



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:00 PM UTC

PDB ID : 1A5G / pdb_00001a5g
Title : HUMAN THROMBIN COMPLEXED WITH NOVEL SYNTHETIC PEP-
TIDE MIMETIC INHIBITOR AND HIRUGEN
Authors : St Charles, R.; Tulinsky, A.; Kahn, M.
Deposited on : 1998-02-16
Resolution : 2.06 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

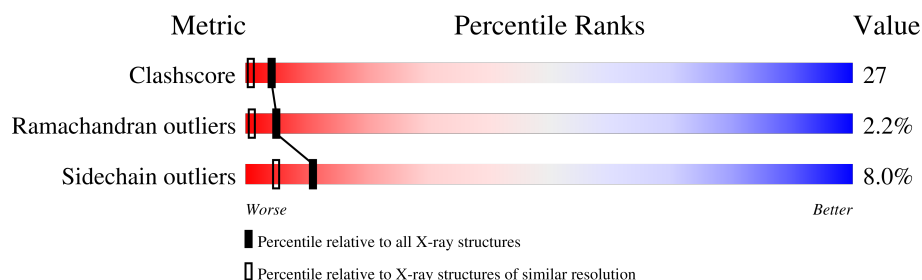
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.06 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	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)

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	25% 39% 11% 25%
2	H	259	42% 37% 14% • •
3	I	12	67% 8% 8% 17%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 2513 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 (SMALL SUBUNIT).

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 (LARGE SUBUNIT).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	250	Total	C	N	O	S	0	0	0
			2022	1290	358	360	14			

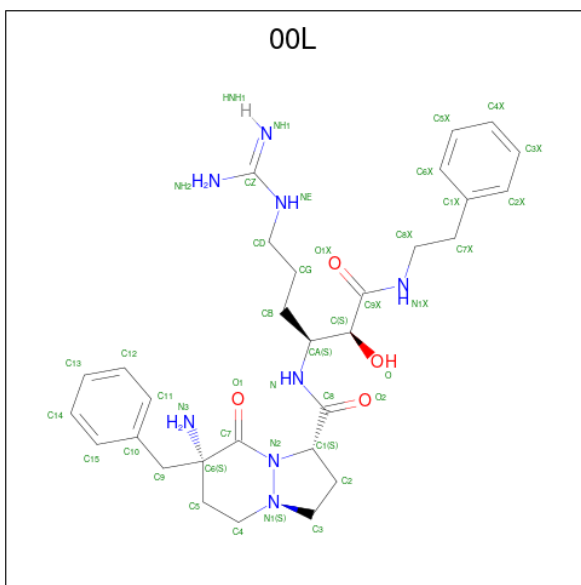
- Molecule 3 is a protein called HIRUGEN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	10	Total	C	N	O	S	0	0	0
			90	56	10	23	1			

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	2	Total	Na	0	0
			2	2		

- Molecule 5 is (1S,7S)-7-amino-7-benzyl-N-[(1S)-4-carbamimidamido-1-[(1S)-1-hydroxy-2-oxo-2-[(2-phenylethyl)amino]ethyl]butyl]-8-oxohexahydro-1H-pyrazolo[1,2-a]pyridazine-1-carboxamide (CCD ID: 00L) (formula: C₃₀H₄₂N₈O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	H	1	Total	C	N	O	0	0
			42	30	8	4		

- Molecule 6 is water.

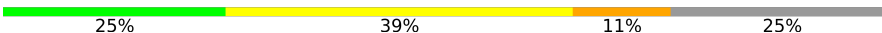
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	L	14	Total O 14 14	0	0
6	H	120	Total O 120 120	0	0
6	I	1	Total O 1 1	0	0

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.

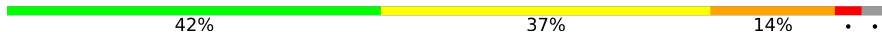
Note EDS was not executed.

