



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:53 PM UTC

PDB ID : 1AWF / pdb_00001awf
Title : NOVEL COVALENT THROMBIN INHIBITOR FROM PLANT EXTRACT
Authors : Jhoti, H.; Cleasby, A.; Wonacott, A.
Deposited on : 1997-10-02
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

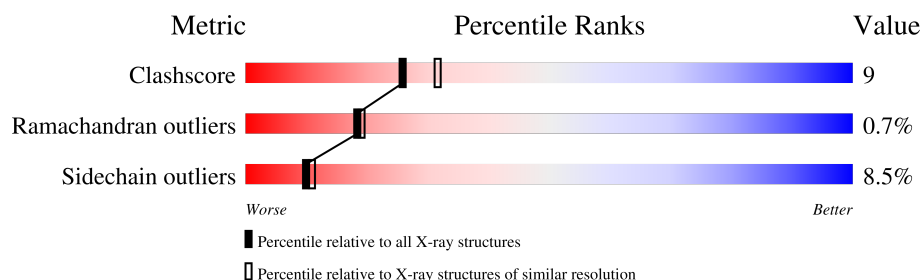
1 Overall quality at a glance

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	L	36	61% 14% 25%
2	H	259	60% 29% 9% .
3	I	10	40% 50% 10%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2682 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 ALPHA THROMBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	27	Total	C	N	O	S	0	0	0
			222	140	36	45	1			

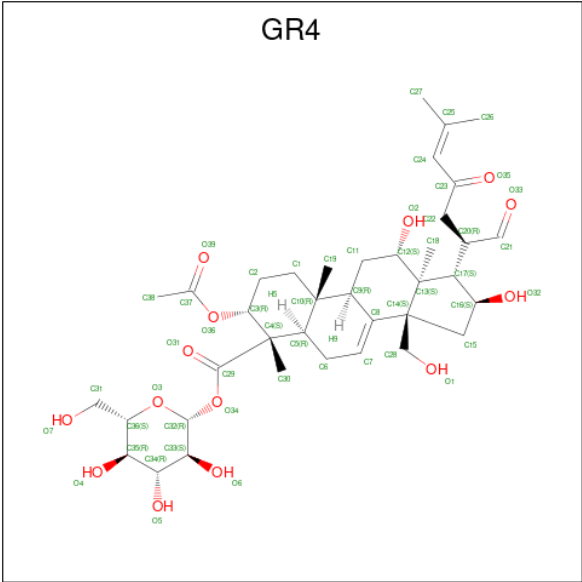
- Molecule 2 is a protein called ALPHA THROMBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	258	Total	C	N	O	S	0	0	0
			2083	1329	369	371	14			

- Molecule 3 is a protein called HIRUGEN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	10	Total	C	N	O	S	0	0	0
			95	59	10	25	1			

- Molecule 4 is R3-ACETOXY-17-(1-FORMYL-5-METHYL-3-OXO-HEX-4-ENYL)-12,16-DI-HYDROXY-14-HYDROXYMETHYL-4,10,13-TRIMETHYL-2,3,4,5,6,9,10,11,12,13,14,15,16,17-TETRADECAHYDRO-1H-CYCLOPENTA[A]PHENANTHRENE-4-CARBOXYLIC ACID IDOPYRANOSYL ESTER (CCD ID: GR4) (formula: C₃₈H₅₆O₁₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	C	O	0	0
			52	38	14		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	37	Total	O	0	0
			37	37		
5	H	185	Total	O	0	0
			185	185		
5	I	8	Total	O	0	0
			8	8		

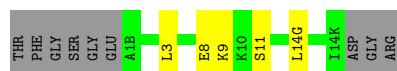
3 Residue-property plots [i](#)

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.

