



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:43 PM UTC

PDB ID : 1E92 / pdb_00001e92
Title : Pteridine reductase 1 from Leishmania major complexed with NADP⁺ and dihydrobiopterin
Authors : Schuettelkopf, A.W.; Hunter, W.N.
Deposited on : 2000-10-04
Resolution : 2.20 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

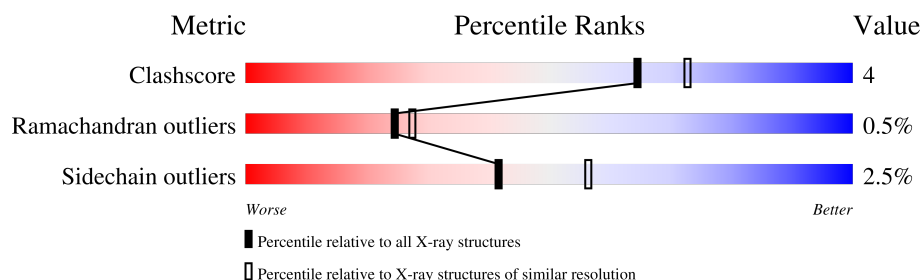
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)

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	288	
1	B	288	
1	C	288	
1	D	288	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

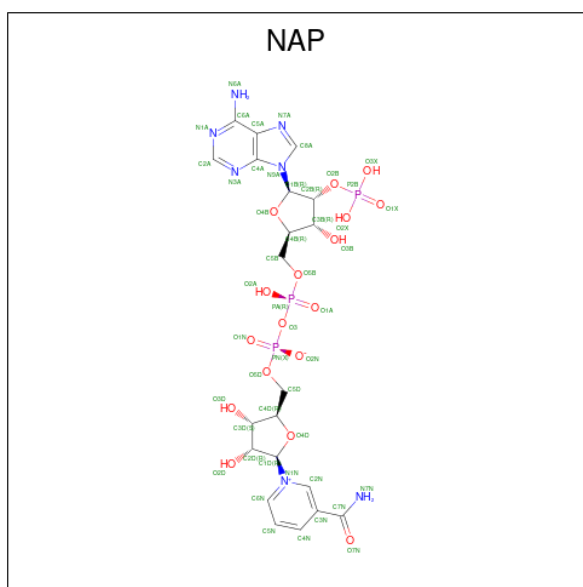
Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	EDO	B	1292	-	X	-	-
4	EDO	B	1293	-	X	-	-

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 PTERIDINE REDUCTASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	268	Total 2006	C 1261	N 359	O 375	S 11	12	1	0
1	B	266	Total 1985	C 1251	N 353	O 370	S 11	4	0	0
1	C	257	Total 1915	C 1205	N 344	O 356	S 10	22	0	0
1	D	256	Total 1906	C 1201	N 342	O 353	S 10	10	0	0

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



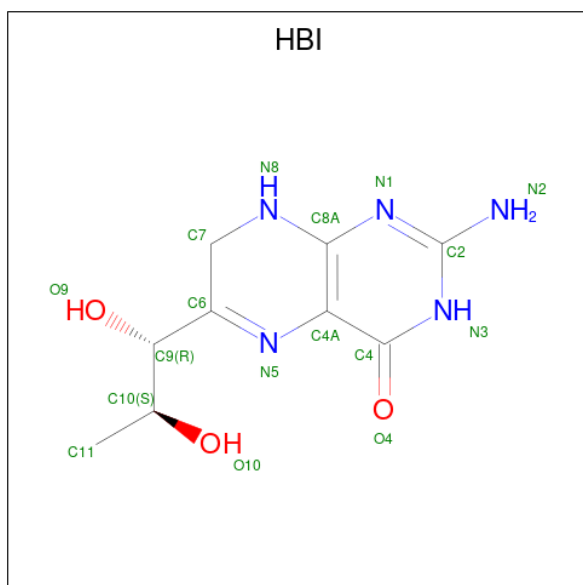
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	B	1	Total 48	C 21	N 7	O 17	P 3	0	0

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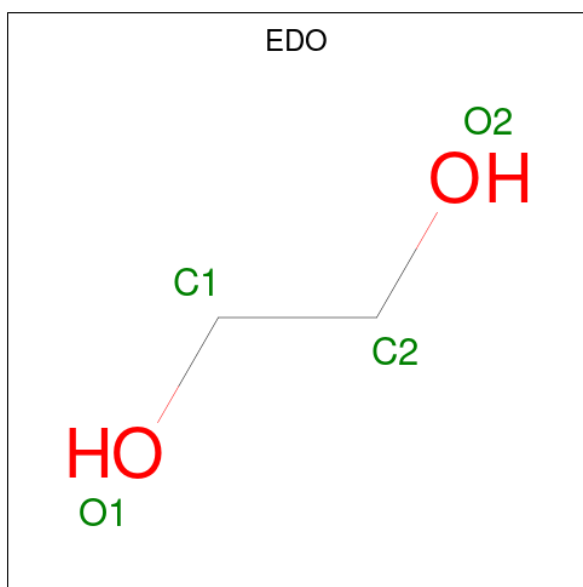
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is 7,8-DIHYDROBIOPTERIN (CCD ID: HBI) (formula: $C_9H_{13}N_5O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			17	9	5	3		
3	B	1	Total	C	N	O	0	0
			17	9	5	3		
3	C	1	Total	C	N	O	0	0
			17	9	5	3		
3	D	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	109	Total	O	0	0
			109	109		
5	B	101	Total	O	0	0
			101	101		
5	C	114	Total	O	0	0
			114	114		
5	D	110	Total	O	0	0
			110	110		

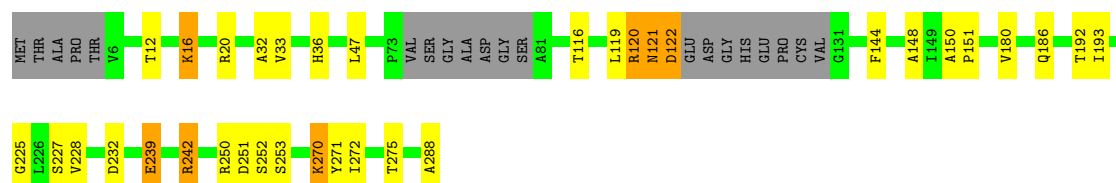
3 Residue-property plots [i](#)

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.

