



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:45 PM UTC

PDB ID : 1QJ7 / pdb_00001qj7
Title : Novel Covalent Active Site Thrombin Inhibitors
Authors : Jhoti, H.; Cleasby, A.
Deposited on : 1999-06-22
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

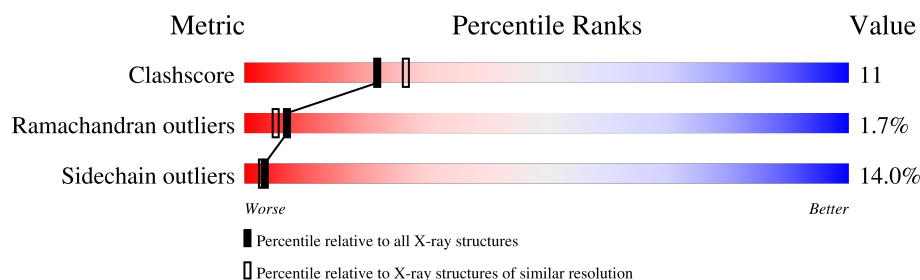
1 Overall quality at a glance

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	36	
2	B	259	
3	I	10	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 2715 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 THROMBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	36	Total	C	N	O	S	0	0	0
			287	177	48	61	1			

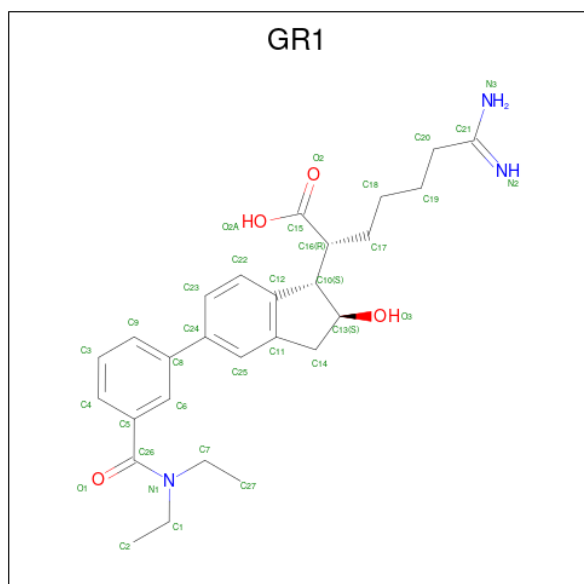
- Molecule 2 is a protein called THROMBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	259	Total	C	N	O	S	0	0	0
			2093	1334	370	375	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
			94	59	10	24	1			

- Molecule 4 is 6-CARBAMIMIDOYL-2-[5-(3-DIETHYLCARBAMOYL-PHENYL)-2-HYDROXY-INDAN-1-YL]-HEXANOIC ACID (CCD ID: GR1) (formula: C₂₇H₃₅N₃O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			33	27	3	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	26	Total	O	0	0
			26	26		
5	B	178	Total	O	0	0
			178	178		
5	I	4	Total	O	0	0
			4	4		

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.