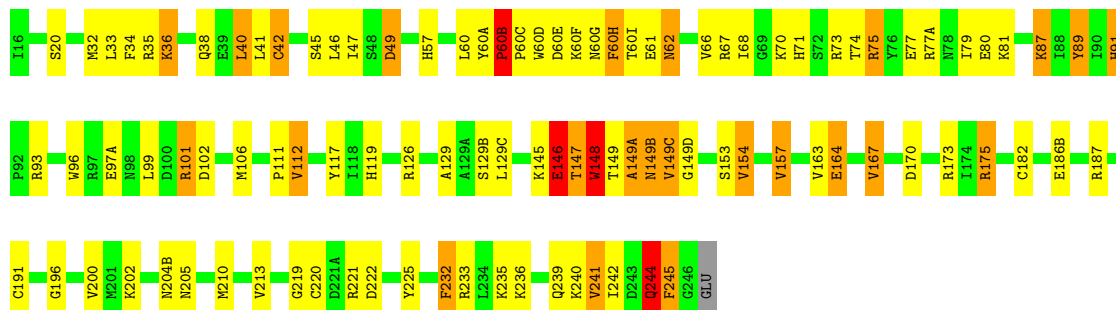
• Molecule 1: ALPHA THROMBIN

Chain L: 

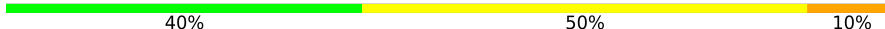


• Molecule 2: ALPHA THROMBIN

Chain H: 



• Molecule 3: HIRUGEN

Chain I: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	71.92Å 71.84Å 73.01Å 90.00° 100.39° 90.00°	Depositor
Resolution (Å)	15.00 – 2.20	Depositor
% Data completeness (in resolution range)	98.0 (15.00-2.20)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.196 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2682	wwPDB-VP
Average B, all atoms (Å ²)	27.0	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: TYS, GR4

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	L	1.12	0/224	1.86	2/298 (0.7%)
2	H	1.25	5/2138 (0.2%)	2.11	73/2891 (2.5%)
3	I	0.86	0/79	2.05	3/103 (2.9%)
All	All	1.22	5/2441 (0.2%)	2.08	78/3292 (2.4%)

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
2	H	0	5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	71	HIS	CG-ND1	-5.93	1.31	1.38
2	H	119	HIS	CG-CD2	5.31	1.41	1.35
2	H	119	HIS	CE1-NE2	5.29	1.37	1.32
2	H	200	VAL	CA-C	-5.28	1.46	1.52
2	H	57	HIS	CG-ND1	-5.05	1.32	1.38

