



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 09:14 pm BST

PDB ID : 1IQF  
Title : Human coagulation factor Xa in complex with M55165  
Authors : Shiromizu, I.; Matsusue, T.  
Deposited on : 2001-07-23  
Resolution : 3.20 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

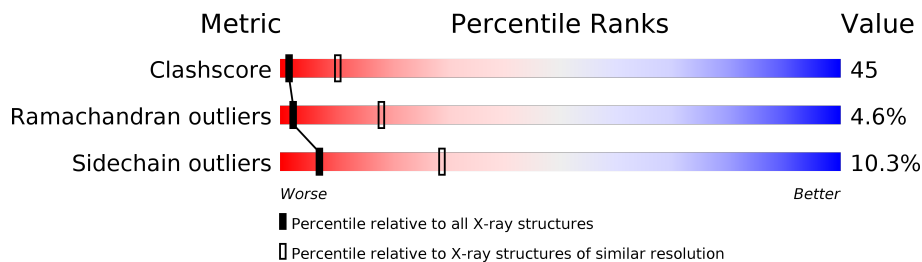
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	235	
2	L	96	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2279 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 coagulation Factor Xa.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	235	1864	1172	327	351	14	0	0	0

- Molecule 2 is a protein called coagulation Factor Xa.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	51	375	226	65	77	7	0	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		

- Molecule 4 is (2R)-4-[(6-CHLORO-2-NAPHTHALENYL)SULFONYL]-6-OXO-1-[[1-(4-PYRIDINYL)-4-PIPERIDINYLMETHYL]-2-PIPERAZINECARBOXYLIC ACID ETHYL ESTER (three-letter code: XMD) (formula: C<sub>28</sub>H<sub>31</sub>ClN<sub>4</sub>O<sub>5</sub>S).





## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	72.29Å 78.04Å 56.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 3.20	Depositor
% Data completeness (in resolution range)	81.0 (8.00-3.20)	Depositor
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNX 2000	Depositor
R, $R_{free}$	0.169 , 0.277	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	2279	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	12.0	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: XMD, CA

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	0.40	0/1902	0.67	0/2560
2	L	0.38	0/381	0.67	0/515
All	All	0.40	0/2283	0.67	0/3075

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1864	0	1821	172	0
2	L	375	0	343	38	0
3	A	1	0	0	0	0
4	A	39	0	31	4	0
All	All	2279	0	2195	202	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 45.