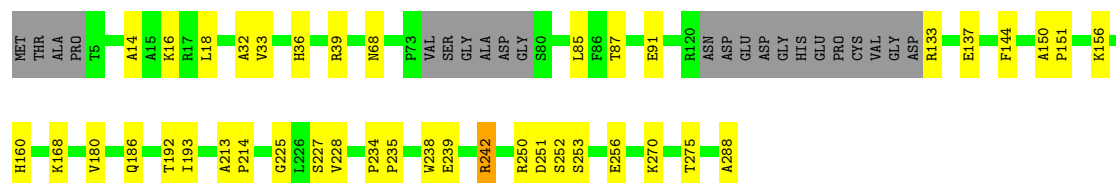
• Molecule 1: PTERIDINE REDUCTASE 1

Chain A: 



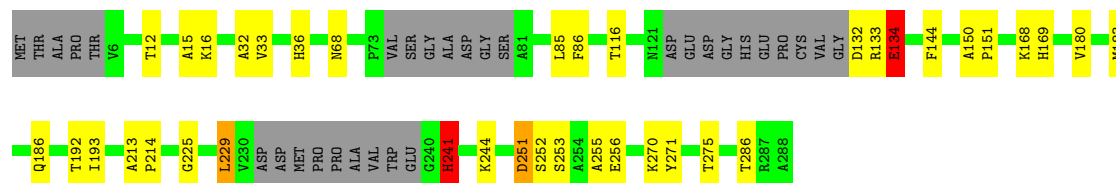
• Molecule 1: PTERIDINE REDUCTASE 1

Chain B: 



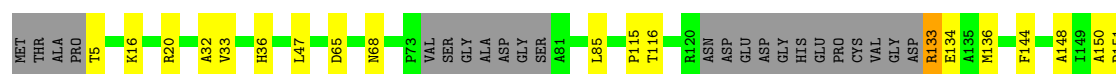
• Molecule 1: PTERIDINE REDUCTASE 1

Chain C: 



• Molecule 1: PTERIDINE REDUCTASE 1

Chain D: 



V180	Q186	P187	L188	T192	I193	G225	V230	ASP	ASP	MET	PRO	PRO	ALA	VAL	TRP	GLU	G240	D251	S252	S253	K270	Y271	T286	R287	A288
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4 Data and refinement statistics

Xtriage (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	94.34Å 103.80Å 137.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.77 – 2.20	Depositor
% Data completeness (in resolution range)	90.5 (27.77-2.20)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.198 , 0.227	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8522	wwPDB-VP
Average B, all atoms (Å ²)	23.0	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: NAP, HBI, EDO

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	0.82	0/2050	1.05	12/2791 (0.4%)
1	B	0.79	0/2024	1.06	11/2757 (0.4%)
1	C	0.78	1/1949 (0.1%)	1.06	16/2650 (0.6%)
1	D	0.76	0/1940	1.07	14/2638 (0.5%)
All	All	0.79	1/7963 (0.0%)	1.06	53/10836 (0.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	255	ALA	CA-CB	5.21	1.61	1.53