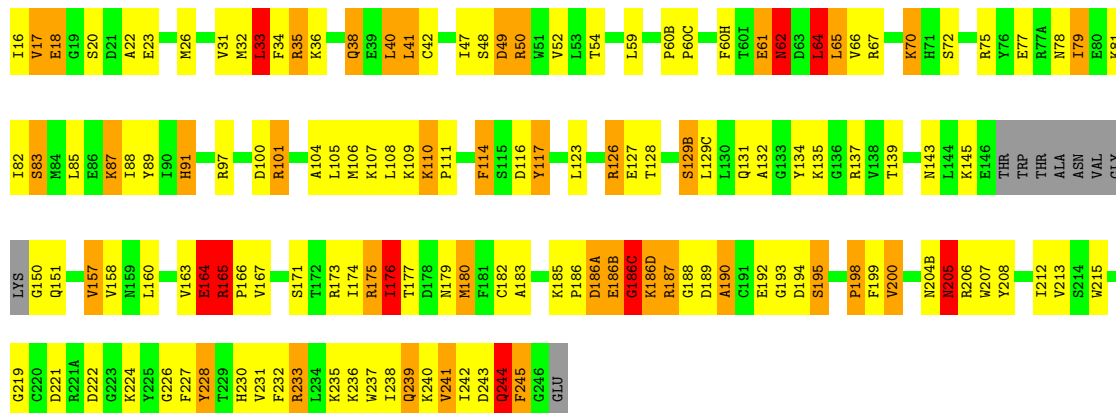
• Molecule 1: ALPHA-THROMBIN (SMALL SUBUNIT)

Chain L: 



• Molecule 2: ALPHA-THROMBIN (LARGE SUBUNIT)

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	70.81Å 72.25Å 72.79Å 90.00° 100.80° 90.00°	Depositor
Resolution (Å)	7.00 – 2.06	Depositor
% Data completeness (in resolution range)	81.0 (7.00-2.06)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROFFT	Depositor
R, R_{free}	0.158 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2513	wwPDB-VP
Average B, all atoms (Å ²)	29.0	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: 00L, NA, TYS

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	1.35	0/224	2.36	15/298 (5.0%)
2	H	1.38	5/2074 (0.2%)	2.31	118/2801 (4.2%)
3	I	1.16	0/74	2.87	7/96 (7.3%)
All	All	1.37	5/2372 (0.2%)	2.33	140/3195 (4.4%)

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	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	48	SER	C-O	5.54	1.29	1.24
2	H	116	ASP	C-O	5.45	1.30	1.24
2	H	198	PRO	CA-CB	5.25	1.59	1.54
2	H	82	ILE	CA-CB	5.14	1.60	1.53
2	H	200	VAL	N-CA	5.04	1.51	1.46

