



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 21, 2024 – 09:46 am BST

PDB ID : 1E60
Title : OXIDIZED DMSO REDUCTASE EXPOSED TO HEPES - Structure II BUFFER
Authors : Bailey, S.; Bennett, B.; Adams, B.; Smith, A.T.; Bray, R.C.
Deposited on : 2000-08-06
Resolution : 2.00 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 : 1.8.4, 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) : 2.36.2

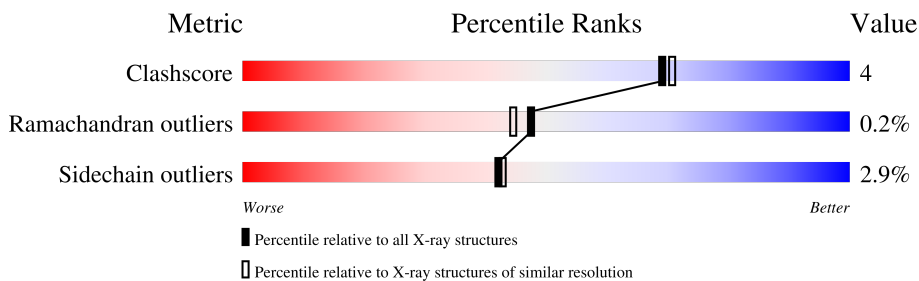
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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 $\leq 5\%$.

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 13400 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	778	5964	3791	1009	1137	27	0	0	0
1	C	770	5904	3752	999	1126	27	0	0	0

There are 26 discrepancies between the modelled and reference sequences:

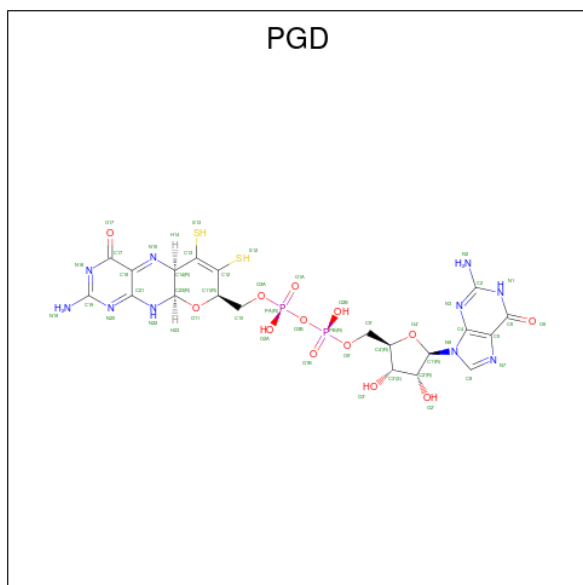
Chain	Residue	Modelled	Actual	Comment	Reference
A	39	SER	THR	conflict	UNP Q52675
A	43	ALA	GLU	conflict	UNP Q52675
A	107	GLU	GLN	conflict	UNP Q52675
A	234	GLU	ASP	conflict	UNP Q52675
A	236	ILE	VAL	conflict	UNP Q52675
A	280	ASP	MET	conflict	UNP Q52675
A	294	GLU	SER	conflict	UNP Q52675
A	295	GLY	ASP	conflict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

Continued on next page...

Continued from previous page...

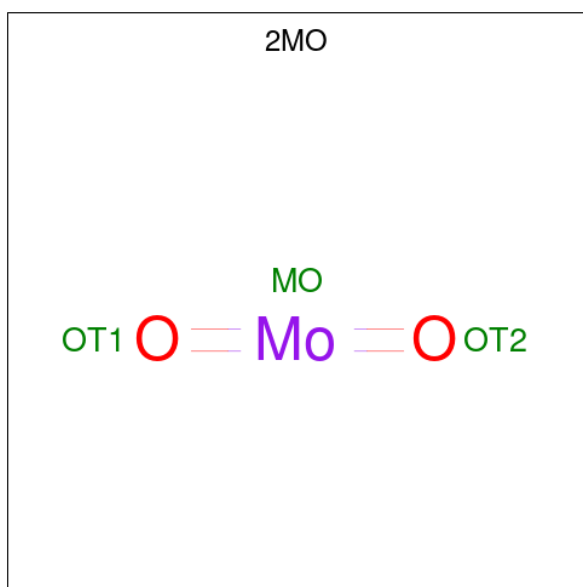
Chain	Residue	Modelled	Actual	Comment	Reference
C	552	ALA	GLY	conflict	UNP Q52675

- 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: C₂₀H₂₄N₁₀O₁₃P₂S₂).



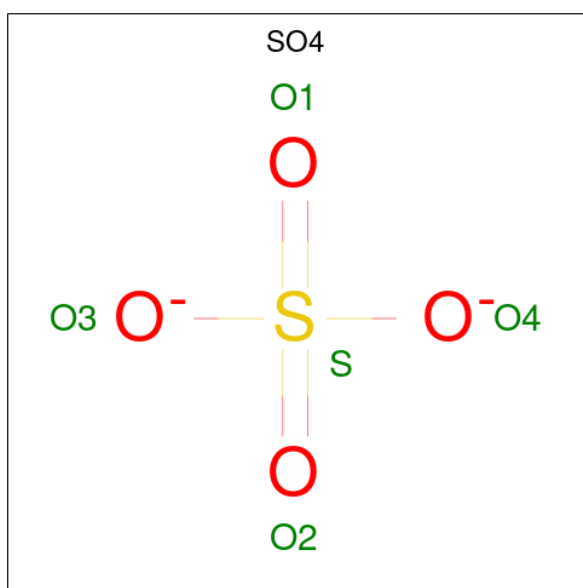
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			S
2	A	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
2	A	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
2	C	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
2	C	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		

- Molecule 3 is MOLYBDENUM (IV)OXIDE (three-letter code: 2MO) (formula: MoO₂).