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	134	GLU	N-CA-C	-10.85	99.76	113.43
1	B	225	GLY	N-CA-C	-9.47	101.59	110.21
1	C	225	GLY	N-CA-C	-8.87	102.14	110.21
1	D	225	GLY	N-CA-C	-8.31	102.64	110.21
1	A	32	ALA	N-CA-C	-8.03	96.47	109.96
1	B	32	ALA	N-CA-C	-7.73	96.97	109.96
1	A	225	GLY	N-CA-C	-7.71	103.19	110.21
1	C	32	ALA	N-CA-C	-7.65	97.10	109.96
1	D	32	ALA	N-CA-C	-7.59	97.21	109.96
1	D	192	THR	N-CA-C	6.86	119.34	111.11
1	C	270	LYS	N-CA-C	6.78	121.00	112.87
1	A	270	LYS	N-CA-C	6.68	120.89	112.87
1	B	186	GLN	N-CA-C	-6.66	97.22	108.94
1	C	192	THR	N-CA-C	6.49	118.89	111.11
1	B	192	THR	N-CA-C	6.40	118.79	111.11
1	D	186	GLN	N-CA-C	-6.34	97.78	108.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	251	ASP	N-CA-C	-6.31	102.65	110.41
1	B	33	VAL	N-CA-C	6.30	116.93	108.11
1	C	133	ARG	N-CA-C	-6.29	106.24	114.04
1	D	33	VAL	N-CA-C	6.24	117.47	108.48
1	A	192	THR	N-CA-C	6.19	118.54	111.11
1	A	186	GLN	N-CA-C	-6.19	98.05	108.94
1	C	186	GLN	N-CA-C	-6.14	98.13	108.94
1	A	16	LYS	N-CA-C	6.12	116.16	108.45
1	C	33	VAL	N-CA-C	6.07	116.61	108.11
1	C	251	ASP	N-CA-C	-6.04	102.98	110.41
1	B	253	SER	N-CA-C	-6.01	102.77	110.53
1	B	16	LYS	N-CA-C	6.01	117.03	108.74
1	A	116	THR	CA-C-N	5.99	126.01	119.90
1	A	116	THR	C-N-CA	5.99	126.01	119.90
1	B	270	LYS	N-CA-C	5.70	119.85	113.01
1	B	14	ALA	N-CA-C	5.62	119.98	113.18
1	A	33	VAL	N-CA-C	5.60	116.19	108.12
1	C	253	SER	N-CA-C	-5.60	102.47	110.59
1	D	270	LYS	N-CA-C	5.56	119.54	112.87
1	B	251	ASP	N-CA-C	-5.46	103.70	110.41
1	D	115	PRO	N-CA-C	5.46	119.65	111.14
1	D	116	THR	CA-C-N	5.45	125.46	119.90
1	D	116	THR	C-N-CA	5.45	125.46	119.90
1	C	134	GLU	N-CA-C	-5.43	106.66	113.28
1	A	251	ASP	N-CA-C	-5.38	103.42	110.53
1	D	253	SER	N-CA-C	-5.36	103.62	110.53
1	C	116	THR	CA-C-N	5.33	125.34	119.90
1	C	116	THR	C-N-CA	5.33	125.34	119.90
1	C	16	LYS	N-CA-C	5.32	115.15	108.45
1	A	253	SER	N-CA-C	-5.23	103.78	110.53
1	A	272	ILE	CB-CA-C	-5.18	104.70	110.96
1	C	15	ALA	N-CA-C	5.17	117.66	111.71
1	B	242	ARG	CB-CA-C	-5.13	102.27	110.79
1	C	183	MET	N-CA-C	5.13	119.64	113.17
1	D	65	ASP	N-CA-C	-5.13	100.81	108.96
1	D	188	LEU	N-CA-C	-5.09	101.67	109.76
1	C	241	HIS	N-CA-C	5.04	121.53	110.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2006	0	2009	21	0
1	B	1985	0	1995	17	0
1	C	1915	0	1931	13	0
1	D	1906	0	1928	19	0
2	A	48	0	25	0	0
2	B	48	0	25	1	0
2	C	48	0	25	0	0
2	D	48	0	25	0	0
3	A	17	0	13	0	0
3	B	17	0	13	0	0
3	C	17	0	13	0	0
3	D	17	0	13	0	0
4	B	12	0	18	1	0
4	D	4	0	6	0	0
5	A	109	0	0	0	0
5	B	101	0	0	0	0
5	C	114	0	0	1	0
5	D	110	0	0	0	0
All	All	8522	0	8039	62	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 (62) 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:119:LEU:HD13	1:A:122:ASP:HB2	1.26	1.10
1:A:119:LEU:HD13	1:A:122:ASP:CB	1.85	1.04
1:D:133:ARG:HH11	1:D:133:ARG:HG2	1.23	1.01
1:D:133:ARG:HH11	1:D:133:ARG:CG	1.94	0.81
1:D:133:ARG:N	1:D:133:ARG:HD3	2.04	0.72
1:A:119:LEU:CD1	1:A:122:ASP:HB2	2.13	0.70
1:D:133:ARG:HG2	1:D:133:ARG:NH1	2.00	0.69
1:C:86:PHE:CD2	1:D:136:MET:HE1	2.30	0.67
1:D:133:ARG:N	1:D:133:ARG:CD	2.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:39:ARG:HH11	1:B:39:ARG:HG2	1.64	0.62
1:D:230:VAL:HG12	1:D:230:VAL:O	1.99	0.61
1:A:270:LYS:HE3	1:C:256:GLU:OE2	2.03	0.59
1:C:229:LEU:HD22	1:C:251:ASP:HB3	1.85	0.58
1:D:150:ALA:HB3	1:D:151:PRO:HD3	1.89	0.54
1:C:168:LYS:HG3	1:C:169:HIS:ND1	2.23	0.54
1:B:227:SER:O	1:B:228:VAL:C	2.51	0.54
5:C:2048:HOH:O	1:D:136:MET:HG3	2.07	0.54
1:A:20[B]:ARG:HG3	1:A:47:LEU:HD22	1.91	0.53
1:B:256:GLU:OE2	1:D:270:LYS:HE3	2.10	0.52
1:D:144:PHE:CE2	1:D:193:ILE:HG23	2.46	0.51
1:A:242:ARG:HB2	1:A:250:ARG:HA	1.92	0.51
1:A:20[A]:ARG:HD2	1:A:47:LEU:HD22	1.93	0.50
1:C:150:ALA:HB3	1:C:151:PRO:HD3	1.94	0.49
1:A:148:ALA:C	1:A:151:PRO:HD2	2.39	0.48
1:C:12:THR:HA	1:C:36:HIS:HB3	1.96	0.48
1:B:238:TRP:O	1:B:242:ARG:HG3	2.14	0.48
1:A:119:LEU:HD13	1:A:122:ASP:HB3	1.87	0.47
1:C:68:ASN:HA	1:C:85:LEU:HD22	1.97	0.47
1:A:239:GLU:OE2	1:A:242:ARG:HD3	2.14	0.47
1:A:227:SER:O	1:A:228:VAL:C	2.58	0.47
1:A:271:TYR:CE2	1:C:252:SER:HB3	2.50	0.47
1:D:133:ARG:HA	1:D:136:MET:HB3	1.96	0.46
1:C:132:ASP:N	1:C:134:GLU:OE2	2.47	0.46
1:A:144:PHE:CE2	1:A:193:ILE:HG23	2.51	0.46
1:A:16:LYS:HA	1:A:20[B]:ARG:HB2	1.98	0.46
1:B:242:ARG:HB3	1:B:250:ARG:HA	1.97	0.46
1:C:144:PHE:CE2	1:C:193:ILE:HG23	2.51	0.46
1:D:133:ARG:CG	1:D:133:ARG:NH1	2.64	0.45
1:B:150:ALA:HB3	1:B:151:PRO:HD3	1.97	0.45
1:B:144:PHE:CE2	1:B:193:ILE:HG23	2.52	0.44
1:D:68:ASN:HA	1:D:85:LEU:HD22	2.00	0.44
1:B:234:PRO:HA	1:B:235:PRO:HD3	1.89	0.43
1:B:156:LYS:HE2	1:B:160:HIS:CE1	2.53	0.43
1:A:232:ASP:O	1:A:232:ASP:CG	2.61	0.43
1:A:12:THR:HA	1:A:36:HIS:HB3	2.00	0.42
1:A:120:ARG:HG3	1:A:121:ASN:OD1	2.19	0.42
1:A:288:ALA:HB2	1:D:286:THR:HB	2.01	0.42
1:D:16:LYS:HA	1:D:20:ARG:HB2	2.01	0.42
1:A:150:ALA:HB3	1:A:151:PRO:HD3	2.01	0.42
1:A:120:ARG:H	1:A:120:ARG:HG2	1.46	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:87:THR:O	1:B:91:GLU:HG3	2.19	0.42
1:D:148:ALA:C	1:D:151:PRO:HD2	2.45	0.42
1:B:68:ASN:HA	1:B:85:LEU:HD22	2.02	0.41
1:A:252:SER:HB3	1:C:271:TYR:CE2	2.56	0.41
1:B:18:LEU:HB2	2:B:1289:NAP:H51N	2.03	0.41
1:B:252:SER:HB3	1:D:271:TYR:CE2	2.56	0.41
1:D:20:ARG:HG3	1:D:47:LEU:HD22	2.03	0.41
1:B:39:ARG:HG2	1:B:39:ARG:NH1	2.31	0.40
1:B:288:ALA:HB2	1:C:286:THR:HB	2.03	0.40
1:B:68:ASN:HD22	4:B:1293:EDO:C1	2.34	0.40
1:B:213:ALA:N	1:B:214:PRO:CD	2.85	0.40
1:C:213:ALA:N	1:C:214:PRO:CD	2.85	0.40