All (140) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	55	ASP	CA-CB-CG	14.99	127.59	112.60
2	H	205	ASN	OD1-CG-ND2	13.71	136.31	122.60
2	H	205	ASN	CA-CB-CG	-10.88	101.72	112.60
2	H	126	ARG	CD-NE-CZ	10.72	139.41	124.40
1	L	1(A)	ASP	CA-CB-CG	-9.93	102.67	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	64	LEU	CA-C-O	9.13	132.14	121.46
1	L	14	ASP	CA-C-O	9.09	132.53	121.81
2	H	52	VAL	CA-C-N	8.65	134.94	123.00
2	H	52	VAL	C-N-CA	8.65	134.94	123.00
1	L	14(E)	GLU	CB-CG-CD	8.43	126.93	112.60
2	H	132	ALA	CA-C-O	-8.38	111.94	121.15
2	H	127	GLU	CB-CG-CD	8.00	126.20	112.60
2	H	67	ARG	NE-CZ-NH1	7.92	129.42	121.50
2	H	157	VAL	CA-C-O	-7.82	112.99	121.28
2	H	117	TYR	CA-C-N	7.82	133.60	123.13
2	H	117	TYR	C-N-CA	7.82	133.60	123.13
2	H	137	ARG	NE-CZ-NH2	7.66	126.10	119.20
2	H	38	GLN	CB-CG-CD	7.58	125.49	112.60
2	H	75	ARG	CD-NE-CZ	7.51	134.92	124.40
2	H	173	ARG	CD-NE-CZ	-7.49	113.91	124.40
2	H	160	LEU	CA-C-O	-7.48	112.57	120.28
1	L	14(C)	GLU	CG-CD-OE2	-7.42	101.32	118.40
2	H	104	ALA	CA-C-O	-7.33	112.78	120.99
2	H	101	ARG	NE-CZ-NH2	-7.20	112.72	119.20
2	H	205	ASN	N-CA-CB	-7.09	101.21	112.63
2	H	175	ARG	CD-NE-CZ	-7.01	114.59	124.40
1	L	14(K)	ILE	CA-C-O	6.99	132.69	120.80
2	H	179	ASN	CA-CB-CG	-6.98	105.62	112.60
3	I	58	GLU	CB-CG-CD	6.98	124.46	112.60
2	H	87	LYS	N-CA-C	6.97	119.85	108.55
1	L	14(K)	ILE	CB-CA-C	6.93	125.46	111.60
2	H	164	GLU	CB-CG-CD	6.92	124.36	112.60
2	H	64	LEU	N-CA-C	6.84	120.66	109.85
2	H	26	MET	CA-C-N	6.84	130.37	122.85
2	H	26	MET	C-N-CA	6.84	130.37	122.85
2	H	176	ILE	CA-CB-CG2	6.83	122.11	110.50
2	H	78	ASN	CA-CB-CG	6.77	119.37	112.60
2	H	192	GLU	CA-C-O	-6.76	113.71	121.15
2	H	158	VAL	CA-C-O	-6.75	114.24	121.19
2	H	18	GLU	O-C-N	6.72	131.35	122.47
2	H	48	SER	CA-C-O	-6.71	113.93	121.25
2	H	75	ARG	O-C-N	-6.67	114.67	122.87
2	H	189	ASP	O-C-N	6.67	129.53	123.26
2	H	135	LYS	CA-C-N	6.65	128.09	122.17
2	H	135	LYS	C-N-CA	6.65	128.09	122.17
2	H	40	LEU	O-C-N	6.65	131.10	122.93
2	H	33	LEU	CB-CA-C	6.63	121.75	110.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	128	THR	N-CA-C	-6.61	103.99	111.07
2	H	164	GLU	CA-CB-CG	6.60	127.29	114.10
2	H	160	LEU	O-C-N	6.59	126.56	121.88
2	H	243	ASP	CA-CB-CG	6.56	119.16	112.60
2	H	231	VAL	CA-C-O	-6.55	114.45	121.27
2	H	116	ASP	CA-CB-CG	6.53	119.12	112.60
2	H	49	ASP	CA-CB-CG	-6.52	106.08	112.60
2	H	230	HIS	CA-C-N	6.51	129.00	120.60
2	H	230	HIS	C-N-CA	6.51	129.00	120.60
2	H	83	SER	CA-C-N	6.44	133.09	122.07
2	H	83	SER	C-N-CA	6.44	133.09	122.07
2	H	75	ARG	CB-CA-C	6.43	120.39	109.72
2	H	18	GLU	CB-CA-C	-6.41	102.91	111.63
2	H	38	GLN	CA-C-O	-6.41	113.06	120.49
2	H	42	CYS	N-CA-CB	-6.36	101.67	111.46
2	H	67	ARG	NH1-CZ-NH2	-6.34	111.06	119.30
1	L	14(C)	GLU	CG-CD-OE1	6.23	132.74	118.40
2	H	205	ASN	CB-CG-ND2	-6.22	107.07	116.40
2	H	243	ASP	CA-C-O	-6.16	113.41	120.24
2	H	17	VAL	CA-C-O	-6.16	113.99	120.39
2	H	75	ARG	NE-CZ-NH2	6.15	124.73	119.20
2	H	145	LYS	O-C-N	6.12	130.37	123.27