All (78) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	149(B)	ASN	N-CA-C	11.77	125.89	109.18
2	H	146	GLU	N-CA-C	11.31	125.46	110.53
2	H	77(A)	ARG	CA-C-N	-10.94	106.11	122.86
2	H	77(A)	ARG	C-N-CA	-10.94	106.11	122.86
2	H	149	THR	N-CA-C	10.80	126.40	111.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	62	ASN	CA-CB-CG	-9.54	103.06	112.60
2	H	157	VAL	CB-CA-C	-8.39	98.12	110.62
2	H	225	TYR	CA-C-N	-8.34	113.48	121.57
2	H	225	TYR	C-N-CA	-8.34	113.48	121.57
2	H	153	SER	CA-C-O	8.27	129.19	120.42
2	H	205	ASN	N-CA-C	8.24	122.77	111.90
2	H	77(A)	ARG	N-CA-C	8.03	124.63	111.37
2	H	154	VAL	N-CA-CB	-7.99	99.01	112.44
2	H	222	ASP	CA-CB-CG	-7.72	104.88	112.60
2	H	147	THR	CA-C-N	-7.52	112.95	123.03
2	H	147	THR	C-N-CA	-7.52	112.95	123.03
2	H	245	PHE	N-CA-C	7.50	120.78	107.80
2	H	97(A)	GLU	N-CA-C	6.89	121.36	112.12
2	H	235	LYS	N-CA-C	6.81	118.79	111.36
2	H	233	ARG	N-CA-C	6.75	119.47	111.71
1	L	11	SER	N-CA-C	6.59	120.26	111.30
2	H	70	LYS	N-CA-C	6.57	119.42	110.55
2	H	74	THR	N-CA-C	6.56	121.57	113.50
2	H	36	LYS	N-CA-C	6.53	118.48	111.36
2	H	187	ARG	N-CA-C	6.46	116.80	108.34
2	H	146	GLU	CB-CG-CD	-6.36	101.79	112.60
2	H	97(A)	GLU	CA-C-N	-6.35	112.59	122.37
2	H	97(A)	GLU	C-N-CA	-6.35	112.59	122.37
2	H	213	VAL	CA-C-N	-6.33	112.42	122.17
2	H	213	VAL	C-N-CA	-6.33	112.42	122.17
2	H	204(B)	ASN	N-CA-C	6.27	120.97	112.88
2	H	66	VAL	N-CA-CB	-6.22	103.53	110.99
2	H	112	VAL	CA-C-N	-6.22	112.89	122.09
2	H	112	VAL	C-N-CA	-6.22	112.89	122.09
2	H	60(B)	PRO	N-CA-C	6.16	118.21	110.70
2	H	47	ILE	CA-C-O	6.16	124.81	118.96
2	H	175	ARG	N-CA-C	6.06	117.88	109.15
2	H	60(H)	PHE	CA-CB-CG	-6.03	107.78	113.80
2	H	149(A)	ALA	N-CA-C	5.98	123.53	110.80
2	H	232	PHE	N-CA-C	5.94	118.52	111.33
2	H	20	SER	CB-CA-C	-5.93	97.44	110.67
2	H	149(B)	ASN	CA-CB-CG	-5.92	106.67	112.60
2	H	182	CYS	N-CA-C	5.92	119.19	109.72
2	H	245	PHE	CA-CB-CG	-5.91	107.89	113.80
2	H	89	TYR	CB-CA-C	-5.89	101.73	110.62
3	I	56	PHE	N-CA-C	5.89	118.79	109.96
2	H	222	ASP	N-CA-C	5.78	118.74	110.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	60	PRO	CA-C-O	5.71	127.82	121.36
2	H	164	GLU	CB-CA-C	-5.71	100.51	109.70
2	H	57	HIS	N-CA-C	5.69	119.70	112.87
2	H	157	VAL	CA-CB-CG2	5.68	120.06	110.40
2	H	81	LYS	CA-C-N	-5.64	116.19	123.19
2	H	81	LYS	C-N-CA	-5.64	116.19	123.19
2	H	106	MET	CA-C-N	-5.60	115.00	122.72
2	H	106	MET	C-N-CA	-5.60	115.00	122.72
3	I	61	GLU	N-CA-C	5.55	118.10	111.71
2	H	91	HIS	N-CA-C	5.54	116.38	109.57
2	H	241	VAL	N-CA-C	5.50	117.97	111.09
2	H	62	ASN	N-CA-C	5.39	119.61	113.19
2	H	186(B)	GLU	C-N-CA	-5.36	111.04	122.30
2	H	170	ASP	N-CA-C	5.31	119.51	113.19
2	H	173	ARG	CB-CA-C	-5.21	100.58	109.65
2	H	153	SER	N-CA-CB	-5.20	102.47	110.16
1	L	8	GLU	CB-CA-C	-5.16	102.22	110.79
2	H	196	GLY	CA-C-N	-5.16	113.77	121.87
2	H	196	GLY	C-N-CA	-5.16	113.77	121.87
2	H	80	GLU	N-CA-C	5.13	117.48	110.55
2	H	93	ARG	N-CA-C	5.12	119.02	112.26
2	H	67	ARG	CA-C-O	5.12	125.77	120.30
2	H	75	ARG	NE-CZ-NH2	-5.09	114.62	119.20
2	H	239	GLN	CB-CA-C	-5.09	102.33	110.79
2	H	49	ASP	CA-C-N	-5.08	111.74	121.15
2	H	49	ASP	C-N-CA	-5.08	111.74	121.15
2	H	73	ARG	N-CA-C	5.07	116.50	111.07
2	H	242	ILE	N-CA-C	5.07	116.53	111.00
2	H	61	GLU	N-CA-C	5.05	116.78	111.28
2	H	244	GLN	N-CA-C	5.04	119.41	113.16
2	H	42	CYS	CB-CA-C	-5.04	101.80	111.78