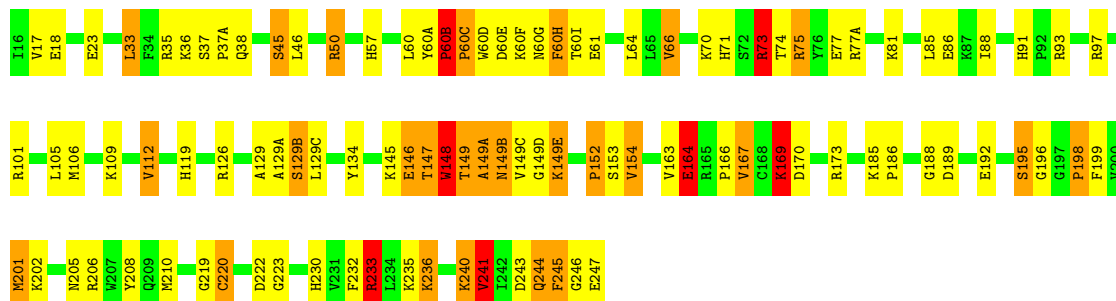
• Molecule 1: THROMBIN

Chain A:  61% 19% 19%



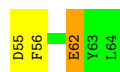
• Molecule 2: THROMBIN

Chain B:  60% 27% 10% •



• Molecule 3: HIRUGEN

Chain I:  70% 20% 10%



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	71.40 Å 72.10 Å 72.80 Å 90.00° 100.70° 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}	0.187 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2715	wwPDB-VP
Average B, all atoms (Å ²)	34.0	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, GR1

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	1.02	0/290	1.79	7/384 (1.8%)
2	B	1.20	5/2148 (0.2%)	2.01	63/2903 (2.2%)
3	I	0.93	0/79	1.64	2/103 (1.9%)
All	All	1.18	5/2517 (0.2%)	1.97	72/3390 (2.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
2	B	0	4
All	All	0	6

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	195	SER	CB-OG	-8.96	1.24	1.42
2	B	71	HIS	CG-ND1	-5.74	1.31	1.38
2	B	119	HIS	CG-CD2	5.59	1.42	1.35
2	B	119	HIS	CE1-NE2	5.20	1.37	1.32
2	B	230	HIS	CE1-NE2	5.05	1.37	1.32