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: O₄S).



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

Continued on next page...

Continued from previous page...

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

- Molecule 5 is water.


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	686	Total	O	0	0
			686	686		
5	C	632	Total	O	0	0
			632	632		

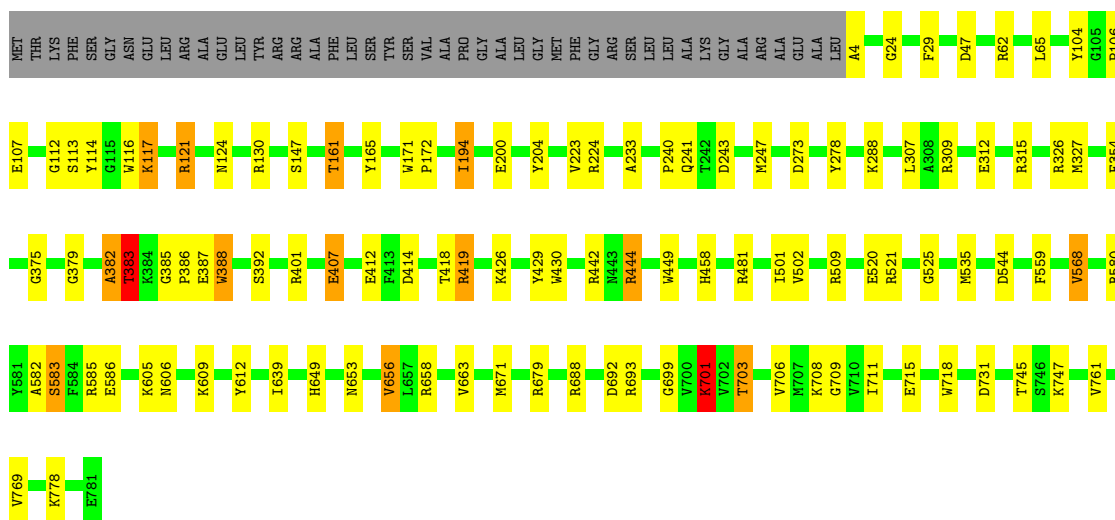
3 Residue-property plots [i](#)

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. 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.

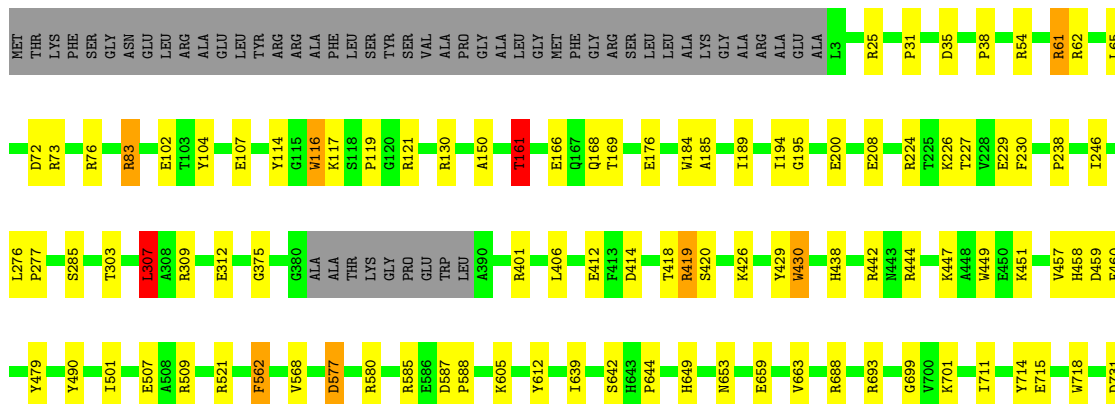
- Molecule 1: Dimethyl sulfoxide/trimethylamine N-oxide reductase

Chain A:  81% 12% • 5%



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

Chain C:  81% 12% • 6%





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, α , β , γ	68.55Å 115.92Å 229.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	98.1 (20.00-2.00)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.194 , 0.241	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	13400	wwPDB-VP
Average B, all atoms (Å ²)	15.0	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: 2MO, SO4, 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	0.62	1/6125 (0.0%)	1.36	68/8338 (0.8%)
1	C	0.61	1/6061 (0.0%)	1.34	44/8248 (0.5%)
All	All	0.62	2/12186 (0.0%)	1.35	112/16586 (0.7%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	312	GLU	CD-OE1	-8.68	1.16	1.25
1	C	312	GLU	CD-OE1	-7.28	1.17	1.25