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	101	ARG	Sidechain
2	H	146	GLU	Peptide
2	H	148	TRP	Peptide
2	H	244	GLN	Peptide
2	H	245	PHE	Peptide

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	L	222	0	225	2	0
2	H	2083	0	2061	34	1
3	I	95	0	74	2	0
4	H	52	0	54	7	0
5	H	185	0	0	1	2
5	I	8	0	0	0	0
5	L	37	0	0	0	0
All	All	2682	0	2414	43	2

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 9.

All (43) 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)
2:H:145:LYS:HD2	2:H:149(C):VAL:O	1.88	0.72
2:H:32:MET:HG3	2:H:40:LEU:HD23	1.77	0.66
2:H:68:ILE:HD12	2:H:112:VAL:HG11	1.79	0.63
2:H:164:GLU:HB2	2:H:167:VAL:HG13	1.83	0.60
2:H:240:LYS:O	2:H:244:GLN:HG3	2.03	0.59
2:H:145:LYS:HG3	2:H:149(B):ASN:HB3	1.85	0.58
2:H:146:GLU:O	2:H:149(B):ASN:HB2	2.05	0.57
4:H:1:GR4:H111	4:H:1:GR4:H281	1.87	0.57
1:L:14(G):LEU:HD21	2:H:202:LYS:HD3	1.88	0.55
2:H:191:CYS:HG	2:H:220:CYS:HG	0.90	0.55
2:H:126:ARG:NH1	2:H:232:PHE:HE2	2.05	0.55
2:H:49:ASP:OD2	2:H:111:PRO:HB3	2.07	0.54
3:I:58:GLU:H	3:I:58:GLU:CD	2.16	0.54
2:H:35:ARG:O	2:H:38:GLN:HA	2.09	0.53
2:H:236:LYS:HB3	5:H:506:HOH:O	2.08	0.53
2:H:60(B):PRO:HG2	2:H:96:TRP:CE2	2.46	0.51
2:H:146:GLU:OE2	2:H:221:ARG:HD3	2.12	0.50
2:H:129:ALA:HA	2:H:210:MET:HE1	1.94	0.50
2:H:236:LYS:O	2:H:240:LYS:HG3	2.12	0.50
2:H:75:ARG:CZ	2:H:77:GLU:HG2	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:148:TRP:HE3	2:H:148:TRP:H	1.61	0.48
2:H:34:PHE:CZ	2:H:38:GLN:HB3	2.49	0.48
2:H:148:TRP:O	4:H:1:GR4:H311	2.13	0.47
2:H:146:GLU:HA	2:H:147:THR:HG23	1.97	0.47
2:H:36:LYS:HE2	2:H:62:ASN:O	2.16	0.45
2:H:147:THR:HA	2:H:149(A):ALA:HA	1.97	0.45
4:H:1:GR4:H303	4:H:1:GR4:H192	1.98	0.45
2:H:148:TRP:HZ3	2:H:219:GLY:HA2	1.81	0.45
2:H:87:LYS:HB3	2:H:89:TYR:CE1	2.51	0.45
4:H:1:GR4:H281	4:H:1:GR4:C11	2.46	0.45
2:H:99:LEU:O	2:H:102:ASP:HB2	2.17	0.45
2:H:149(B):ASN:OD1	2:H:149(C):VAL:HG22	2.17	0.44
4:H:1:GR4:O36	4:H:1:GR4:H32	2.18	0.43
4:H:1:GR4:H183	4:H:1:GR4:H9	2.01	0.43
2:H:163:VAL:CG1	2:H:167:VAL:HG22	2.49	0.42
2:H:148:TRP:HH2	2:H:219:GLY:H	1.67	0.41
2:H:33:LEU:HB2	2:H:42:CYS:O	2.20	0.41
2:H:35:ARG:HD2	2:H:41:LEU:HD21	2.03	0.41
2:H:79:ILE:HG23	2:H:117:TYR:CD2	2.56	0.41
4:H:1:GR4:C7	4:H:1:GR4:H191	2.51	0.41
3:I:61:GLU:HA	3:I:64:LEU:HD12	2.02	0.41
2:H:91:HIS:CE1	2:H:101:ARG:HD3	2.56	0.40
1:L:3:LEU:HB2	1:L:9:LYS:HE3	2.03	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:371:HOH:O	5:H:401:HOH:O[2_656]	2.14	0.06
2:H:175:ARG:NH2	5:H:523:HOH:O[2_556]	2.19	0.01