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	77(A)	ARG	CA-C-N	-9.83	107.81	122.86
2	B	77(A)	ARG	C-N-CA	-9.83	107.81	122.86
2	B	154	VAL	N-CA-CB	-8.93	97.47	112.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	241	VAL	N-CA-C	8.89	119.70	110.72
2	B	60(B)	PRO	N-CA-C	8.12	120.61	110.70
2	B	205	ASN	N-CA-C	7.72	122.04	112.47
2	B	244	GLN	N-CA-C	7.56	122.33	113.18
2	B	93	ARG	N-CA-C	7.33	121.08	112.72
2	B	74	THR	N-CA-C	7.30	122.31	113.41
2	B	70	LYS	N-CA-C	7.09	121.02	110.52
2	B	66	VAL	N-CA-CB	-6.99	102.61	110.99
2	B	149(A)	ALA	N-CA-C	6.92	120.41	110.24
2	B	169	LYS	CB-CA-C	6.81	122.43	110.85
2	B	146	GLU	N-CA-C	6.66	120.02	110.24
2	B	77(A)	ARG	N-CA-C	6.65	122.34	111.37
2	B	205	ASN	CA-CB-CG	-6.58	106.03	112.60
2	B	170	ASP	N-CA-C	6.55	120.87	113.01
2	B	18	GLU	CA-C-N	-6.43	115.90	122.27
2	B	18	GLU	C-N-CA	-6.43	115.90	122.27
2	B	97	ARG	N-CA-C	6.39	118.25	111.28
1	A	4	ARG	N-CA-C	6.34	117.63	109.65
2	B	245	PHE	N-CA-C	6.30	118.58	107.61
2	B	164	GLU	N-CA-C	6.25	119.31	110.50
2	B	109	LYS	N-CA-C	6.12	117.95	111.28
2	B	129(B)	SER	N-CA-C	6.02	118.80	111.82
2	B	232	PHE	N-CA-C	5.96	118.26	111.11
2	B	129(A)	ALA	N-CA-C	5.85	117.33	111.07
2	B	112	VAL	CB-CA-C	-5.83	103.58	111.63
2	B	241	VAL	CA-C-N	-5.82	111.09	120.64
2	B	241	VAL	C-N-CA	-5.82	111.09	120.64
2	B	149(B)	ASN	N-CA-C	5.79	118.90	109.59
2	B	154	VAL	CA-CB-CG1	5.77	120.22	110.40
2	B	60(H)	PHE	CA-CB-CG	-5.75	108.05	113.80
2	B	189	ASP	CA-CB-CG	5.73	118.33	112.60
1	A	14(A)	LYS	N-CA-C	5.72	120.13	113.20
2	B	208	TYR	CA-C-N	-5.70	114.83	122.42
2	B	208	TYR	C-N-CA	-5.70	114.83	122.42
2	B	198	PRO	N-CA-C	5.69	119.40	110.80
2	B	195	SER	CA-CB-OG	5.67	122.43	111.10
2	B	149	THR	N-CA-CB	5.66	120.05	110.49
1	A	1(C)	GLU	N-CA-C	5.65	118.21	110.24
2	B	222	ASP	N-CA-C	5.65	118.21	110.24
1	A	14(H)	GLU	N-CA-C	5.65	120.01	113.18
2	B	66	VAL	N-CA-C	5.63	116.42	108.36
3	I	56	PHE	CA-CB-CG	-5.58	108.22	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	220	CYS	CB-CA-C	-5.55	101.59	110.14
3	I	62	GLU	CB-CA-C	-5.54	99.57	110.10
1	A	1(A)	ASP	CA-CB-CG	-5.54	107.06	112.60
2	B	73	ARG	N-CA-CB	-5.54	101.98	110.01
2	B	23	GLU	CA-CB-CG	-5.52	103.06	114.10
1	A	8	GLU	N-CA-C	5.47	117.95	111.33
2	B	235	LYS	N-CA-C	5.46	117.23	111.28
2	B	57	HIS	N-CA-C	5.45	119.19	112.54
2	B	153	SER	CA-C-O	5.42	125.95	119.60
2	B	152	PRO	CA-C-N	-5.39	111.61	121.52
2	B	152	PRO	C-N-CA	-5.39	111.61	121.52
2	B	169	LYS	CA-CB-CG	5.38	124.87	114.10
2	B	33	LEU	CA-C-N	-5.35	115.22	122.77
2	B	33	LEU	C-N-CA	-5.35	115.22	122.77
2	B	243	ASP	N-CA-C	5.35	117.19	111.36
2	B	129(B)	SER	CB-CA-C	-5.28	100.54	110.67
2	B	75	ARG	CB-CG-CD	5.26	123.40	111.30
2	B	233	ARG	NE-CZ-NH2	-5.23	114.50	119.20
2	B	173	ARG	CB-CA-C	-5.22	100.61	110.01
2	B	45	SER	N-CA-C	5.22	117.18	108.99
2	B	201	MET	CG-SD-CE	-5.20	89.46	100.90
2	B	36	LYS	N-CA-C	5.15	116.97	111.36
1	A	1(C)	GLU	C-N-CA	5.05	134.33	121.70
2	B	196	GLY	CA-C-N	-5.04	114.17	121.42
2	B	196	GLY	C-N-CA	-5.04	114.17	121.42
2	B	73	ARG	N-CA-C	5.01	116.44	111.07
2	B	149(E)	LYS	CA-C-O	5.00	124.84	118.54

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1(G)	PHE	Peptide
1	A	14(K)	ILE	Peptide
2	B	148	TRP	Peptide
2	B	233	ARG	Sidechain
2	B	244	GLN	Peptide
2	B	73	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	287	0	279	7	0
2	B	2093	0	2070	43	0
3	I	94	0	73	1	0
4	B	33	0	33	4	0
5	A	26	0	0	0	0
5	B	178	0	0	0	0
5	I	4	0	0	0	0
All	All	2715	0	2455	49	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 11.