2	H	171	SER	CA-C-O	6.08	126.09	119.15
2	H	18	GLU	CA-C-O	-6.08	113.44	120.98
2	H	180	MET	O-C-N	6.01	130.25	123.27
1	L	14(B)	THR	CA-C-O	-6.00	112.91	119.08
2	H	233	ARG	NE-CZ-NH2	5.97	124.58	119.20
2	H	35	ARG	NE-CZ-NH2	-5.97	113.83	119.20
2	H	187	ARG	CD-NE-CZ	-5.97	116.04	124.40
3	I	64	LEU	CB-CA-C	5.96	121.42	110.10
2	H	186(C)	GLY	C-N-CA	5.90	136.44	121.70
2	H	175	ARG	NE-CZ-NH1	-5.88	115.62	121.50
2	H	190	ALA	N-CA-C	-5.87	102.95	110.53
2	H	20	SER	CA-C-O	-5.86	115.00	121.33
2	H	165	ARG	CA-C-N	5.85	125.06	118.97
2	H	165	ARG	C-N-CA	5.85	125.06	118.97
2	H	61	GLU	O-C-N	-5.81	115.96	122.12
2	H	87	LYS	CB-CA-C	-5.78	99.45	109.86
2	H	222	ASP	CA-CB-CG	-5.75	106.85	112.60
2	H	81	LYS	CA-C-O	5.74	126.56	120.36
2	H	242	ILE	CB-CA-C	5.71	120.11	112.22
2	H	91	HIS	CA-C-O	5.71	125.11	119.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	14(G)	LEU	CB-CA-C	5.69	120.35	110.68
2	H	50	ARG	CD-NE-CZ	-5.69	116.43	124.40
1	L	8	GLU	N-CA-C	5.69	117.93	111.11
3	I	59	ILE	CA-C-N	5.66	125.95	119.83
3	I	59	ILE	C-N-CA	5.66	125.95	119.83
2	H	175	ARG	CA-C-N	5.59	129.59	122.37
2	H	175	ARG	C-N-CA	5.59	129.59	122.37
2	H	239	GLN	CA-C-O	5.59	127.22	121.07
1	L	13	GLU	CA-C-O	-5.57	114.81	120.71
2	H	61	GLU	N-CA-CB	-5.56	101.72	110.06
2	H	193	GLY	CA-C-O	-5.55	113.33	119.27
2	H	207	TRP	O-C-N	5.54	129.53	123.27
2	H	54	THR	CA-CB-CG2	5.53	119.90	110.50
2	H	228	TYR	CA-C-O	-5.51	114.89	121.11
2	H	62	ASN	OD1-CG-ND2	5.49	128.09	122.60
2	H	186(D)	LYS	N-CA-C	-5.49	99.10	110.80
2	H	105	LEU	CA-C-O	-5.43	115.02	121.16
2	H	213	VAL	O-C-N	-5.43	116.85	122.66
2	H	134	TYR	CA-C-O	-5.42	115.65	121.56
2	H	40	LEU	CA-C-N	5.39	130.77	122.42
2	H	40	LEU	C-N-CA	5.39	130.77	122.42
2	H	114	PHE	CA-CB-CG	-5.37	108.43	113.80
2	H	164	GLU	CA-C-N	5.36	127.65	120.58
2	H	164	GLU	C-N-CA	5.36	127.65	120.58
2	H	132	ALA	O-C-N	5.35	129.50	122.97
2	H	123	LEU	N-CA-C	-5.35	103.33	110.07
1	L	14(K)	ILE	N-CA-CB	-5.27	102.54	111.50
2	H	104	ALA	O-C-N	5.24	129.25	123.33
2	H	33	LEU	N-CA-CB	-5.23	101.89	110.21
2	H	244	GLN	CA-CB-CG	5.22	124.54	114.10
1	L	14	ASP	CB-CA-C	5.20	120.11	109.76
1	L	13	GLU	CB-CA-C	-5.20	100.02	109.38
2	H	22	ALA	N-CA-CB	-5.17	102.58	110.45
2	H	60(H)	PHE	CA-CB-CG	5.17	118.97	113.80
1	L	14(J)	TYR	CA-C-O	5.17	127.91	120.51
2	H	70	LYS	O-C-N	5.17	128.73	122.94
2	H	110	LYS	O-C-N	5.16	125.02	121.71
2	H	186(D)	LYS	CB-CA-C	5.13	120.62	110.42
2	H	174	ILE	CA-CB-CG2	5.11	119.18	110.50
2	H	205	ASN	CB-CA-C	-5.10	102.75	111.26
2	H	47	ILE	CB-CG1-CD1	5.08	124.48	113.80
2	H	180	MET	CA-C-O	-5.07	115.18	121.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	199	PHE	N-CA-C	-5.06	99.03	107.99
2	H	245	PHE	CA-CB-CG	-5.06	108.74	113.80
2	H	165	ARG	O-C-N	5.06	125.71	120.70
2	H	75	ARG	CG-CD-NE	5.05	123.11	112.00
2	H	219	GLY	N-CA-C	-5.05	103.08	112.37
2	H	100	ASP	CA-CB-CG	-5.04	107.56	112.60
2	H	208	TYR	N-CA-CB	-5.04	102.06	110.83
3	I	57	GLU	N-CA-CB	5.04	117.44	109.83
3	I	58	GLU	CA-C-O	-5.01	115.67	121.19