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	L	25/36 (69%)	22 (88%)	3 (12%)	0	100	100
2	H	256/259 (99%)	237 (93%)	17 (7%)	2 (1%)	16	16
3	I	7/10 (70%)	6 (86%)	1 (14%)	0	100	100
All	All	288/305 (94%)	265 (92%)	21 (7%)	2 (1%)	18	19

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	149(D)	GLY
2	H	149(C)	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	L	25/31 (81%)	25 (100%)	0	100	100
2	H	224/225 (100%)	202 (90%)	22 (10%)	7	8
3	I	9/9 (100%)	9 (100%)	0	100	100
All	All	258/265 (97%)	236 (92%)	22 (8%)	10	11

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	40	LEU
2	H	45	SER
2	H	46	LEU
2	H	60	LEU
2	H	60(A)	TYR
2	H	60(B)	PRO
2	H	60(C)	PRO
2	H	60(D)	TRP
2	H	60(E)	ASP

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Mol	Chain	Res	Type
2	H	60(F)	LYS
2	H	60(G)	ASN
2	H	60(H)	PHE
2	H	60(I)	THR
2	H	87	LYS
2	H	129(B)	SER
2	H	129(C)	LEU
2	H	148	TRP
2	H	154	VAL
2	H	157	VAL
2	H	167	VAL
2	H	241	VAL
2	H	244	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	H	204(B)	ASN
2	H	244	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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	TYS	I	63	3	15,16,17	0.87	1 (6%)	15,22,24	1.09	1 (6%)

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	TYS	I	63	3	-	1/10/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	63	TYS	OH-CZ	2.33	1.46	1.42

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	63	TYS	CE2-CD2-CG	-2.03	118.33	121.00

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	I	63	TYS	CZ-OH-S-O3

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	GR4	H	1	2	56,56,56	1.31	3 (5%)	78,89,89	1.72	20 (25%)

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
4	GR4	H	1	2	-	6/33/132/132	0/5/5/5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	1	GR4	O1-C28	-6.83	1.20	1.42
4	H	1	GR4	C10-C5	-2.65	1.52	1.56
4	H	1	GR4	C22-C20	2.49	1.57	1.54

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	1	GR4	O1-C28-C14	4.65	128.32	113.24
4	H	1	GR4	O36-C3-C4	4.27	114.41	107.24
4	H	1	GR4	O34-C32-C33	3.65	118.09	107.49
4	H	1	GR4	C3-O36-C37	3.24	122.68	117.84
4	H	1	GR4	O35-C23-C24	-3.21	116.94	123.03
4	H	1	GR4	C11-C9-C8	3.15	113.87	110.11
4	H	1	GR4	C5-C4-C3	3.10	114.23	109.20
4	H	1	GR4	O6-C33-C32	2.92	117.03	110.08
4	H	1	GR4	C13-C17-C16	-2.86	101.68	103.98
4	H	1	GR4	C6-C5-C4	2.86	116.52	112.82
4	H	1	GR4	O3-C36-C31	2.72	113.19	106.44
4	H	1	GR4	C2-C3-C4	-2.66	108.95	112.78
4	H	1	GR4	C20-C17-C16	2.60	116.81	113.77
4	H	1	GR4	C13-C14-C8	-2.45	108.82	110.75
4	H	1	GR4	C34-C35-C36	2.41	114.60	110.23
4	H	1	GR4	C31-C36-C35	-2.40	107.12	113.02
4	H	1	GR4	C14-C8-C9	-2.37	114.19	119.51
4	H	1	GR4	C10-C9-C8	-2.24	109.12	112.54
4	H	1	GR4	C18-C13-C12	2.09	112.89	109.14
4	H	1	GR4	O36-C37-O39	2.03	126.92	122.99

There are no chirality outliers.