All (112) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	62	ARG	NE-CZ-NH2	-17.45	111.58	120.30
1	C	62	ARG	NE-CZ-NH1	13.12	126.86	120.30
1	A	224	ARG	NE-CZ-NH1	12.79	126.70	120.30
1	C	130	ARG	NE-CZ-NH1	12.12	126.36	120.30
1	C	577	ASP	CB-CG-OD1	11.81	128.93	118.30
1	A	312	GLU	OE1-CD-OE2	-11.40	109.62	123.30
1	A	444	ARG	NE-CZ-NH1	11.15	125.88	120.30
1	A	658	ARG	NE-CZ-NH1	10.97	125.78	120.30
1	C	312	GLU	OE1-CD-OE2	-10.87	110.25	123.30
1	C	309	ARG	NE-CZ-NH2	-10.62	114.99	120.30
1	C	83	ARG	NE-CZ-NH1	10.22	125.41	120.30
1	C	521	ARG	NE-CZ-NH2	-10.06	115.27	120.30
1	A	509	ARG	NE-CZ-NH2	-10.02	115.29	120.30
1	C	130	ARG	NE-CZ-NH2	-10.01	115.30	120.30
1	A	481	ARG	NE-CZ-NH1	9.52	125.06	120.30
1	A	224	ARG	NE-CZ-NH2	-9.36	115.62	120.30
1	C	61	ARG	NE-CZ-NH1	9.36	124.98	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	121	ARG	NE-CZ-NH1	9.25	124.93	120.30
1	C	509	ARG	NE-CZ-NH2	-9.25	115.67	120.30
1	A	224	ARG	CD-NE-CZ	9.04	136.26	123.60
1	A	121	ARG	NE-CZ-NH2	-8.96	115.82	120.30
1	A	568	VAL	CB-CA-C	-8.86	94.58	111.40
1	A	383	THR	N-CA-CB	8.84	127.10	110.30
1	A	419	ARG	NE-CZ-NH1	8.80	124.70	120.30
1	A	312	GLU	CG-CD-OE2	8.77	135.84	118.30
1	A	583	SER	CB-CA-C	8.23	125.74	110.10
1	A	419	ARG	CA-CB-CG	7.97	130.94	113.40
1	C	224	ARG	CD-NE-CZ	7.78	134.49	123.60
1	C	312	GLU	CG-CD-OE2	7.68	133.66	118.30
1	C	72	ASP	CB-CG-OD1	7.62	125.16	118.30
1	A	693	ARG	NE-CZ-NH2	-7.22	116.69	120.30
1	C	521	ARG	NE-CZ-NH1	7.16	123.88	120.30
1	A	388	TRP	CA-CB-CG	7.12	127.23	113.70
1	A	47	ASP	CB-CG-OD2	7.04	124.64	118.30
1	C	73	ARG	NE-CZ-NH1	-7.03	116.79	120.30
1	A	703	THR	CB-CA-C	-6.96	92.82	111.60
1	A	114	TYR	CB-CG-CD1	-6.95	116.83	121.00
1	A	407	GLU	OE1-CD-OE2	-6.78	115.16	123.30
1	C	521	ARG	CD-NE-CZ	6.72	133.01	123.60
1	A	165	TYR	CB-CG-CD2	-6.71	116.97	121.00
1	A	693	ARG	CG-CD-NE	6.68	125.83	111.80
1	C	401	ARG	NE-CZ-NH2	-6.67	116.96	120.30
1	A	692	ASP	CB-CG-OD1	6.59	124.23	118.30
1	C	442	ARG	NE-CZ-NH2	-6.58	117.01	120.30
1	C	459	ASP	CB-CG-OD1	6.52	124.17	118.30
1	A	769	VAL	N-CA-CB	-6.52	97.16	111.50
1	C	458	HIS	N-CA-CB	6.47	122.25	110.60
1	A	194	ILE	CA-CB-CG2	6.46	123.83	110.90
1	A	442	ARG	NE-CZ-NH2	-6.44	117.08	120.30
1	A	444	ARG	CD-NE-CZ	6.39	132.55	123.60
1	C	54	ARG	NE-CZ-NH1	6.35	123.48	120.30
1	C	208	GLU	OE1-CD-OE2	-6.28	115.77	123.30
1	C	585	ARG	NE-CZ-NH2	-6.27	117.17	120.30
1	A	62	ARG	NE-CZ-NH2	-6.21	117.19	120.30
1	A	580	ARG	NE-CZ-NH2	-6.20	117.20	120.30
1	C	76	ARG	NE-CZ-NH1	6.20	123.40	120.30
1	C	25	ARG	NE-CZ-NH1	6.19	123.39	120.30
1	C	490	TYR	CB-CG-CD1	-6.18	117.29	121.00
1	A	326	ARG	NE-CZ-NH1	6.15	123.37	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	401	ARG	NE-CZ-NH2	-6.04	117.28	120.30
1	A	309	ARG	NE-CZ-NH2	-6.03	117.28	120.30
1	C	307	LEU	CA-CB-CG	6.01	129.13	115.30
1	A	679	ARG	NE-CZ-NH1	5.98	123.29	120.30
1	A	731	ASP	CB-CG-OD1	5.95	123.65	118.30
1	C	688	ARG	NE-CZ-NH1	-5.91	117.35	120.30
1	C	612	TYR	CB-CG-CD1	5.89	124.54	121.00
1	C	114	TYR	CA-CB-CG	-5.87	102.24	113.40
1	C	577	ASP	OD1-CG-OD2	-5.82	112.25	123.30
1	A	701	LYS	CA-CB-CG	5.75	126.06	113.40
1	C	731	ASP	CB-CG-OD1	5.67	123.40	118.30