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	165	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	L	222	0	225	12	0
2	H	2022	0	1997	108	0
3	I	90	0	69	6	0
4	H	2	0	0	0	0
5	H	42	0	41	8	0
6	H	120	0	0	8	0
6	I	1	0	0	0	0
6	L	14	0	0	0	0
All	All	2513	0	2332	126	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 27.

All (126) 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:195:SER:OG	5:H:372:00L:H41	1.00	1.18
1:L:14(J):TYR:C	1:L:14(K):ILE:HG13	1.59	1.10
2:H:139:THR:HG22	2:H:157:VAL:HG22	1.25	1.10
2:H:85:LEU:HD13	2:H:106:MET:HE2	1.11	1.06
2:H:85:LEU:HD13	2:H:106:MET:CE	1.89	1.03
2:H:50:ARG:HH21	2:H:109:LYS:C	1.67	1.02
2:H:85:LEU:CD1	2:H:106:MET:HE2	1.90	1.00
1:L:14(I):SER:C	1:L:14(K):ILE:H	1.61	0.99
2:H:50:ARG:NH2	2:H:109:LYS:O	1.96	0.98
2:H:244:GLN:HG2	2:H:245:PHE:CD2	2.01	0.95
2:H:244:GLN:HG2	2:H:245:PHE:CE2	2.02	0.93
1:L:14(J):TYR:C	1:L:14(K):ILE:CG1	2.43	0.92
2:H:139:THR:CG2	2:H:157:VAL:HG22	2.02	0.90
2:H:195:SER:HG	5:H:372:00L:H41	1.12	0.89
2:H:195:SER:CB	5:H:372:00L:H41	2.06	0.86
2:H:186(A):ASP:OD1	2:H:186(B):GLU:N	2.09	0.86
2:H:85:LEU:CD1	2:H:106:MET:CE	2.50	0.85
2:H:186(A):ASP:O	2:H:186(C):GLY:N	2.10	0.84
2:H:187:ARG:NH2	2:H:221:ASP:O	2.09	0.84
2:H:50:ARG:NH1	2:H:107:LYS:HE2	1.93	0.84
2:H:50:ARG:NH2	2:H:109:LYS:C	2.36	0.82
2:H:97:ARG:HD2	6:H:500:HOH:O	1.80	0.81
2:H:41:LEU:O	5:H:372:00L:H2X	1.80	0.80
1:L:14(A):LYS:HB2	2:H:23:GLU:OE2	1.82	0.80
2:H:165:ARG:NH1	2:H:180:MET:O	2.14	0.77
2:H:139:THR:HG22	2:H:157:VAL:CG2	2.11	0.77
1:L:14(I):SER:C	1:L:14(K):ILE:N	2.39	0.75
2:H:186(A):ASP:OD1	2:H:186(A):ASP:C	2.34	0.71
2:H:187:ARG:NE	2:H:221:ASP:OD2	2.20	0.71
2:H:87:LYS:HB3	2:H:89:TYR:CE1	2.28	0.69
2:H:35:ARG:O	2:H:38:GLN:HA	1.92	0.69
2:H:244:GLN:CG	2:H:245:PHE:CE2	2.77	0.67
2:H:195:SER:OG	5:H:372:00L:C9X	2.42	0.67
2:H:244:GLN:NE2	2:H:245:PHE:CZ	2.63	0.66
1:L:14(J):TYR:O	1:L:14(K):ILE:HD12	1.95	0.66
2:H:41:LEU:CD2	2:H:64:LEU:CD2	2.74	0.66
2:H:50:ARG:NH2	2:H:108:LEU:O	2.28	0.66
2:H:186(A):ASP:CG	2:H:186(B):GLU:N	2.52	0.66
2:H:59:LEU:HD22	2:H:88:ILE:HD13	1.79	0.64
2:H:237:TRP:O	2:H:241:VAL:HG13	1.98	0.63
2:H:204(B):ASN:ND2	2:H:206:ARG:H	1.97	0.63
1:L:14(D):ARG:O	1:L:14(H):GLU:HG3	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:36:LYS:HE2	2:H:65:LEU:HD13	1.81	0.62
1:L:14(J):TYR:O	1:L:14(K):ILE:CD1	2.48	0.62
2:H:165:ARG:NH2	2:H:177:THR:O	2.32	0.62
2:H:17:VAL:O	2:H:188:GLY:HA2	2.00	0.62
2:H:18:GLU:HG3	2:H:187:ARG:HB2	1.82	0.61
2:H:186(A):ASP:C	2:H:186(C):GLY:H	2.07	0.61
2:H:165:ARG:N	2:H:166:PRO:CD	2.65	0.59
2:H:41:LEU:HD23	2:H:64:LEU:CD2	2.33	0.59
2:H:66:VAL:HG13	2:H:85:LEU:HD21	1.83	0.59
2:H:126:ARG:HA	2:H:232:PHE:CZ	2.39	0.57
2:H:32:MET:HG3	2:H:40:LEU:CD1	2.34	0.57
2:H:129(B):SER:O	2:H:131:GLN:NE2	2.36	0.56
2:H:175:ARG:NH1	6:H:498:HOH:O	2.29	0.56
2:H:204(B):ASN:O	2:H:205:ASN:HB2	2.06	0.56
2:H:18:GLU:HG3	2:H:187:ARG:CB	2.37	0.55
2:H:50:ARG:CZ	2:H:108:LEU:O	2.54	0.55
3:I:58:GLU:H	3:I:58:GLU:CD	2.14	0.55
2:H:85:LEU:HD11	2:H:106:MET:CE	2.37	0.55
2:H:244:GLN:CD	2:H:245:PHE:CE2	2.85	0.55