All (6) torsion outliers are listed below:

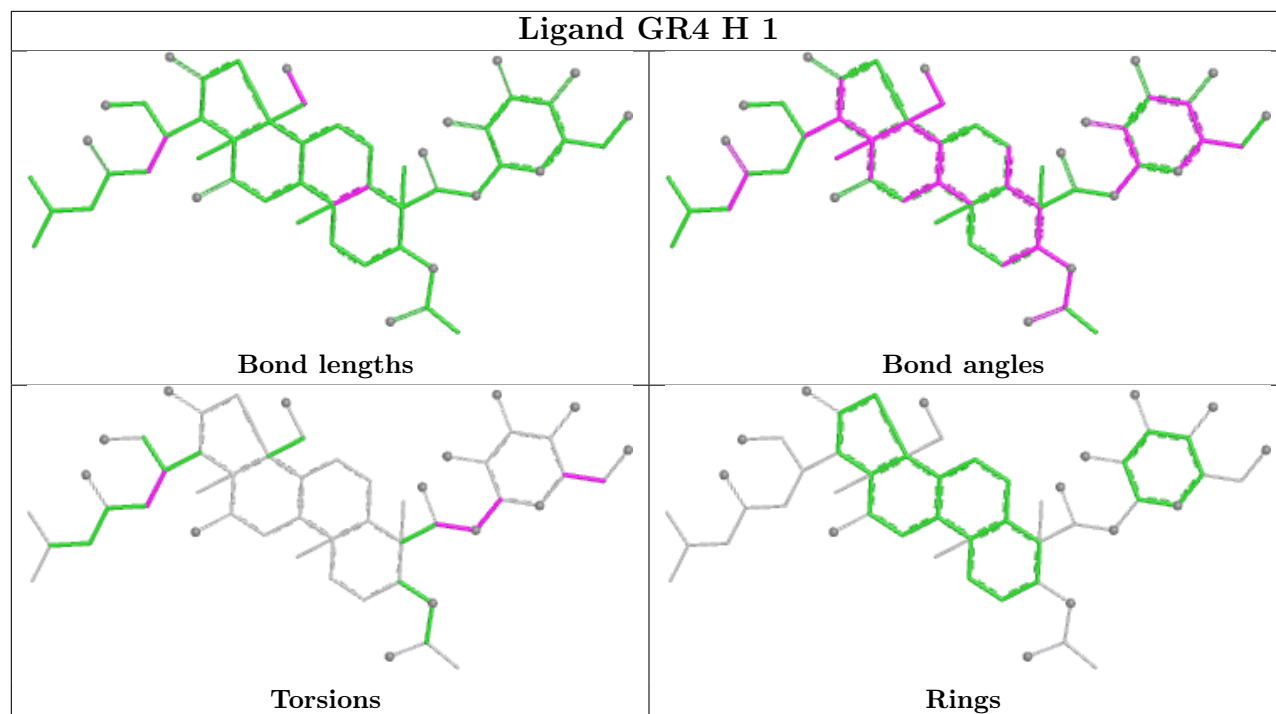
Mol	Chain	Res	Type	Atoms
4	H	1	GR4	C21-C20-C22-C23
4	H	1	GR4	C4-C29-O34-C32
4	H	1	GR4	O31-C29-O34-C32
4	H	1	GR4	C33-C32-O34-C29
4	H	1	GR4	O7-C31-C36-C35
4	H	1	GR4	O7-C31-C36-O3

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	1	GR4	7	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.