1	A	401	ARG	NE-CZ-NH1	5.64	123.12	120.30
1	A	458	HIS	N-CA-CB	5.64	120.75	110.60
1	C	580	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	A	204	TYR	CB-CG-CD2	5.62	124.37	121.00
1	C	102	GLU	CB-CG-CD	5.62	129.38	114.20
1	A	568	VAL	N-CA-CB	5.62	123.86	111.50
1	A	130	ARG	NE-CZ-NH1	5.59	123.10	120.30
1	C	116	TRP	CA-CB-CG	-5.59	103.08	113.70
1	A	612	TYR	CB-CG-CD1	5.57	124.34	121.00
1	A	688	ARG	NE-CZ-NH2	-5.55	117.52	120.30
1	A	580	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	A	679	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	A	204	TYR	CB-CG-CD1	-5.47	117.72	121.00
1	A	29	PHE	CB-CG-CD1	5.47	124.63	120.80
1	A	688	ARG	CD-NE-CZ	5.45	131.22	123.60
1	A	521	ARG	NE-CZ-NH1	5.44	123.02	120.30
1	A	419	ARG	N-CA-CB	5.42	120.36	110.60
1	C	444	ARG	NE-CZ-NH2	-5.42	117.59	120.30
1	C	612	TYR	CB-CG-CD2	-5.39	117.77	121.00
1	A	165	TYR	CB-CG-CD1	5.39	124.23	121.00
1	A	407	GLU	CG-CD-OE2	5.35	129.00	118.30
1	C	76	ARG	CG-CD-NE	5.35	123.03	111.80
1	A	385	GLY	N-CA-C	-5.31	99.82	113.10
1	C	161	THR	N-CA-CB	5.29	120.35	110.30
1	A	419	ARG	CB-CA-C	-5.28	99.84	110.40
1	A	693	ARG	CD-NE-CZ	5.28	130.98	123.60
1	A	585	ARG	NE-CZ-NH1	5.23	122.91	120.30
1	C	693	ARG	NE-CZ-NH2	-5.22	117.69	120.30
1	A	273	ASP	CB-CG-OD1	5.21	122.99	118.30
1	A	354	PHE	CB-CG-CD2	5.18	124.42	120.80
1	A	161	THR	N-CA-CB	5.14	120.06	110.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	544	ASP	CB-CG-OD2	-5.13	113.68	118.30
1	A	656	VAL	CB-CA-C	-5.13	101.64	111.40
1	A	114	TYR	CA-CB-CG	-5.13	103.66	113.40
1	C	460	PHE	N-CA-CB	5.12	119.81	110.60
1	A	481	ARG	NE-CZ-NH2	-5.09	117.76	120.30
1	C	490	TYR	CB-CG-CD2	5.08	124.05	121.00
1	A	382	ALA	CA-C-N	5.08	128.38	117.20
1	A	412	GLU	OE1-CD-OE2	5.08	129.40	123.30
1	C	35	ASP	CB-CG-OD2	-5.06	113.75	118.30
1	A	658	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	A	233	ALA	CB-CA-C	-5.03	102.56	110.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	5964	0	5763	44	0
1	C	5904	0	5706	42	0
2	A	94	0	42	4	0
2	C	94	0	42	2	0
3	A	3	0	0	0	0
3	C	3	0	0	0	0
4	A	10	0	0	1	0
4	C	10	0	0	0	0
5	A	686	0	0	4	0
5	C	632	0	0	5	0
All	All	13400	0	11553	86	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 (86) 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:407:GLU:OE1	1:A:444:ARG:NH2	2.09	0.83
1:C:562:PHE:HD1	1:C:568:VAL:HG23	1.49	0.77
1:C:562:PHE:CD1	1:C:568:VAL:HG23	2.22	0.74
1:A:535:MET:HE1	1:A:559:PHE:HZ	1.57	0.69
1:C:414:ASP:OD1	1:C:419:ARG:HG2	1.93	0.67
1:C:176:GLU:HG3	5:C:2074:HOH:O	1.94	0.66
1:C:189:ILE:HD12	1:C:227:THR:HA	1.76	0.65
1:A:701:LYS:HD3	5:A:2616:HOH:O	1.97	0.63
1:C:194:ILE:C	1:C:194:ILE:HD12	2.20	0.62
1:A:535:MET:HE1	1:A:559:PHE:CZ	2.35	0.61
1:C:568:VAL:HG22	5:C:2452:HOH:O	1.99	0.61
1:A:407:GLU:HG2	5:A:2382:HOH:O	2.02	0.60
1:A:106:PRO:HB2	1:A:388:TRP:CZ3	2.37	0.60
1:A:107:GLU:HG3	1:A:388:TRP:CE2	2.38	0.58
1:C:121:ARG:HB3	1:C:375:GLY:HA3	1.85	0.58
1:A:414:ASP:OD2	1:A:747:LYS:HE3	2.04	0.57
1:A:383:THR:HG23	5:A:2153:HOH:O	2.05	0.57
1:C:479:TYR:HB3	1:C:501:ILE:HD12	1.87	0.57
1:A:582:ALA:O	1:A:586:GLU:HB3	2.05	0.56
1:A:653:ASN:ND2	1:A:718:TRP:H	2.08	0.52
