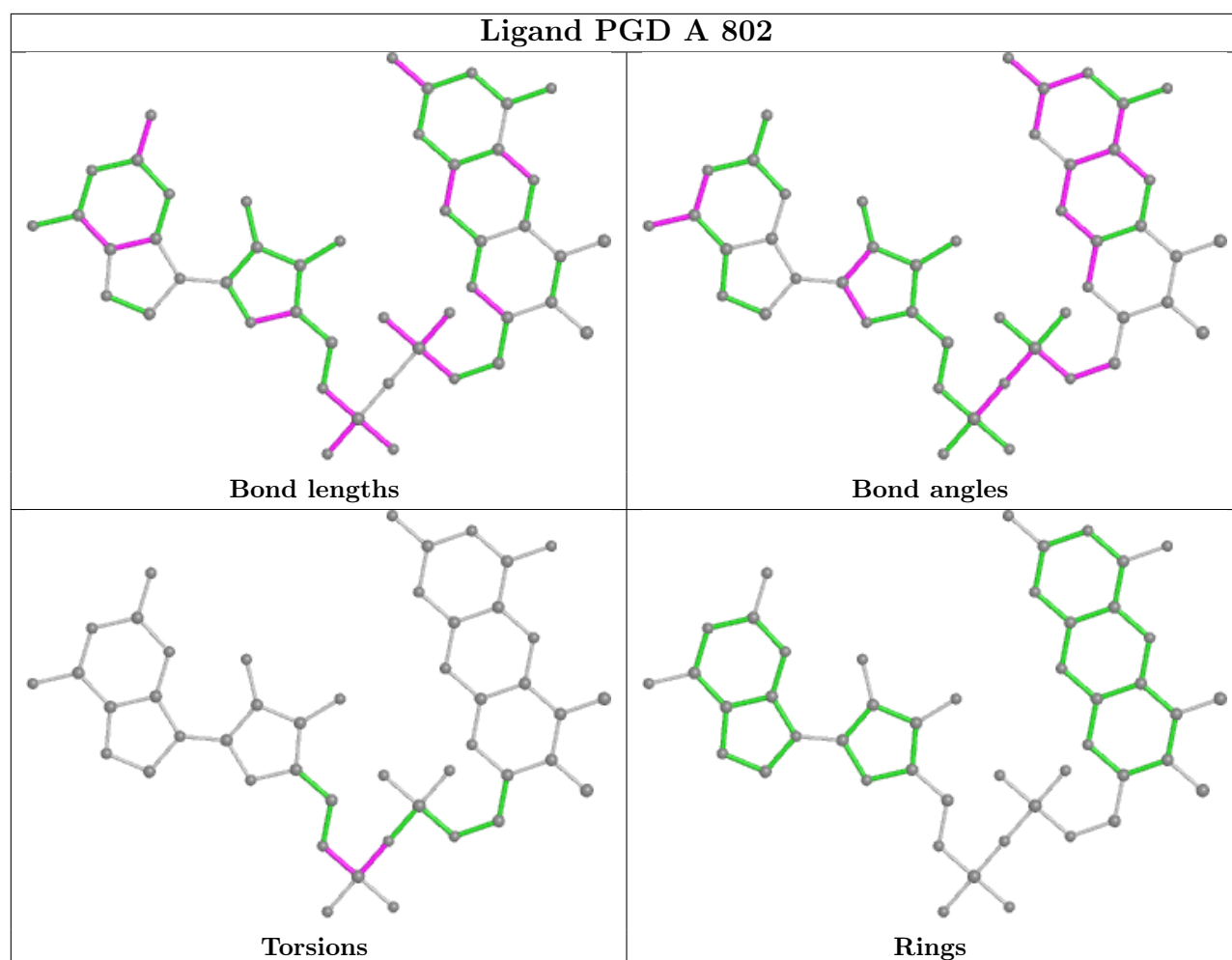
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.











## 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 is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.