2:H:186(A):ASP:CG	2:H:186(B):GLU:H	2.16	0.54
2:H:49:ASP:N	2:H:49:ASP:OD1	2.32	0.54
3:I:61:GLU:C	3:I:63:TYS:N	2.66	0.53
2:H:87:LYS:HB3	2:H:89:TYR:HE1	1.71	0.53
2:H:126:ARG:HB3	6:H:501:HOH:O	2.09	0.52
1:L:14(J):TYR:O	1:L:14(K):ILE:CG1	2.58	0.52
2:H:163:VAL:HG23	2:H:183:ALA:HA	1.92	0.51
2:H:59:LEU:HD22	2:H:88:ILE:CD1	2.40	0.51
2:H:236:LYS:HB2	6:H:517:HOH:O	2.11	0.51
2:H:114:PHE:CD1	2:H:114:PHE:N	2.74	0.50
2:H:70:LYS:HE3	2:H:72:SER:O	2.10	0.50
2:H:41:LEU:CD2	2:H:64:LEU:HD21	2.42	0.49
2:H:204(B):ASN:C	2:H:204(B):ASN:HD22	2.21	0.49
2:H:237:TRP:O	2:H:241:VAL:CG1	2.60	0.49
2:H:235:LYS:HA	2:H:238:ILE:HD12	1.95	0.49
2:H:187:ARG:HE	2:H:221:ASP:CG	2.18	0.49
1:L:1(A):ASP:OD2	1:L:9:LYS:HE2	2.13	0.49
2:H:34:PHE:HE1	3:I:56:PHE:CD2	2.31	0.49
2:H:110:LYS:HB3	2:H:111:PRO:HD2	1.95	0.48
3:I:62:GLU:OE1	3:I:62:GLU:N	2.39	0.48
2:H:49:ASP:HB3	2:H:114:PHE:CZ	2.48	0.48
2:H:167:VAL:HG11	2:H:185:LYS:HE2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:186:PRO:HD3	6:H:438:HOH:O	2.14	0.48
2:H:224:LYS:HE2	6:H:528:HOH:O	2.14	0.47
2:H:198:PRO:HB2	2:H:200:VAL:HG13	1.95	0.47
2:H:186(B):GLU:O	2:H:186(C):GLY:C	2.58	0.47
2:H:32:MET:HG3	2:H:40:LEU:HD13	1.97	0.46
2:H:204(B):ASN:HD22	2:H:206:ARG:H	1.63	0.46
2:H:244:GLN:HG2	2:H:245:PHE:CZ	2.49	0.46
2:H:244:GLN:CG	2:H:245:PHE:CZ	2.99	0.46
2:H:91:HIS:CE1	2:H:101:ARG:HD3	2.51	0.46
2:H:194:ASP:O	2:H:195:SER:C	2.57	0.46
2:H:31:VAL:HG12	2:H:32:MET:N	2.30	0.45
2:H:204(B):ASN:O	2:H:205:ASN:CB	2.64	0.45
2:H:164:GLU:H	2:H:164:GLU:CD	2.25	0.44
2:H:244:GLN:CD	2:H:245:PHE:CZ	2.94	0.44
2:H:151:GLN:NE2	6:H:518:HOH:O	2.47	0.44
2:H:182:CYS:HB3	2:H:227:PHE:CE2	2.52	0.44
2:H:33:LEU:HD23	2:H:33:LEU:HA	1.50	0.44
2:H:195:SER:CB	5:H:372:00L:C	2.78	0.44
1:L:4:ARG:HB2	1:L:8:GLU:OE1	2.18	0.43
2:H:186(B):GLU:O	2:H:186(C):GLY:O	2.36	0.43
3:I:60:PRO:O	3:I:63:TYS:HB3	2.19	0.43
2:H:50:ARG:HH11	2:H:107:LYS:HE2	1.75	0.43
2:H:79:ILE:HG23	2:H:117:TYR:CD2	2.54	0.43
2:H:49:ASP:O	2:H:111:PRO:HA	2.19	0.43
2:H:16:ILE:HD13	2:H:190:ALA:HA	2.01	0.43
2:H:176:ILE:CD1	2:H:215:TRP:HZ2	2.32	0.43
2:H:35:ARG:HB2	2:H:41:LEU:HD13	2.00	0.42
2:H:164:GLU:C	2:H:166:PRO:HD2	2.44	0.42
2:H:176:ILE:HD11	2:H:215:TRP:CZ2	2.54	0.42
2:H:50:ARG:HH21	2:H:110:LYS:N	2.14	0.42
2:H:204(B):ASN:HD22	2:H:205:ASN:N	2.17	0.42
5:H:372:00L:N1X	5:H:372:00L:C6X	2.83	0.42
2:H:186(A):ASP:C	2:H:186(C):GLY:N	2.65	0.42
2:H:244:GLN:HG2	2:H:245:PHE:CG	2.49	0.41
2:H:85:LEU:HD11	2:H:106:MET:HE1	2.01	0.41
2:H:36:LYS:HE3	2:H:62:ASN:O	2.21	0.41
2:H:60(B):PRO:N	2:H:60(C):PRO:CD	2.82	0.41
2:H:182:CYS:HB2	2:H:226:GLY:O	2.20	0.41
5:H:372:00L:H6X	5:H:372:00L:H8XA	1.65	0.41
2:H:143:ASN:HA	2:H:150:GLY:O	2.20	0.41
2:H:212:ILE:O	2:H:228:TYR:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:3:LEU:HD22	6:H:535:HOH:O	2.20	0.40
3:I:60:PRO:HG2	3:I:63:TYS:HE2	2.04	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	L	25/36 (69%)	22 (88%)	3 (12%)	0	100	100
2	H	246/259 (95%)	232 (94%)	8 (3%)	6 (2%)	4	1
3	I	7/12 (58%)	7 (100%)	0	0	100	100
All	All	278/307 (91%)	261 (94%)	11 (4%)	6 (2%)	5	1