All (202) 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:96:LYS:H	1:A:96:LYS:HD3	1.21	1.04
2:L:87:LYS:HG2	2:L:88:LEU:H	1.23	1.01
2:L:103:GLU:O	2:L:104:GLN:HG2	1.68	0.92
1:A:120:PRO:O	2:L:132:CYS:HA	1.70	0.91
2:L:113:ARG:NH1	2:L:113:ARG:H	1.71	0.89
1:A:81:ALA:HB2	1:A:115:ARG:HH22	1.36	0.88
2:L:113:ARG:HH11	2:L:113:ARG:H	1.22	0.87
1:A:21:GLU:HB3	1:A:23:LYS:NZ	1.96	0.81
2:L:87:LYS:N	2:L:106:SER:HA	1.97	0.79
1:A:55:ALA:H	1:A:196:GLY:HA2	1.49	0.78
1:A:217:GLU:OE1	1:A:224:LYS:HD3	1.85	0.77
2:L:97:ASP:OD1	2:L:123:ALA:HA	1.85	0.76
1:A:45:THR:OG1	1:A:198:PRO:HB3	1.85	0.75
1:A:137:ILE:HB	1:A:200:VAL:HG23	1.67	0.75
1:A:71:ARG:HH11	1:A:71:ARG:HB3	1.52	0.75
1:A:47:LEU:HD11	1:A:53:LEU:HB2	1.69	0.74
1:A:122:CYS:O	1:A:209:VAL:HG23	1.88	0.73
1:A:240:ARG:HD3	1:A:245:ARG:HD3	1.70	0.73
1:A:35:ASN:ND2	1:A:37:GLU:H	1.88	0.72
1:A:183:ALA:HB3	1:A:228:TYR:CE1	2.25	0.71
1:A:50:PHE:CZ	1:A:111:PRO:HG3	2.26	0.71
1:A:202:ARG:NE	1:A:205:ASP:H	1.88	0.71
1:A:202:ARG:CZ	1:A:205:ASP:H	2.04	0.70
1:A:195:SER:HA	1:A:213:VAL:HG12	1.73	0.70
1:A:210:THR:O	1:A:231:VAL:HB	1.91	0.70
1:A:81:ALA:HB2	1:A:115:ARG:NH2	2.09	0.68
1:A:123:LEU:HD23	2:L:113:ARG:NH2	2.08	0.68
1:A:212:ILE:HB	1:A:229:THR:HB	1.74	0.68
1:A:217:GLU:O	1:A:222:ARG:HD2	1.93	0.68
1:A:35:ASN:HD21	1:A:37:GLU:CG	2.07	0.68
1:A:164:ASP:OD2	1:A:166:ASN:HB2	1.96	0.66
1:A:224:LYS:HE3	1:A:225:TYR:H	1.60	0.66
1:A:238:ILE:O	1:A:242:MET:HG2	1.94	0.66
1:A:165:ARG:HH12	1:A:176:ILE:HG22	1.60	0.65
2:L:87:LYS:CA	2:L:106:SER:HA	2.27	0.65
1:A:134:LYS:HE3	1:A:134:LYS:HA	1.78	0.65
1:A:33:LEU:HD12	1:A:42:CYS:HB3	1.80	0.64
1:A:195:SER:HA	1:A:213:VAL:CG1	2.28	0.64
1:A:202:ARG:HH21	1:A:205:ASP:CG	1.99	0.64
2:L:88:LEU:HD23	2:L:91:LEU:HD22	1.80	0.64
1:A:108:LEU:HD12	1:A:112:ILE:HG13	1.81	0.63
2:L:87:LYS:HG2	2:L:88:LEU:N	2.05	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:ARG:HB3	1:A:71:ARG:NH1	2.14	0.62
1:A:202:ARG:NH2	1:A:205:ASP:H	1.97	0.62
1:A:215:TRP:CZ2	1:A:227:ILE:HG21	2.35	0.62
1:A:163:VAL:HB	1:A:182:CYS:HB3	1.82	0.62
1:A:202:ARG:HH21	1:A:205:ASP:N	1.98	0.62
2:L:88:LEU:C	2:L:90:SER:H	2.03	0.61
1:A:222:ARG:HH22	4:A:401:XMD:H183	1.65	0.61
1:A:202:ARG:NH2	1:A:205:ASP:N	2.49	0.61
1:A:115:ARG:HG2	1:A:116:MET:O	2.01	0.61
1:A:35:ASN:HD21	1:A:37:GLU:CD	2.04	0.61
1:A:202:ARG:HB2	1:A:207:TYR:CE2	2.36	0.61
1:A:232:THR:HA	1:A:235:LEU:HD13	1.83	0.61
1:A:150:ARG:HG3	1:A:150:ARG:HH21	1.66	0.60
2:L:87:LYS:CG	2:L:88:LEU:H	2.03	0.60
1:A:115:ARG:HD3	1:A:118:VAL:HB	1.83	0.60
1:A:21:GLU:HB3	1:A:23:LYS:HZ2	1.65	0.60
1:A:217:GLU:HA	4:A:401:XMD:O19	2.01	0.60
1:A:124(A):GLU:OE1	1:A:126:ASP:N	2.35	0.60
1:A:80:GLU:N	1:A:80:GLU:OE2	2.29	0.59
1:A:171:SER:HB2	1:A:223(A):GLY:O	2.02	0.59
1:A:23:LYS:O	1:A:26:GLU:HB2	2.04	0.58
1:A:91:HIS:HB2	1:A:103:ILE:HG23	1.85	0.57
1:A:165:ARG:O	1:A:169:LYS:HE2	2.04	0.57
1:A:55:ALA:O	1:A:58:CYS:HB2	2.04	0.57
1:A:116:MET:HG2	1:A:117:ASN:OD1	2.05	0.56
1:A:131(B):MET:HA	1:A:162:TYR:CZ	2.41	0.56
1:A:72:ASN:ND2	1:A:154:ARG:NE	2.53	0.56
1:A:209:VAL:O	1:A:231:VAL:HG11	2.06	0.56
1:A:186:LYS:HE2	1:A:188:GLU:OE2	2.06	0.56
1:A:33:LEU:HD12	1:A:42:CYS:CB	2.35	0.56