All (49) 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:B:75:ARG:HD2	2:B:77:GLU:HG2	1.43	0.97
2:B:166:PRO:HA	2:B:169:LYS:HD2	1.56	0.88
2:B:201:MET:HE3	2:B:210:MET:HG3	1.58	0.86
2:B:199:PHE:HE1	2:B:201:MET:HE2	1.43	0.82
1:A:1(C):GLU:HA	1:A:1(B):ALA:HB3	1.72	0.71
1:A:3:LEU:HB3	1:A:9:LYS:HD3	1.74	0.69
2:B:45:SER:HB3	2:B:198:PRO:HG3	1.78	0.64
1:A:1(G):PHE:HB3	1:A:1(B):ALA:HB2	1.81	0.62
2:B:147:THR:HA	2:B:149(A):ALA:HA	1.83	0.60
2:B:164:GLU:HG2	2:B:167:VAL:HG13	1.88	0.55
2:B:75:ARG:HD2	2:B:77:GLU:CG	2.29	0.54
2:B:148:TRP:CZ3	2:B:220:CYS:SG	3.01	0.53
2:B:149(D):GLY:C	2:B:149(E):LYS:HD2	2.35	0.52
4:B:1248:GR1:H22	4:B:1248:GR1:H171	1.91	0.51
1:A:14(G):LEU:HD21	2:B:202:LYS:HD3	1.93	0.50
2:B:236:LYS:HE3	2:B:240:LYS:HD3	1.94	0.50
2:B:145:LYS:NZ	2:B:149(D):GLY:HA3	2.27	0.49
2:B:233:ARG:HH11	2:B:233:ARG:HB3	1.77	0.49
2:B:85:LEU:HG	2:B:106:MET:HE2	1.94	0.48
2:B:35:ARG:O	2:B:38:GLN:HA	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:148:TRP:HZ2	4:B:1248:GR1:H22	1.79	0.47
2:B:146:GLU:OE2	2:B:148:TRP:HB2	2.14	0.47
2:B:146:GLU:HG2	2:B:148:TRP:H	1.79	0.47
2:B:199:PHE:CE1	2:B:201:MET:HE2	2.35	0.46
1:A:1(C):GLU:HA	1:A:1(B):ALA:CB	2.45	0.46
2:B:129:ALA:HA	2:B:210:MET:HE1	1.96	0.46
2:B:245:PHE:HA	2:B:246:GLY:HA3	1.72	0.45
2:B:61:GLU:HG3	2:B:88:ILE:HG13	1.98	0.45
2:B:105:LEU:HD13	2:B:241:VAL:HG22	1.99	0.44
2:B:145:LYS:HB3	2:B:149(B):ASN:HB3	1.99	0.44
2:B:91:HIS:CE1	2:B:101:ARG:HD2	2.53	0.44
2:B:145:LYS:HZ2	2:B:149(D):GLY:HA3	1.81	0.44
2:B:73:ARG:HD3	2:B:152:PRO:O	2.17	0.44
2:B:37:SER:HA	2:B:37(A):PRO:C	2.42	0.44
2:B:219:GLY:O	4:B:1248:GR1:N2	2.51	0.43
2:B:134:TYR:CD1	2:B:134:TYR:N	2.86	0.43
2:B:148:TRP:CZ2	4:B:1248:GR1:H171	2.54	0.43
1:A:3:LEU:HD13	2:B:206:ARG:HG2	2.00	0.42
2:B:60(B):PRO:O	2:B:60(C):PRO:C	2.62	0.42
2:B:164:GLU:HG2	2:B:167:VAL:CG1	2.49	0.42
2:B:186:PRO:HG3	2:B:223:GLY:H	1.85	0.42
2:B:148:TRP:CZ3	2:B:192:GLU:HB2	2.54	0.41
2:B:50:ARG:HE	2:B:50:ARG:HB2	1.77	0.41
2:B:17:VAL:O	2:B:188:GLY:HA2	2.19	0.41
2:B:134:TYR:N	2:B:134:TYR:HD1	2.19	0.41
1:A:14(H):GLU:HB2	1:A:14(L):ASP:OD2	2.20	0.41
2:B:73:ARG:HH22	3:I:55:ASP:CG	2.28	0.41
2:B:148:TRP:CD1	2:B:219:GLY:H	2.39	0.40
2:B:163:VAL:CG1	2:B:167:VAL:HG22	2.52	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	34/36 (94%)	30 (88%)	1 (3%)	3 (9%)	0	0
2	B	257/259 (99%)	242 (94%)	13 (5%)	2 (1%)	16	16
3	I	7/10 (70%)	7 (100%)	0	0	100	100
All	All	298/305 (98%)	279 (94%)	14 (5%)	5 (2%)	7	5