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	263/288 (91%)	248 (94%)	14 (5%)	1 (0%)	30	34
1	B	260/288 (90%)	247 (95%)	12 (5%)	1 (0%)	30	34
1	C	249/288 (86%)	234 (94%)	13 (5%)	2 (1%)	16	16
1	D	248/288 (86%)	236 (95%)	11 (4%)	1 (0%)	30	34
All	All	1020/1152 (88%)	965 (95%)	50 (5%)	5 (0%)	24	27

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	241	HIS
1	A	180	VAL
1	B	180	VAL

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Mol	Chain	Res	Type
1	C	180	VAL
1	D	180	VAL

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	209/223 (94%)	203 (97%)	6 (3%)	37	51
1	B	207/223 (93%)	201 (97%)	6 (3%)	37	51
1	C	199/223 (89%)	194 (98%)	5 (2%)	42	56
1	D	198/223 (89%)	195 (98%)	3 (2%)	57	73
All	All	813/892 (91%)	793 (98%)	20 (2%)	42	56

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	120	ARG
1	A	121	ASN
1	A	122	ASP
1	A	239	GLU
1	A	242	ARG
1	A	275	THR
1	B	36	HIS
1	B	133	ARG
1	B	137	GLU
1	B	168	LYS
1	B	239	GLU
1	B	275	THR
1	C	134	GLU
1	C	229	LEU
1	C	241	HIS
1	C	244	LYS
1	C	275	THR
1	D	5	THR
1	D	36	HIS

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Mol	Chain	Res	Type
1	D	133	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	108	ASN
1	A	249	GLN
1	B	68	ASN
1	B	108	ASN
1	C	38	HIS
1	C	108	ASN
1	C	216	GLN
1	D	108	ASN
1	D	216	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

12 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	HBI	D	1290	-	15,18,18	3.55	8 (53%)	14,26,26	2.09	6 (42%)
2	NAP	A	1289	-	50,52,52	2.20	12 (24%)	71,80,80	1.56	10 (14%)
4	EDO	B	1291	-	3,3,3	2.15	2 (66%)	2,2,2	0.65	0
2	NAP	D	1289	-	50,52,52	2.24	12 (24%)	71,80,80	1.61	9 (12%)
4	EDO	B	1292	-	3,3,3	2.18	2 (66%)	2,2,2	0.61	0
4	EDO	B	1293	-	3,3,3	2.45	2 (66%)	2,2,2	0.39	0
3	HBI	A	1290	-	15,18,18	3.59	10 (66%)	14,26,26	1.97	6 (42%)
3	HBI	C	1290	-	15,18,18	3.62	9 (60%)	14,26,26	2.10	6 (42%)
3	HBI	B	1290	-	15,18,18	3.59	10 (66%)	14,26,26	2.15	6 (42%)
2	NAP	B	1289	-	50,52,52	2.07	13 (26%)	71,80,80	1.60	10 (14%)
4	EDO	D	1291	-	3,3,3	2.38	2 (66%)	2,2,2	0.42	0
2	NAP	C	1289	-	50,52,52	2.01	10 (20%)	71,80,80	1.58	9 (12%)

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	HBI	D	1290	-	-	4/4/17/17	0/2/2/2
2	NAP	A	1289	-	-	0/35/67/67	0/5/5/5
4	EDO	B	1291	-	-	0/1/1/1	-
2	NAP	D	1289	-	-	0/35/67/67	0/5/5/5
4	EDO	B	1292	-	-	1/1/1/1	-
4	EDO	B	1293	-	-	1/1/1/1	-
3	HBI	A	1290	-	-	4/4/17/17	0/2/2/2
3	HBI	C	1290	-	-	4/4/17/17	0/2/2/2
3	HBI	B	1290	-	-	4/4/17/17	0/2/2/2
2	NAP	B	1289	-	-	0/35/67/67	0/5/5/5
4	EDO	D	1291	-	-	0/1/1/1	-
2	NAP	C	1289	-	-	0/35/67/67	0/5/5/5