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	186(B)	GLU
2	H	186(C)	GLY
2	H	77	GLU
2	H	186(D)	LYS
2	H	195	SER
2	H	186(A)	ASP

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L	25/31 (81%)	24 (96%)	1 (4%)	28	22
2	H	218/225 (97%)	200 (92%)	18 (8%)	10	4
3	I	8/10 (80%)	7 (88%)	1 (12%)	4	1
All	All	251/266 (94%)	231 (92%)	20 (8%)	11	5

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

Mol	Chain	Res	Type
1	L	6	LEU
2	H	33	LEU
2	H	41	LEU
2	H	61	GLU
2	H	62	ASN
2	H	64	LEU
2	H	65	LEU
2	H	79	ILE
2	H	83	SER
2	H	129(B)	SER
2	H	129(C)	LEU
2	H	164	GLU
2	H	176	ILE
2	H	205	ASN
2	H	233	ARG
2	H	239	GLN
2	H	240	LYS
2	H	241	VAL
2	H	244	GLN
3	I	58	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
2	H	38	GLN
2	H	62	ASN
2	H	151	GLN
2	H	156	GLN
2	H	204(B)	ASN
2	H	239	GLN
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	1.54	2 (13%)	15,22,24	1.42	2 (13%)

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	-	2/10/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	63	TYS	OH-S	3.82	1.65	1.58
3	I	63	TYS	OH-CZ	-3.56	1.36	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	63	TYS	OH-S-O2	-2.35	100.41	107.56
3	I	63	TYS	O2-S-O1	2.06	120.20	112.24

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	I	63	TYS	CA-CB-CG-CD1
3	I	63	TYS	CZ-OH-S-O2

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	63	TYS	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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
5	00L	H	372	2	41,45,45	1.98	9 (21%)	46,62,62	2.23	14 (30%)

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
5	00L	H	372	2	-	5/33/63/63	0/4/4/4

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	372	00L	O-C	-7.04	1.28	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	372	00L	C9X-N1X	5.60	1.46	1.33
5	H	372	00L	C5-C6	-2.96	1.51	1.54
5	H	372	00L	N2-N1	-2.50	1.41	1.44
5	H	372	00L	C7X-C1X	2.14	1.57	1.51
5	H	372	00L	O1X-C9X	-2.12	1.19	1.23
5	H	372	00L	C4X-C5X	2.09	1.42	1.38
5	H	372	00L	CA-N	2.06	1.49	1.46
5	H	372	00L	C8-N	2.00	1.38	1.34

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	H	372	00L	C8X-N1X-C9X	-6.00	111.76	122.55
5	H	372	00L	O-C-CA	5.70	124.49	108.43
5	H	372	00L	C8X-C7X-C1X	-4.43	102.84	112.83
5	H	372	00L	C1-C8-N	4.39	126.15	116.52
5	H	372	00L	C2-C1-C8	3.72	119.12	111.21
5	H	372	00L	C5-C4-N1	3.15	113.10	109.20
5	H	372	00L	C-C9X-N1X	-3.14	110.40	116.64
5	H	372	00L	C7-N2-N1	3.08	125.72	120.31
5	H	372	00L	C1-N2-C7	-3.03	120.66	124.94
5	H	372	00L	O2-C8-C1	-2.66	114.28	120.69
5	H	372	00L	O1X-C9X-N1X	2.55	128.37	122.98
5	H	372	00L	C2X-C1X-C6X	2.54	122.01	118.23
5	H	372	00L	CG-CB-CA	-2.45	109.28	113.94
5	H	372	00L	CB-CA-N	2.09	113.01	110.30

There are no chirality outliers.