1:C:732:LYS:HD2	1:C:769:VAL:HG13	1.92	0.51
1:C:406:LEU:O	1:C:451:LYS:HD2	2.10	0.51
1:A:414:ASP:OD1	1:A:419:ARG:HG2	2.11	0.51
1:C:653:ASN:ND2	1:C:718:TRP:H	2.09	0.51
1:A:663:VAL:HB	1:A:699:GLY:HA3	1.93	0.50
1:A:671:MET:HE1	1:A:761:VAL:HG11	1.93	0.50
1:C:642:SER:HB2	2:C:802:PGD:O1B	2.11	0.50
1:C:663:VAL:HB	1:C:699:GLY:HA3	1.93	0.50
1:A:520:GLU:OE1	1:A:525:GLY:HA3	2.12	0.49
1:C:781:GLU:OE1	5:C:2624:HOH:O	2.20	0.49
1:C:161:THR:HB	1:C:166:GLU:OE2	2.13	0.49
1:C:107:GLU:CD	1:C:107:GLU:H	2.16	0.48
1:C:303:THR:HG22	1:C:307:LEU:HD22	1.95	0.48
1:A:107:GLU:HG3	1:A:388:TRP:NE1	2.28	0.48
1:A:121:ARG:HB3	1:A:375:GLY:HA3	1.95	0.48
1:A:535:MET:CE	1:A:559:PHE:CZ	2.97	0.48
1:C:104:TYR:CD2	1:C:426:LYS:HG3	2.49	0.48
1:A:639:ILE:HG12	1:A:711:ILE:HD11	1.94	0.47
1:A:107:GLU:HG2	1:A:392:SER:HB3	1.96	0.47
1:A:117:LYS:HE2	1:A:124:ASN:OD1	2.14	0.47
1:A:315:ARG:HA	4:A:902:SO4:O2	2.15	0.47
1:A:147:SER:HA	2:A:801:PGD:S13	2.55	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:GLY:O	1:A:382:ALA:HB3	2.15	0.47
1:C:168:GLN:O	1:C:169:THR:C	2.53	0.46
1:C:150:ALA:HB2	1:C:745:THR:HG21	1.96	0.46
1:C:412:GLU:HA	1:C:420:SER:O	2.15	0.46
1:C:663:VAL:CG2	1:C:701:LYS:HE3	2.45	0.46
1:A:4:ALA:HB3	1:A:24:GLY:HA2	1.96	0.46
1:C:31:PRO:HB3	1:C:38:PRO:HB3	1.99	0.45
1:C:184:TRP:O	1:C:185:ALA:HB3	2.17	0.45
1:C:430:TRP:O	1:C:457:VAL:HA	2.17	0.45
1:A:194:ILE:HD12	1:A:194:ILE:C	2.37	0.45
1:C:104:TYR:CE2	1:C:426:LYS:HG3	2.53	0.44
1:A:708:LYS:HG2	5:A:2248:HOH:O	2.17	0.44
1:C:238:PRO:HB3	1:C:246:ILE:CD1	2.48	0.44
1:A:327:MET:O	1:A:745:THR:HG22	2.18	0.44
1:A:104:TYR:CD2	1:A:426:LYS:HG3	2.53	0.44
1:C:447:LYS:HD3	5:C:2359:HOH:O	2.17	0.43
1:A:104:TYR:CE2	1:A:426:LYS:HG3	2.53	0.43
1:C:194:ILE:HD12	1:C:195:GLY:N	2.33	0.43
1:C:189:ILE:HD11	1:C:230:PHE:CB	2.49	0.42
1:A:243:ASP:O	1:A:247:MET:HG3	2.19	0.42
1:A:278:TYR:CZ	1:A:288:LYS:HE2	2.54	0.42
1:C:116:TRP:O	1:C:117:LYS:C	2.57	0.42
1:C:605:LYS:HG3	5:C:2267:HOH:O	2.19	0.42
1:A:606:ASN:HD22	1:A:606:ASN:HA	1.67	0.42
1:C:276:LEU:HB3	1:C:277:PRO:HD3	2.02	0.41
1:C:83:ARG:NH2	1:C:507:GLU:OE2	2.53	0.41
1:A:171:TRP:N	1:A:172:PRO:HD2	2.35	0.41
1:C:238:PRO:HB3	1:C:246:ILE:HD11	2.03	0.41
1:C:649:HIS:CG	2:C:801:PGD:H102	2.55	0.41
1:A:501:ILE:HG22	1:A:502:VAL:HG13	2.02	0.41
1:A:112:GLY:O	1:A:113:SER:C	2.58	0.41
1:A:147:SER:OG	2:A:802:PGD:S12	2.77	0.41
1:A:223:VAL:HG22	1:A:706:VAL:HG12	2.02	0.41
1:A:241:GLN:HG2	1:A:327:MET:SD	2.61	0.41
1:A:116:TRP:HB2	2:A:801:PGD:O2B	2.21	0.41
1:A:605:LYS:HB3	1:A:609:LYS:NZ	2.36	0.41
1:A:708:LYS:HG3	1:A:709:GLY:N	2.35	0.41
1:C:121:ARG:HB3	1:C:375:GLY:CA	2.50	0.41
1:C:116:TRP:CZ3	1:C:194:ILE:HD13	2.55	0.41
1:A:649:HIS:CG	2:A:801:PGD:H102	2.55	0.40
1:C:639:ILE:HG12	1:C:711:ILE:HD11	2.02	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:PRO:O	1:A:241:GLN:HB2	2.21	0.40
1:C:644:PRO:HA	1:C:714:TYR:CG	2.55	0.40
1:C:587:ASP:HA	1:C:588:PRO:HD2	1.97	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	776/823 (94%)	746 (96%)	28 (4%)	2 (0%)	41 37
1	C	766/823 (93%)	745 (97%)	20 (3%)	1 (0%)	51 49
All	All	1542/1646 (94%)	1491 (97%)	48 (3%)	3 (0%)	47 44