All (92) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1289	NAP	C2N-N1N	10.10	1.46	1.35
2	A	1289	NAP	C2N-N1N	9.85	1.45	1.35
2	C	1289	NAP	C2N-N1N	8.74	1.44	1.35
2	B	1289	NAP	C2N-N1N	8.63	1.44	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1290	HBI	C7-C6	7.84	1.58	1.49
3	B	1290	HBI	C7-C6	7.56	1.58	1.49
3	D	1290	HBI	C7-C6	7.21	1.58	1.49
3	A	1290	HBI	C7-C6	7.10	1.58	1.49
3	A	1290	HBI	O4-C4	7.02	1.36	1.23
3	C	1290	HBI	O4-C4	6.64	1.36	1.23
3	D	1290	HBI	O4-C4	6.52	1.35	1.23
3	B	1290	HBI	C7-N8	6.08	1.54	1.45
3	B	1290	HBI	O4-C4	5.98	1.34	1.23
3	C	1290	HBI	C7-N8	5.90	1.54	1.45
3	D	1290	HBI	C7-N8	5.83	1.54	1.45
3	A	1290	HBI	C7-N8	5.25	1.53	1.45
2	A	1289	NAP	O4D-C1D	5.20	1.47	1.40
2	D	1289	NAP	C3N-C7N	4.18	1.56	1.50
2	A	1289	NAP	C5A-N7A	-4.14	1.31	1.39
2	D	1289	NAP	P2B-O2B	3.94	1.66	1.59
2	B	1289	NAP	C6N-N1N	3.94	1.44	1.35
2	C	1289	NAP	O4D-C1D	3.87	1.46	1.40
2	D	1289	NAP	O4D-C1D	3.86	1.46	1.40
2	C	1289	NAP	C8A-N7A	3.71	1.38	1.31
3	D	1290	HBI	C2-N2	3.66	1.42	1.34
2	C	1289	NAP	C4N-C3N	3.62	1.44	1.39
3	D	1290	HBI	C4A-N5	3.62	1.45	1.37
2	A	1289	NAP	C6N-N1N	3.60	1.43	1.35
2	D	1289	NAP	C8A-N7A	3.57	1.38	1.31
2	B	1289	NAP	P2B-O2B	3.54	1.65	1.59
2	B	1289	NAP	C3N-C7N	3.48	1.55	1.50
2	D	1289	NAP	C4N-C3N	3.46	1.44	1.39
2	C	1289	NAP	C6N-N1N	3.46	1.43	1.35
3	B	1290	HBI	C4A-N5	3.45	1.45	1.37
3	B	1290	HBI	C2-N2	3.43	1.42	1.34
2	A	1289	NAP	C3N-C7N	3.42	1.55	1.50
3	C	1290	HBI	C2-N2	3.40	1.42	1.34
2	D	1289	NAP	C6N-N1N	3.39	1.43	1.35
2	C	1289	NAP	C5A-N7A	-3.37	1.32	1.39
3	A	1290	HBI	C6-N5	3.32	1.33	1.28
3	A	1290	HBI	C2-N2	3.31	1.41	1.34
2	B	1289	NAP	C5A-N7A	-3.23	1.33	1.39
4	B	1293	EDO	O2-C2	3.22	1.58	1.42
3	A	1290	HBI	C4A-N5	3.21	1.44	1.37
3	A	1290	HBI	O9-C9	3.20	1.48	1.42
2	B	1289	NAP	C4A-N3A	3.19	1.40	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1289	NAP	C5A-N7A	-3.19	1.33	1.39
3	D	1290	HBI	C6-N5	3.18	1.33	1.28
4	D	1291	EDO	O2-C2	3.12	1.58	1.42
2	A	1289	NAP	C5N-C4N	3.09	1.44	1.38
3	C	1290	HBI	C4A-N5	3.08	1.44	1.37
2	A	1289	NAP	PN-O3	3.06	1.62	1.59
2	D	1289	NAP	C5N-C4N	3.05	1.44	1.38
2	C	1289	NAP	C5N-C4N	3.01	1.44	1.38
3	B	1290	HBI	O9-C9	2.98	1.48	1.42
2	B	1289	NAP	C8A-N7A	2.98	1.37	1.31
2	B	1289	NAP	C4N-C3N	2.95	1.43	1.39
2	C	1289	NAP	C3N-C7N	2.94	1.55	1.50
3	D	1290	HBI	C4A-C8A	2.89	1.47	1.40
3	B	1290	HBI	C6-N5	2.86	1.33	1.28
4	B	1291	EDO	O2-C2	2.84	1.56	1.42
4	B	1292	EDO	O2-C2	2.83	1.56	1.42
3	C	1290	HBI	O9-C9	2.82	1.47	1.42
3	B	1290	HBI	C4A-C8A	2.80	1.47	1.40
2	B	1289	NAP	PA-O3	2.78	1.62	1.59
2	A	1289	NAP	C4A-N3A	2.78	1.39	1.34
3	C	1290	HBI	C6-N5	2.74	1.32	1.28
2	B	1289	NAP	C5N-C4N	2.74	1.43	1.38
3	A	1290	HBI	C4A-C8A	2.71	1.46	1.40
3	D	1290	HBI	O9-C9	2.69	1.47	1.42
2	C	1289	NAP	P2B-O2B	2.61	1.64	1.59
4	D	1291	EDO	O1-C1	2.57	1.55	1.42
3	C	1290	HBI	C4A-C8A	2.55	1.46	1.40
4	B	1293	EDO	O1-C1	2.50	1.54	1.42
3	B	1290	HBI	O10-C10	2.48	1.49	1.43
2	A	1289	NAP	C8A-N7A	2.46	1.36	1.31
3	A	1290	HBI	C11-C10	2.46	1.58	1.51
2	D	1289	NAP	O4B-C4B	-2.45	1.39	1.45
2	D	1289	NAP	PA-O3	2.44	1.62	1.59
2	A	1289	NAP	PA-O2A	-2.40	1.44	1.55
4	B	1292	EDO	O1-C1	2.35	1.54	1.42
4	B	1291	EDO	O1-C1	2.32	1.53	1.42
2	A	1289	NAP	C4A-N9A	-2.30	1.32	1.37
3	B	1290	HBI	C11-C10	2.24	1.58	1.51
2	B	1289	NAP	PA-O2A	-2.22	1.45	1.55
2	D	1289	NAP	C4A-N3A	2.21	1.38	1.34
2	B	1289	NAP	O4D-C1D	2.18	1.43	1.40
3	A	1290	HBI	C4-N3	-2.12	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1290	HBI	C4-N3	-2.09	1.34	1.38
2	C	1289	NAP	PA-O3	2.08	1.61	1.59
2	A	1289	NAP	P2B-O2B	2.06	1.63	1.59
2	B	1289	NAP	O4B-C4B	-2.05	1.40	1.45