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	149	THR
2	B	149(C)	VAL
1	A	14(L)	ASP
1	A	1(B)	ALA
1	A	14(K)	ILE

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	31/31 (100%)	29 (94%)	2 (6%)	15	18
2	B	225/225 (100%)	191 (85%)	34 (15%)	3	2
3	I	9/9 (100%)	8 (89%)	1 (11%)	6	6
All	All	265/265 (100%)	228 (86%)	37 (14%)	3	3

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	15	ARG
2	B	33	LEU
2	B	46	LEU
2	B	50	ARG
2	B	60	LEU
2	B	60(A)	TYR
2	B	60(B)	PRO

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Mol	Chain	Res	Type
2	B	60(C)	PRO
2	B	60(D)	TRP
2	B	60(E)	ASP
2	B	60(F)	LYS
2	B	60(G)	ASN
2	B	60(H)	PHE
2	B	60(I)	THR
2	B	64	LEU
2	B	66	VAL
2	B	81	LYS
2	B	86	GLU
2	B	112	VAL
2	B	126	ARG
2	B	129(B)	SER
2	B	129(C)	LEU
2	B	147	THR
2	B	148	TRP
2	B	154	VAL
2	B	164	GLU
2	B	167	VAL
2	B	169	LYS
2	B	185	LYS
2	B	195	SER
2	B	233	ARG
2	B	236	LYS
2	B	240	LYS
2	B	241	VAL
2	B	247	GLU
3	I	62	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	143	ASN
2	B	204(B)	ASN
2	B	239	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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	11,15,17	0.72	0	10,19,24	0.88	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	TYS	I	63	3	-	0/7/10/13	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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	GR1	B	1248	2	34,35,36	1.02	4 (11%)	41,48,50	1.89	13 (31%)

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	GR1	B	1248	2	-	7/29/41/43	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1248	GR1	C10-C13	2.76	1.58	1.55
4	B	1248	GR1	C21-N2	2.42	1.32	1.27
4	B	1248	GR1	C16-C15	2.40	1.54	1.50
4	B	1248	GR1	C21-N3	2.01	1.36	1.33

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1248	GR1	O3-C13-C10	4.60	120.32	110.48
4	B	1248	GR1	O2-C15-C16	-4.47	115.13	125.19
4	B	1248	GR1	C12-C10-C16	3.73	120.56	112.90
4	B	1248	GR1	C11-C12-C10	-3.23	108.21	110.84
4	B	1248	GR1	C24-C25-C11	-2.88	117.64	121.88
4	B	1248	GR1	C6-C5-C26	-2.70	114.14	120.13
4	B	1248	GR1	C23-C22-C12	-2.41	117.13	121.12
4	B	1248	GR1	C20-C21-N3	2.38	123.27	117.15
4	B	1248	GR1	O1-C26-N1	-2.32	118.70	122.35
4	B	1248	GR1	C1-N1-C7	2.28	121.64	116.33
4	B	1248	GR1	C5-C26-N1	2.27	121.49	118.66
4	B	1248	GR1	C6-C8-C24	-2.14	117.25	120.84
4	B	1248	GR1	C11-C14-C13	-2.08	101.53	103.43

There are no chirality outliers.