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	386	PRO
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.

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	616/648 (95%)	599 (97%)	17 (3%)	43	44
1	C	611/648 (94%)	592 (97%)	19 (3%)	40	40
All	All	1227/1296 (95%)	1191 (97%)	36 (3%)	42	43

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	LEU
1	A	161	THR
1	A	200	GLU
1	A	307	LEU
1	A	383	THR
1	A	387	GLU
1	A	418	THR
1	A	429	TYR
1	A	430	TRP
1	A	449	TRP
1	A	568	VAL
1	A	583	SER
1	A	656	VAL
1	A	701	LYS
1	A	703	THR
1	A	715	GLU
1	A	778	LYS
1	C	61	ARG
1	C	65	LEU
1	C	119	PRO
1	C	161	THR
1	C	200	GLU
1	C	226	LYS
1	C	229	GLU
1	C	285	SER
1	C	307	LEU
1	C	418	THR
1	C	419	ARG
1	C	429	TYR
1	C	430	TRP
1	C	438	HIS
1	C	449	TRP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	562	PHE
1	C	577	ASP
1	C	659	GLU
1	C	715	GLU

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	606	ASN
1	A	653	ASN
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](#)

10 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
4	SO4	C	901	-	4,4,4	0.53	0	6,6,6	0.63	0
2	PGD	C	802	-	40,52,52	2.78	15 (37%)	38,81,81	1.69	7 (18%)
2	PGD	A	801	3	40,52,52	2.66	16 (40%)	38,81,81	2.01	9 (23%)
4	SO4	C	902	-	4,4,4	0.63	0	6,6,6	0.43	0
3	2MO	C	803	2,1	0,2,2	-	-	-	-	-
2	PGD	A	802	-	40,52,52	2.76	17 (42%)	38,81,81	1.85	10 (26%)
2	PGD	C	801	3	40,52,52	2.63	13 (32%)	38,81,81	1.94	12 (31%)
4	SO4	A	902	-	4,4,4	0.58	0	6,6,6	0.21	0
4	SO4	A	901	-	4,4,4	0.28	0	6,6,6	0.35	0
3	2MO	A	803	2,1	0,2,2	-	-	-	-	-

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
2	PGD	A	801	3	-	6/18/82/82	0/6/6/6
2	PGD	C	801	3	-	7/18/82/82	0/6/6/6
2	PGD	C	802	-	-	3/18/82/82	0/6/6/6
2	PGD	A	802	-	-	2/18/82/82	0/6/6/6

All (61) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	802	PGD	C21-N22	7.75	1.43	1.35
2	A	802	PGD	C16-N15	7.62	1.46	1.28
2	C	801	PGD	C16-N15	7.58	1.46	1.28
2	A	801	PGD	C21-N22	7.43	1.43	1.35
2	C	802	PGD	C16-N15	7.39	1.45	1.28
2	A	801	PGD	C16-N15	6.83	1.44	1.28
2	C	802	PGD	C21-N22	6.55	1.42	1.35
2	A	801	PGD	PA-O1A	6.32	1.73	1.50
2	C	801	PGD	PB-O1B	6.12	1.72	1.50
2	C	801	PGD	PA-O1A	6.07	1.72	1.50
2	C	801	PGD	C21-N22	5.67	1.41	1.35
2	C	802	PGD	PB-O1B	5.58	1.70	1.50
2	C	802	PGD	PA-O1A	5.28	1.69	1.50
2	A	802	PGD	PB-O1B	4.98	1.68	1.50
2	A	801	PGD	PB-O1B	4.94	1.68	1.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	802	PGD	O11-C11	-4.61	1.37	1.43
2	A	802	PGD	PA-O1A	4.60	1.67	1.50
2	A	802	PGD	C5-C6	-4.25	1.38	1.47
2	C	801	PGD	C5-C6	-4.21	1.38	1.47
2	A	801	PGD	C5-C6	-4.05	1.39	1.47
2	C	801	PGD	PB-O5'	3.96	1.75	1.59
2	C	802	PGD	PA-O3A	3.91	1.75	1.59
2	A	801	PGD	PB-O5'	3.78	1.74	1.59
2	C	802	PGD	C5-C6	-3.63	1.40	1.47
2	C	802	PGD	PB-O5'	3.63	1.74	1.59
2	A	802	PGD	PA-O2A	3.63	1.72	1.55
2	A	802	PGD	PB-O5'	3.52	1.73	1.59
2	A	802	PGD	PB-O2B	3.48	1.71	1.55
2	C	802	PGD	C10-C11	3.44	1.56	1.52
2	A	801	PGD	PA-O3A	3.40	1.73	1.59
2	C	801	PGD	C2-N2	3.36	1.42	1.34
2	A	802	PGD	C2-N2	3.16	1.41	1.34
2	C	802	PGD	PB-O2B	3.12	1.70	1.55
2	C	802	PGD	PA-O2A	3.12	1.70	1.55
2	A	802	PGD	PA-O3A	3.09	1.71	1.59
2	C	802	PGD	C2-N2	3.06	1.41	1.34
2	A	801	PGD	PB-O2B	2.98	1.69	1.55
2	C	802	PGD	C5-C4	-2.89	1.35	1.43
2	A	801	PGD	C2-N2	2.89	1.41	1.34
2	C	801	PGD	C5-C4	-2.89	1.35	1.43
2	A	801	PGD	C5-C4	-2.80	1.35	1.43
2	C	801	PGD	C19-N19	2.76	1.42	1.34
2	A	802	PGD	C5-C4	-2.76	1.36	1.43
2	C	802	PGD	C19-N19	2.75	1.42	1.34
2	C	801	PGD	PA-O2A	2.73	1.68	1.55
2	C	801	PGD	PA-O3A	2.70	1.70	1.59
2	A	802	PGD	O11-C11	-2.63	1.40	1.43
2	A	802	PGD	C21-N20	2.59	1.37	1.32
2	A	801	PGD	PA-O2A	2.55	1.67	1.55
2	A	801	PGD	C19-N19	2.53	1.41	1.34
2	A	802	PGD	O4'-C1'	2.48	1.44	1.41
2	A	802	PGD	C10-C11	2.36	1.55	1.52
2	A	801	PGD	C2-N3	2.35	1.38	1.33
2	A	801	PGD	C10-C11	2.33	1.55	1.52
2	A	802	PGD	O11-C23	-2.27	1.40	1.43
2	A	801	PGD	O4'-C1'	2.26	1.44	1.41
2	C	802	PGD	O4'-C1'	2.24	1.44	1.41

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	802	PGD	C19-N19	2.23	1.40	1.34
2	C	801	PGD	PB-O2B	2.22	1.65	1.55
2	C	801	PGD	O4'-C1'	2.16	1.44	1.41
2	A	801	PGD	O11-C23	-2.07	1.40	1.43