All (62) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1289	NAP	C5A-C4A-N3A	-5.97	118.50	126.72
2	D	1289	NAP	C5A-C4A-N3A	-5.97	118.50	126.72
2	A	1289	NAP	C5A-C4A-N3A	-5.59	119.02	126.72
2	B	1289	NAP	C5A-C4A-N3A	-5.56	119.06	126.72
2	D	1289	NAP	N3A-C2A-N1A	-5.18	120.74	128.58
2	B	1289	NAP	N3A-C2A-N1A	-5.11	120.84	128.58
2	C	1289	NAP	N3A-C2A-N1A	-5.07	120.91	128.58
2	A	1289	NAP	N3A-C2A-N1A	-5.02	120.98	128.58
2	D	1289	NAP	N3A-C4A-N9A	4.60	134.98	127.17
2	B	1289	NAP	O4B-C1B-N9A	4.46	116.65	108.09
2	C	1289	NAP	N3A-C4A-N9A	4.44	134.73	127.17
2	B	1289	NAP	N3A-C4A-N9A	4.43	134.70	127.17
2	A	1289	NAP	N3A-C4A-N9A	4.34	134.55	127.17
2	C	1289	NAP	O4B-C1B-N9A	4.28	116.31	108.09
2	D	1289	NAP	O4B-C1B-N9A	4.17	116.09	108.09
2	A	1289	NAP	O4B-C1B-N9A	3.96	115.69	108.09
3	B	1290	HBI	C2-N3-C4	-3.94	117.97	125.11
2	C	1289	NAP	C2A-N3A-C4A	3.89	121.34	111.83
2	D	1289	NAP	C2A-N3A-C4A	3.82	121.17	111.83
3	C	1290	HBI	C2-N3-C4	-3.67	118.46	125.11
3	D	1290	HBI	C2-N3-C4	-3.67	118.46	125.11
2	A	1289	NAP	C2A-N3A-C4A	3.49	120.35	111.83
3	A	1290	HBI	C2-N3-C4	-3.48	118.80	125.11
3	B	1290	HBI	C4A-N5-C6	3.42	123.40	116.08
2	B	1289	NAP	C2A-N3A-C4A	3.38	120.09	111.83
3	C	1290	HBI	C4A-N5-C6	3.34	123.24	116.08
3	A	1290	HBI	C4A-N5-C6	3.33	123.21	116.08
3	B	1290	HBI	C4A-C4-N3	3.20	121.39	113.25
3	D	1290	HBI	C4A-C4-N3	3.11	121.18	113.25
3	D	1290	HBI	C4A-N5-C6	3.09	122.71	116.08
3	A	1290	HBI	C4A-C4-N3	3.03	120.96	113.25
2	A	1289	NAP	N9A-C8A-N7A	-3.02	109.64	113.94
3	C	1290	HBI	C4A-C4-N3	3.02	120.95	113.25
3	B	1290	HBI	C2-N1-C8A	2.97	118.60	113.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1289	NAP	N9A-C8A-N7A	-2.95	109.75	113.94
3	C	1290	HBI	C2-N1-C8A	2.94	118.55	113.36
3	D	1290	HBI	C2-N1-C8A	2.79	118.29	113.36
3	D	1290	HBI	O4-C4-C4A	-2.75	119.28	126.53
2	C	1289	NAP	N9A-C8A-N7A	-2.72	110.08	113.94
3	A	1290	HBI	C2-N1-C8A	2.68	118.08	113.36
3	C	1290	HBI	O4-C4-C4A	-2.65	119.53	126.53
2	B	1289	NAP	N9A-C8A-N7A	-2.63	110.21	113.94
3	C	1290	HBI	N2-C2-N1	-2.59	114.61	119.67
2	D	1289	NAP	C5N-C4N-C3N	2.56	122.89	120.36
2	B	1289	NAP	C5N-C4N-C3N	2.56	122.88	120.36
3	D	1290	HBI	N2-C2-N1	-2.53	114.74	119.67
3	B	1290	HBI	N2-C2-N1	-2.52	114.75	119.67
3	B	1290	HBI	O4-C4-C4A	-2.50	119.92	126.53
2	A	1289	NAP	C5N-C4N-C3N	2.50	122.82	120.36
2	A	1289	NAP	C6A-C5A-C4A	2.40	120.45	117.18
2	C	1289	NAP	C5N-C4N-C3N	2.39	122.71	120.36
2	D	1289	NAP	O3X-P2B-O2X	2.38	116.73	107.80
2	B	1289	NAP	C6A-C5A-C4A	2.34	120.37	117.18
2	C	1289	NAP	C6A-C5A-C4A	2.33	120.36	117.18
2	B	1289	NAP	O3X-P2B-O2X	2.31	116.45	107.80
2	D	1289	NAP	C6A-C5A-C4A	2.21	120.20	117.18
3	A	1290	HBI	O4-C4-C4A	-2.14	120.90	126.53
2	C	1289	NAP	O3X-P2B-O2X	2.13	115.78	107.80
2	A	1289	NAP	C6A-C5A-N7A	-2.13	127.99	132.09
2	A	1289	NAP	O3X-P2B-O2X	2.12	115.77	107.80
3	A	1290	HBI	N2-C2-N1	-2.09	115.60	119.67
2	B	1289	NAP	C4A-N9A-C1B	-2.05	121.85	126.63

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1290	HBI	C11-C10-C9-C6
3	B	1290	HBI	C11-C10-C9-C6
3	C	1290	HBI	C11-C10-C9-C6
3	D	1290	HBI	C11-C10-C9-C6
3	D	1290	HBI	C11-C10-C9-O9
4	B	1292	EDO	O1-C1-C2-O2
4	B	1293	EDO	O1-C1-C2-O2
3	A	1290	HBI	O10-C10-C9-C6
3	B	1290	HBI	O10-C10-C9-C6

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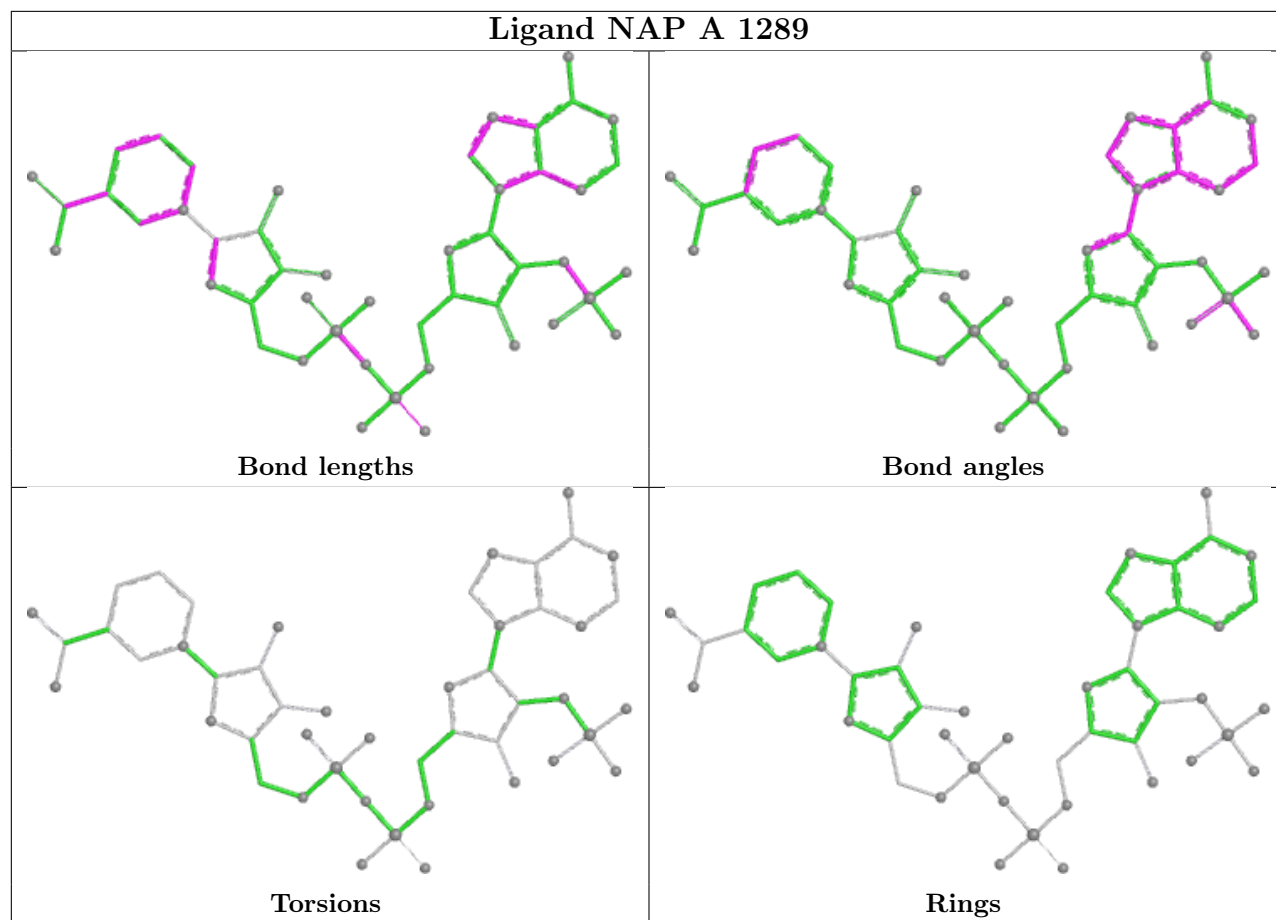
Mol	Chain	Res	Type	Atoms
3	C	1290	HBI	O10-C10-C9-C6
3	D	1290	HBI	O10-C10-C9-C6
3	B	1290	HBI	C11-C10-C9-O9
3	C	1290	HBI	O10-C10-C9-O9
3	C	1290	HBI	C11-C10-C9-O9
3	A	1290	HBI	O10-C10-C9-O9
3	B	1290	HBI	O10-C10-C9-O9
3	D	1290	HBI	O10-C10-C9-O9
3	A	1290	HBI	C11-C10-C9-O9