All (7) torsion outliers are listed below:

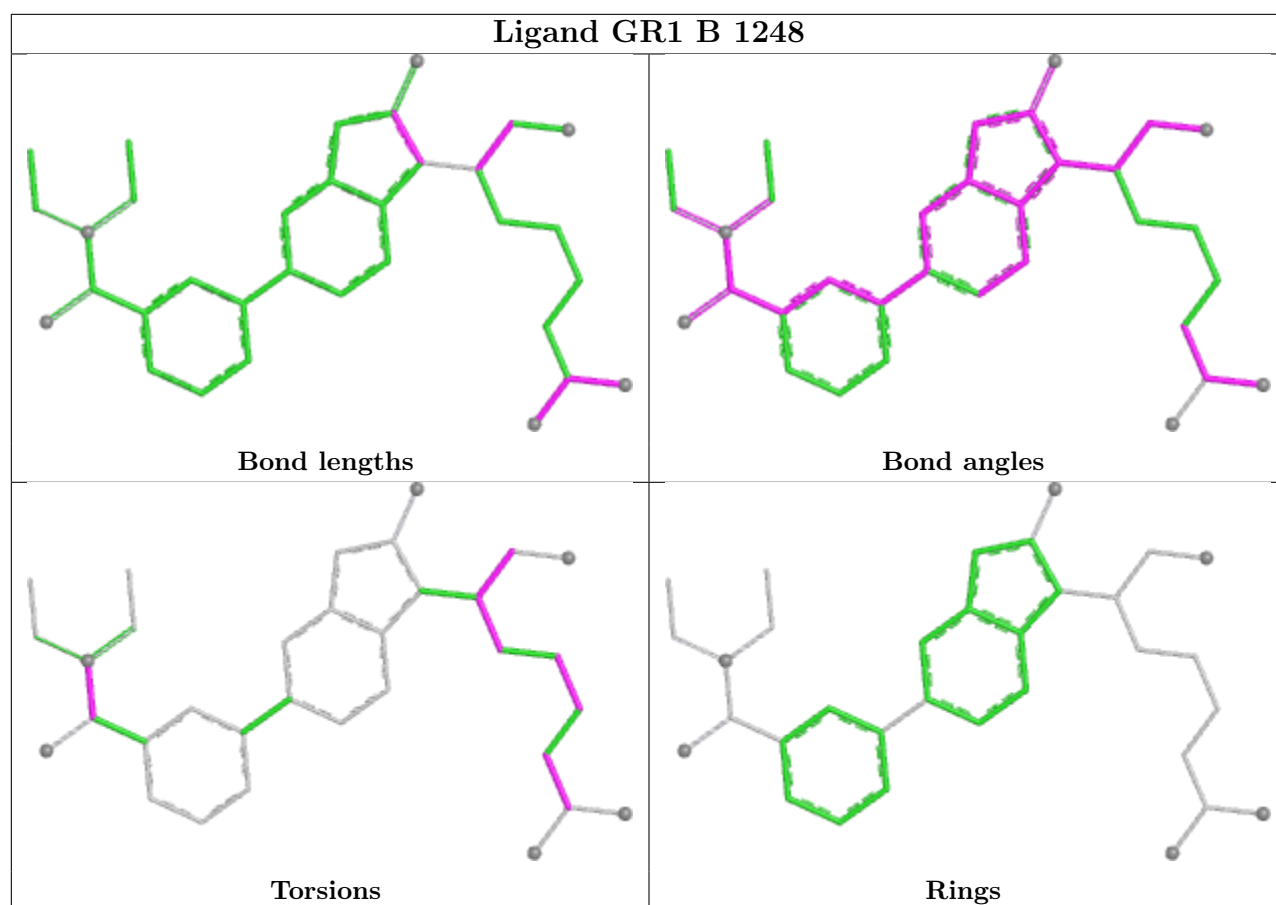
Mol	Chain	Res	Type	Atoms
4	B	1248	GR1	C17-C18-C19-C20
4	B	1248	GR1	C5-C26-N1-C1
4	B	1248	GR1	O1-C26-N1-C1
4	B	1248	GR1	C10-C16-C17-C18
4	B	1248	GR1	C19-C20-C21-N3
4	B	1248	GR1	O2-C15-C16-C10
4	B	1248	GR1	O2-C15-C16-C17

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1248	GR1	4	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.