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	PGD	C17-C16-N15	6.37	125.06	118.06
2	C	802	PGD	C17-C16-N15	5.69	124.31	118.06
2	C	801	PGD	C17-C16-N15	5.35	123.94	118.06
2	C	802	PGD	N20-C19-N18	-4.44	119.22	126.43
2	C	801	PGD	N20-C19-N18	-4.30	119.46	126.43
2	A	801	PGD	N20-C19-N18	-4.26	119.52	126.43
2	A	802	PGD	O6-C6-N1	-4.00	115.92	120.65
2	A	801	PGD	O6-C6-N1	-3.93	116.01	120.65
2	A	802	PGD	C17-C16-N15	3.63	122.04	118.06
2	A	802	PGD	O4'-C1'-C2'	-3.60	101.66	106.93
2	C	801	PGD	C2-N1-C6	-3.51	118.64	125.10
2	A	802	PGD	O11-C23-C14	3.28	113.38	108.73
2	A	801	PGD	N19-C19-N18	3.17	122.04	117.06
2	A	802	PGD	N20-C19-N18	-3.02	121.53	126.43
2	C	801	PGD	O4'-C1'-C2'	-2.92	102.67	106.93
2	A	801	PGD	C16-C21-N22	2.89	123.64	116.62
2	C	801	PGD	N19-C19-N18	2.79	121.46	117.06
2	A	801	PGD	C23-C14-N15	2.79	115.39	111.33
2	C	801	PGD	C5-C6-N1	2.78	118.87	113.95
2	C	802	PGD	PA-O3A-C10	-2.77	105.46	121.68
2	C	802	PGD	O4'-C1'-C2'	-2.65	103.05	106.93
2	A	802	PGD	O11-C23-N22	-2.63	105.86	108.57
2	C	801	PGD	C23-C14-N15	2.59	115.11	111.33
2	A	802	PGD	C2-N1-C6	-2.59	120.33	125.10
2	A	801	PGD	O4'-C1'-C2'	-2.58	103.15	106.93
2	C	801	PGD	PB-O5'-C5'	-2.58	106.57	121.68
2	C	802	PGD	N19-C19-N18	2.52	121.02	117.06
2	A	801	PGD	O11-C23-N22	-2.36	106.14	108.57
2	C	801	PGD	O6-C6-N1	-2.31	117.92	120.65
2	C	801	PGD	O4'-C4'-C3'	2.29	109.64	105.11
2	C	802	PGD	C5'-C4'-C3'	-2.24	106.78	115.18
2	A	802	PGD	N19-C19-N18	2.23	120.57	117.06
2	A	802	PGD	PA-O3A-C10	-2.20	108.79	121.68
2	C	801	PGD	C16-C21-N22	2.20	121.95	116.62

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	801	PGD	O11-C23-C14	2.10	111.70	108.73
2	A	802	PGD	C5-C6-N1	2.06	117.58	113.95
2	A	801	PGD	O17-C17-N18	-2.05	116.74	120.23
2	C	802	PGD	C16-C21-N22	2.04	121.56	116.62

There are no chirality outliers.

All (18) 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-O1B
2	A	801	PGD	C5'-O5'-PB-O2B
2	A	802	PGD	O3A-C10-C11-C12
2	C	801	PGD	PA-O3B-PB-O5'
2	C	801	PGD	C5'-O5'-PB-O1B
2	C	801	PGD	C5'-O5'-PB-O2B
2	A	801	PGD	O3A-C10-C11-C12
2	C	801	PGD	O3A-C10-C11-C12
2	C	802	PGD	O3A-C10-C11-C12
2	C	801	PGD	O4'-C4'-C5'-O5'
2	A	802	PGD	O3A-C10-C11-O11
2	C	801	PGD	O3A-C10-C11-O11
2	C	802	PGD	O3A-C10-C11-O11
2	A	801	PGD	C5'-O5'-PB-O3B
2	C	801	PGD	C5'-O5'-PB-O3B
2	A	801	PGD	O4'-C4'-C5'-O5'
2	C	802	PGD	O4'-C4'-C5'-O5'

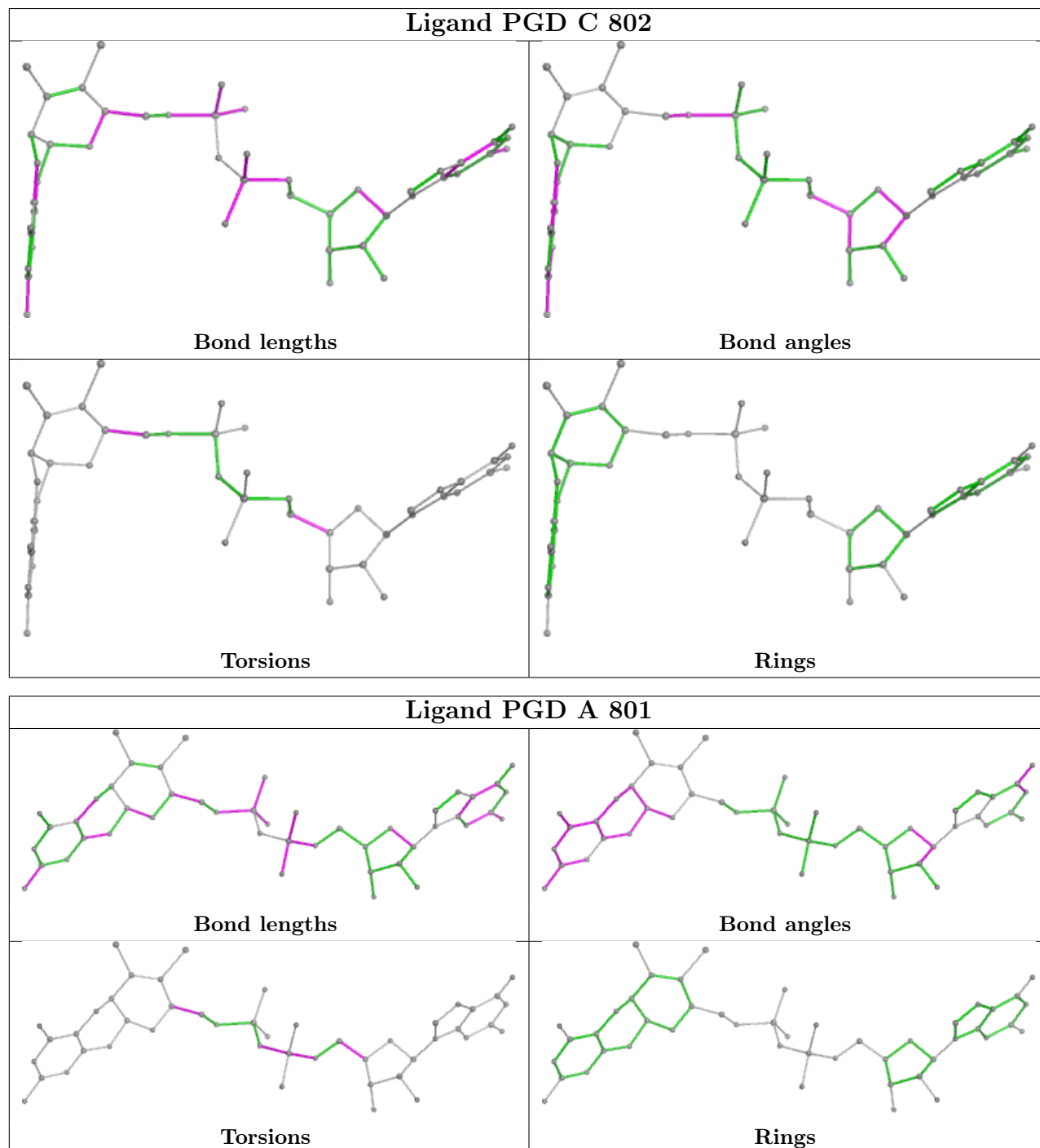
There are no ring outliers.