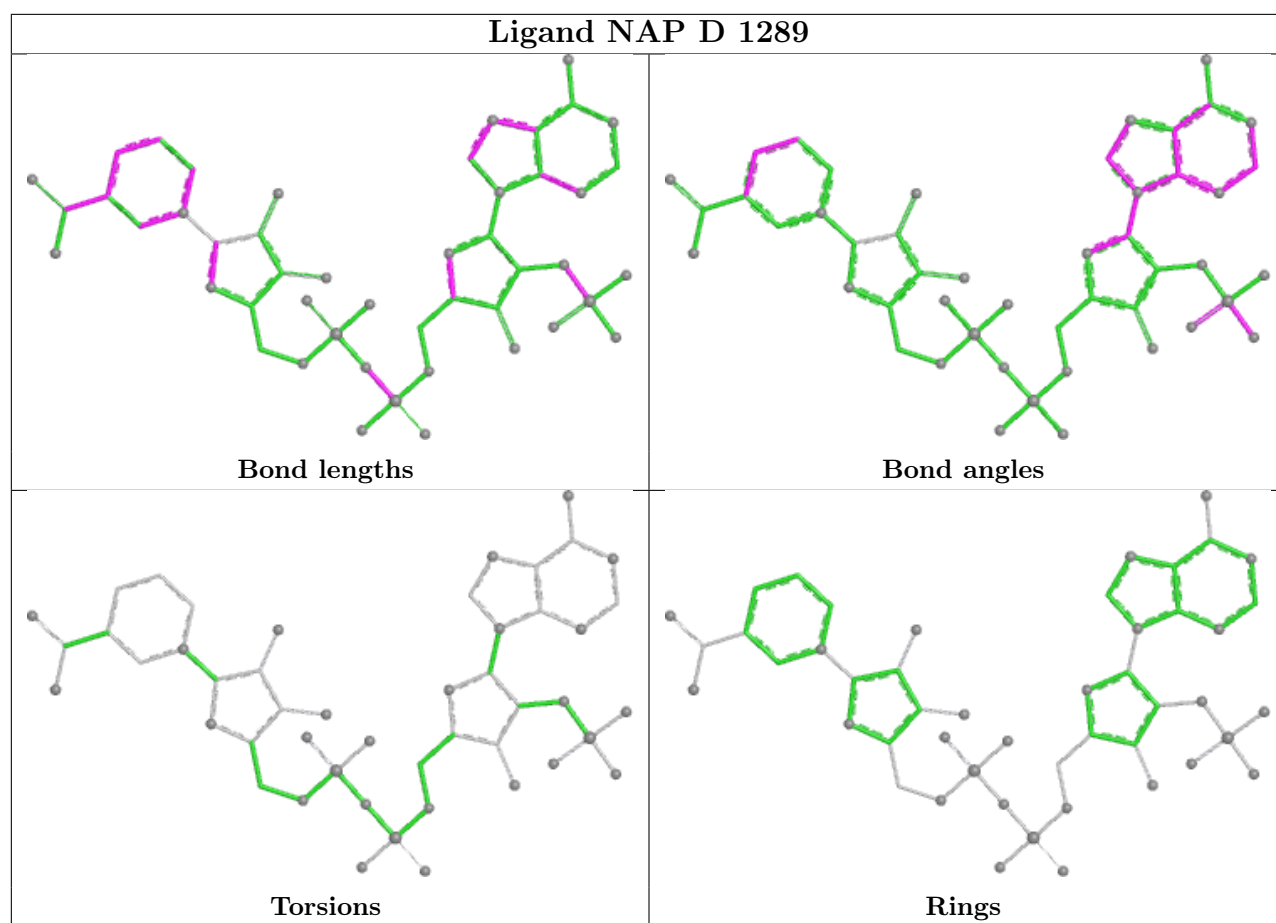
There are no ring outliers.