All (5) torsion outliers are listed below:

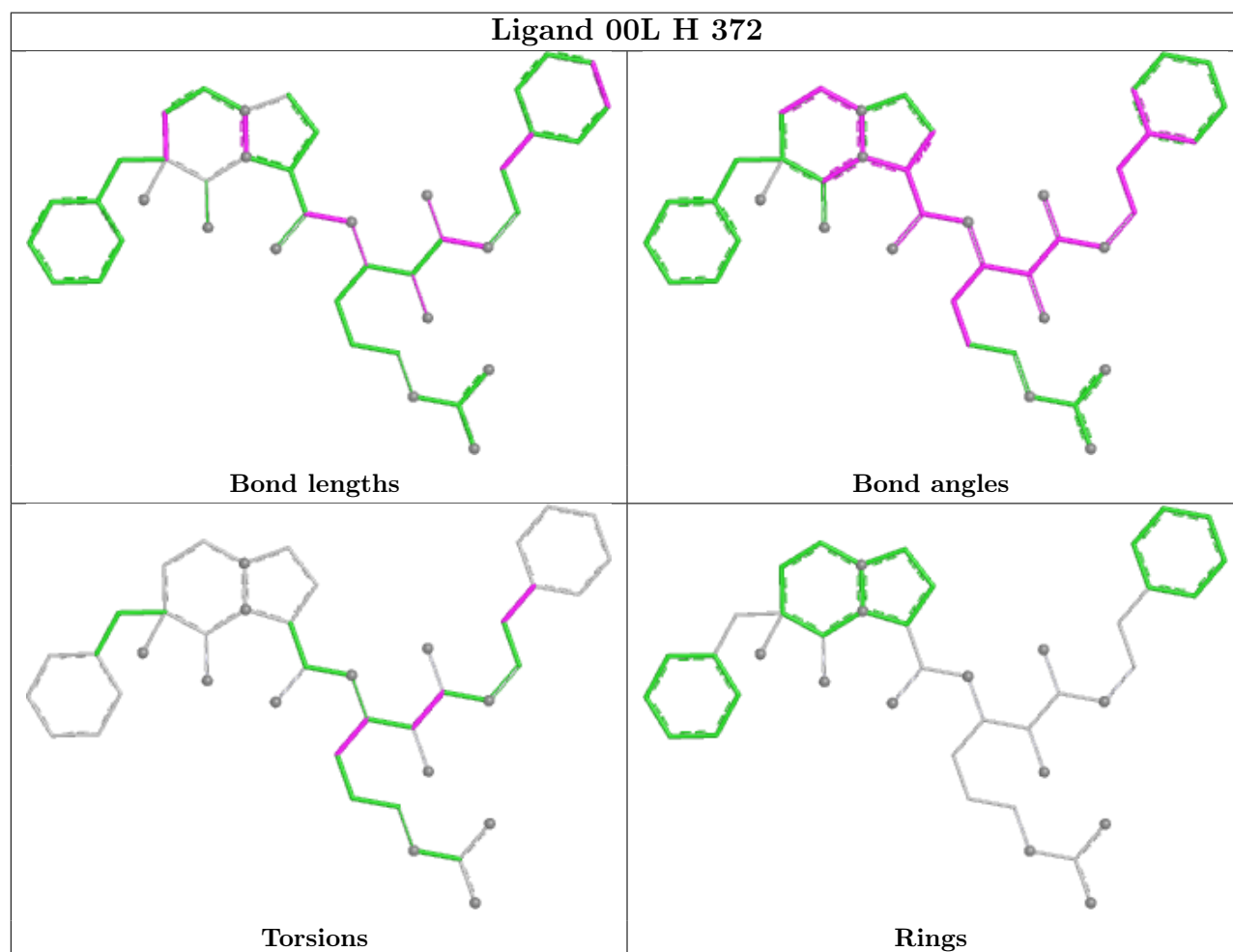
Mol	Chain	Res	Type	Atoms
5	H	372	00L	O-C-C9X-O1X
5	H	372	00L	O-C-C9X-N1X
5	H	372	00L	N-CA-CB-CG
5	H	372	00L	C6X-C1X-C7X-C8X
5	H	372	00L	C2X-C1X-C7X-C8X

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	H	372	00L	8	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 ⓘ

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.