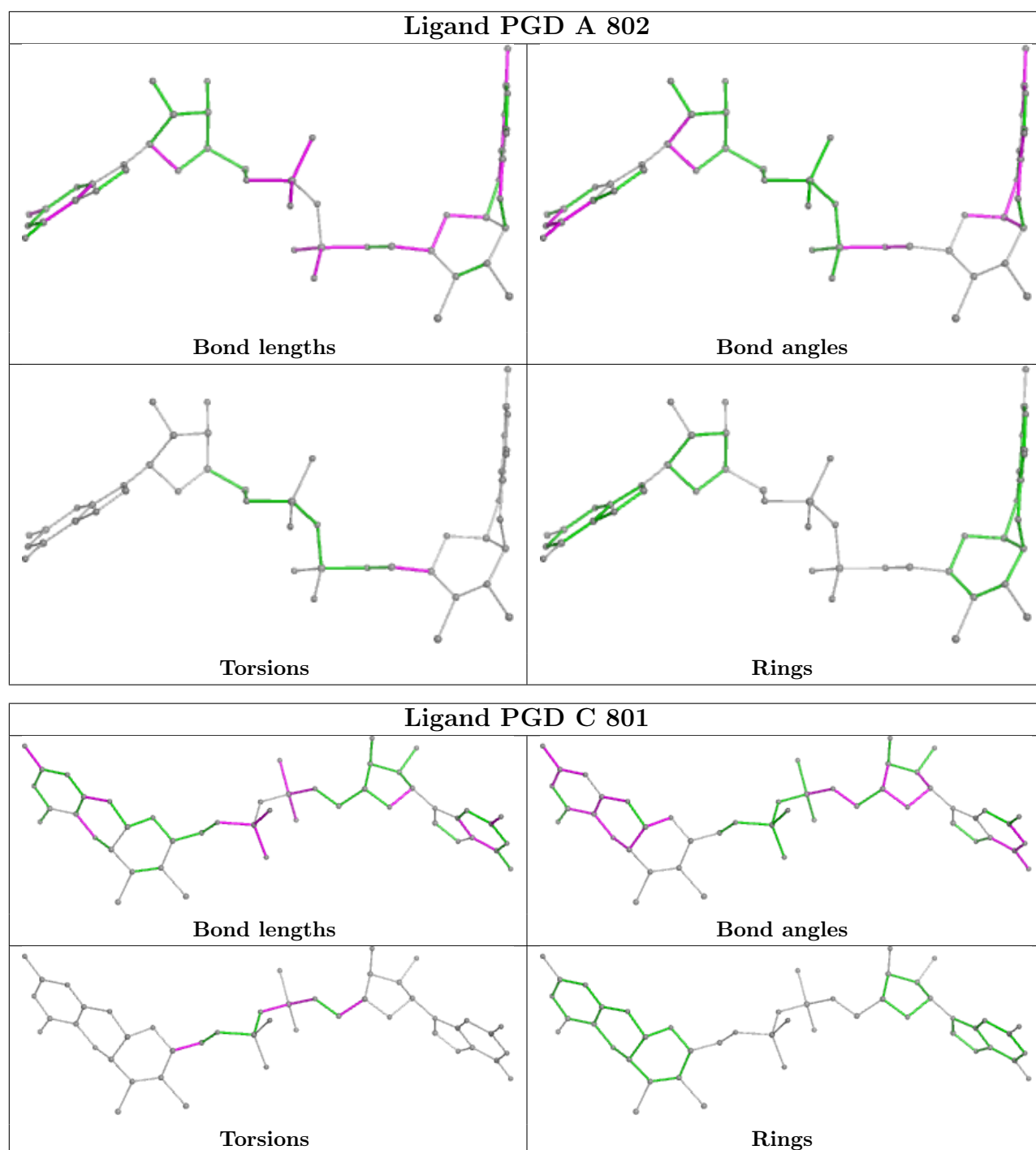
5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	802	PGD	1	0
2	A	801	PGD	3	0
2	A	802	PGD	1	0
2	C	801	PGD	1	0
4	A	902	SO4	1	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 [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.