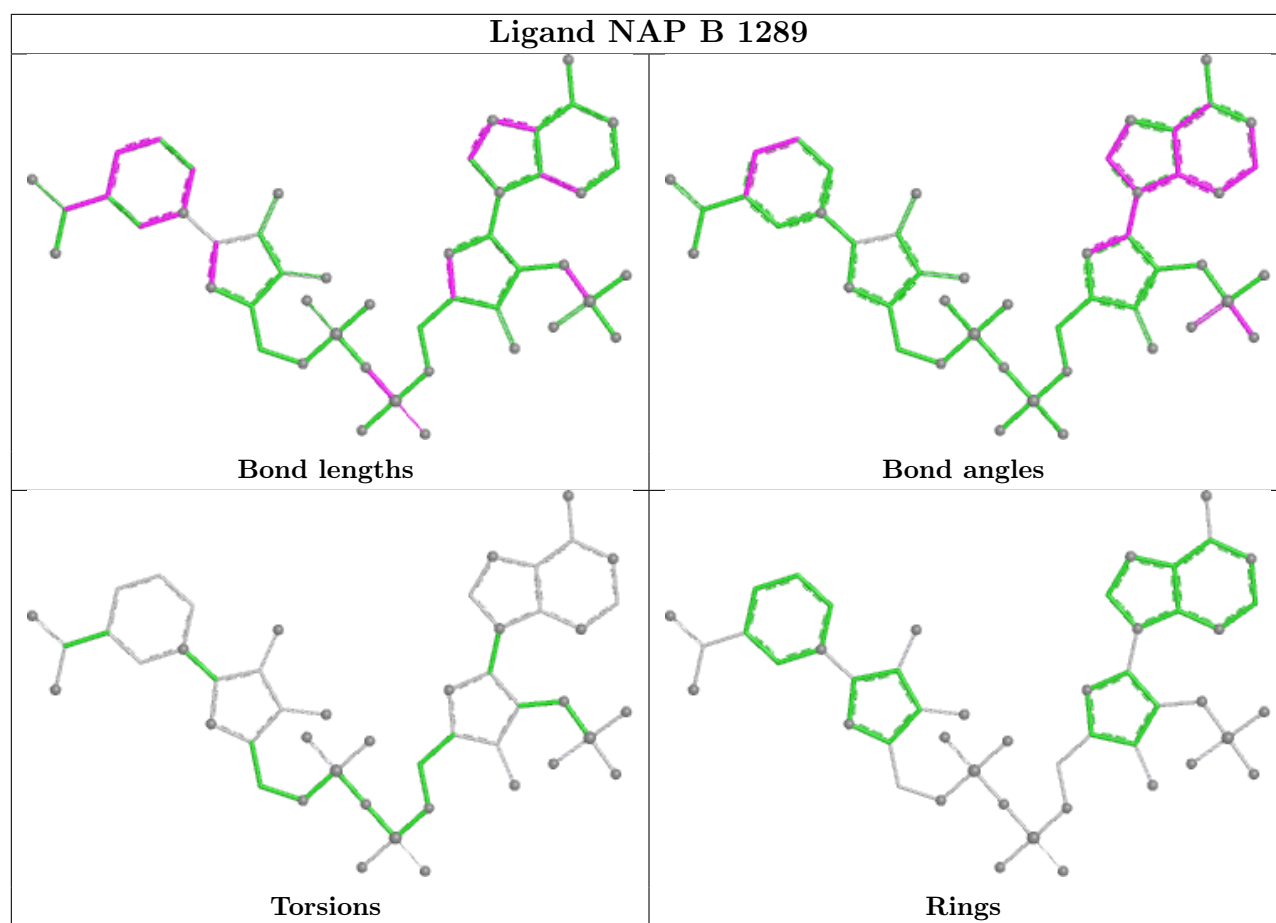
2 monomers are involved in 2 short contacts:

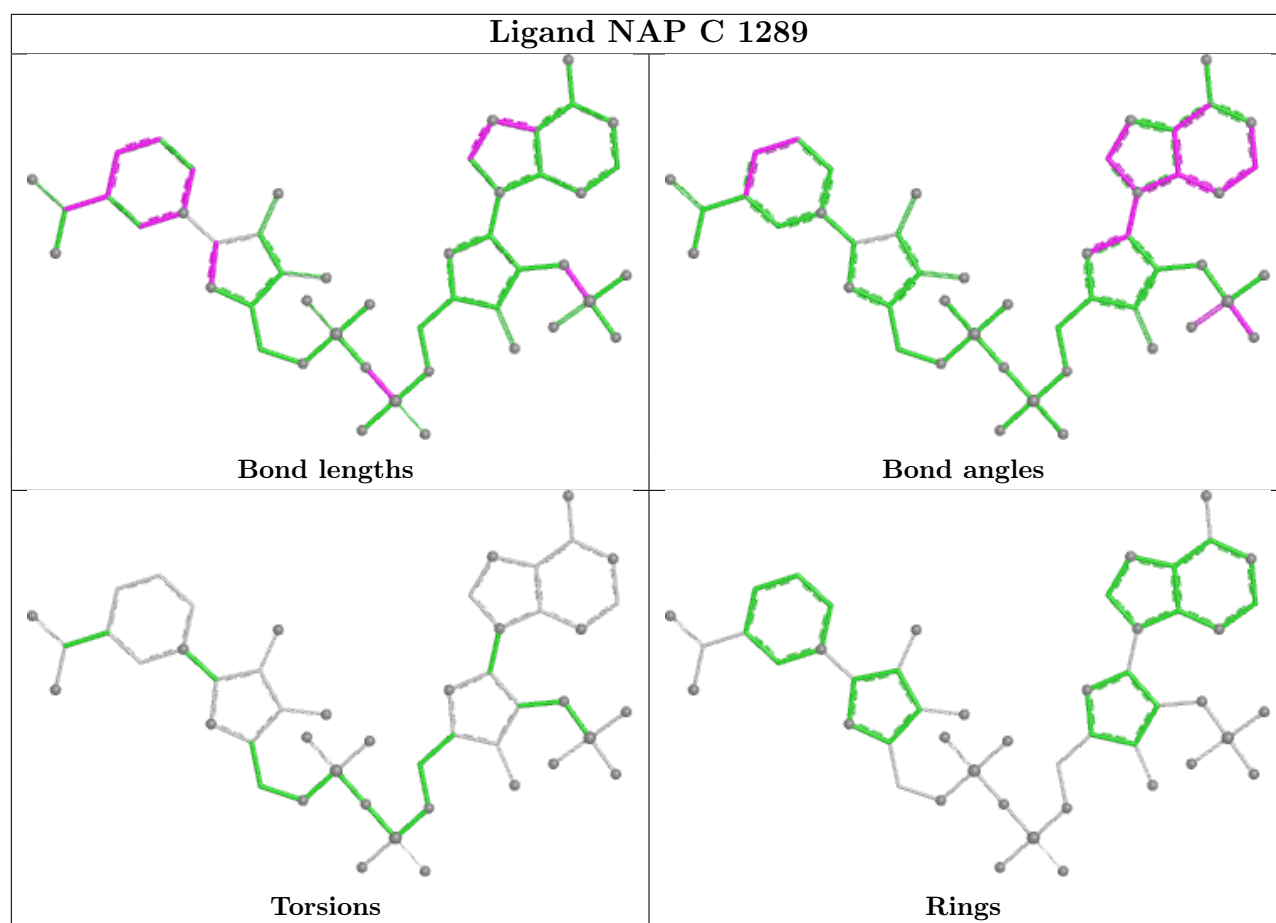
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1293	EDO	1	0
2	B	1289	NAP	1	0

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

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.