1:A:21:GLU:HB3	1:A:23:LYS:HZ3	1.71	0.56
1:A:74:GLU:OE2	1:A:75:GLN:HG3	2.05	0.55
2:L:97:ASP:CG	2:L:123:ALA:HA	2.26	0.55
1:A:56:ALA:HB2	1:A:103:ILE:N	2.22	0.55
1:A:16:ILE:HD13	1:A:190:ALA:HA	1.87	0.55
1:A:224:LYS:HE3	1:A:225:TYR:N	2.21	0.55
1:A:241:SER:O	1:A:244:THR:N	2.36	0.55
1:A:115:ARG:HD3	1:A:118:VAL:CG2	2.37	0.54
1:A:59:LEU:HD13	1:A:88:VAL:HG21	1.90	0.54
1:A:158:LEU:CD2	1:A:158:LEU:C	2.76	0.54
1:A:28:PRO:HG2	1:A:29:TRP:CE3	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:PHE:HE2	1:A:106:LEU:HD13	1.73	0.54
1:A:65:LYS:HE2	1:A:84:GLU:HG2	1.90	0.53
1:A:56:ALA:HB2	1:A:103:ILE:O	2.08	0.53
1:A:30:GLN:HG2	1:A:155:LEU:CD1	2.37	0.53
1:A:100:ASP:O	1:A:101:PHE:HB2	2.07	0.53
1:A:37:GLU:O	1:A:39:GLU:HG3	2.08	0.53
1:A:222:ARG:NH2	4:A:401:XMD:H183	2.23	0.53
1:A:56:ALA:HB3	1:A:102:ASP:HA	1.91	0.52
2:L:117:LEU:HD12	2:L:123:ALA:O	2.09	0.52
1:A:163:VAL:HB	1:A:182:CYS:CB	2.39	0.52
1:A:34:ILE:HG13	1:A:65:LYS:HB2	1.91	0.52
1:A:23:LYS:HB2	1:A:26:GLU:OE1	2.09	0.52
2:L:87:LYS:HB2	2:L:105:ASN:O	2.09	0.52
1:A:128:ALA:HA	1:A:131(A):LEU:HD22	1.91	0.52
1:A:98:THR:O	1:A:99:TYR:HB2	2.09	0.51
2:L:93:ASN:ND2	2:L:96:CYS:HB2	2.25	0.51
1:A:138:VAL:HG12	1:A:158:LEU:O	2.10	0.51
1:A:35:ASN:O	1:A:38:ASN:N	2.40	0.51
1:A:158:LEU:HD22	1:A:160:VAL:HG13	1.93	0.51
1:A:153:THR:HG22	1:A:154:ARG:HD3	1.93	0.51
1:A:80:GLU:H	1:A:80:GLU:CD	2.14	0.51
2:L:118:ALA:HB3	2:L:120:ASN:OD1	2.11	0.51
2:L:87:LYS:HB2	2:L:105:ASN:C	2.31	0.51
1:A:92:ASN:N	1:A:92:ASN:OD1	2.44	0.51
2:L:103:GLU:HG2	2:L:104:GLN:HE21	1.76	0.50
1:A:16:ILE:N	1:A:143:ARG:O	2.44	0.50
1:A:185(A):ASP:OD2	1:A:185(A):ASP:O	2.30	0.50
1:A:81:ALA:CB	1:A:115:ARG:HH22	2.17	0.50
1:A:165:ARG:NH1	1:A:176:ILE:HG22	2.27	0.50
1:A:202:ARG:HE	1:A:205:ASP:H	1.58	0.50
1:A:35:ASN:HD21	1:A:37:GLU:CB	2.24	0.50
1:A:124:PRO:HA	2:L:99:PHE:CE1	2.47	0.50
1:A:165:ARG:NH2	1:A:169:LYS:NZ	2.61	0.49
1:A:215:TRP:CZ3	1:A:227:ILE:HG13	2.48	0.49
1:A:115:ARG:HD3	1:A:118:VAL:CB	2.42	0.49
1:A:82:VAL:HG12	1:A:83:HIS:N	2.27	0.49
1:A:30:GLN:HE21	1:A:155:LEU:HD11	1.77	0.49
1:A:215:TRP:CE2	1:A:227:ILE:HG21	2.48	0.49
1:A:131(A):LEU:O	1:A:133:GLN:HB2	2.13	0.48
1:A:96:LYS:H	1:A:96:LYS:CD	1.96	0.48
2:L:113:ARG:CZ	2:L:113:ARG:HB2	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:230:LYS:HD3	1:A:233:ALA:HB2	1.95	0.48
2:L:101:HIS:HB2	2:L:108:VAL:O	2.13	0.48
1:A:25:GLY:HA3	2:L:136:THR:O	2.12	0.48
1:A:158:LEU:HD11	1:A:188:GLU:HB3	1.96	0.48
1:A:83:HIS:CG	1:A:108:LEU:HD13	2.49	0.48
1:A:179:ASN:HB3	1:A:234:PHE:CE2	2.48	0.48
1:A:56:ALA:HB2	1:A:103:ILE:H	1.77	0.48
2:L:103:GLU:C	2:L:104:GLN:HG2	2.32	0.48
1:A:58:CYS:C	1:A:60:TYR:H	2.17	0.48
1:A:99:TYR:HD1	1:A:215:TRP:CD1	2.32	0.48
1:A:244:THR:O	1:A:245:ARG:HB2	2.14	0.48
1:A:141:PHE:CZ	1:A:155:LEU:HB2	2.49	0.48
2:L:87:LYS:HA	2:L:106:SER:HA	1.94	0.48
2:L:94:GLY:HA3	2:L:107:VAL:HG11	1.95	0.47
1:A:95:THR:HG22	1:A:97:GLU:OE1	2.14	0.47
1:A:239:ASP:C	1:A:241:SER:N	2.67	0.47
1:A:124:PRO:HB3	1:A:208:PHE:CD1	2.49	0.47
1:A:64:PHE:CE2	1:A:106:LEU:HD13	2.49	0.47
1:A:210:THR:C	1:A:231:VAL:HB	2.34	0.47
1:A:165:ARG:NH2	1:A:169:LYS:HZ1	2.13	0.47
1:A:94:PHE:O	1:A:95:THR:HG23	2.15	0.46
1:A:178:GLN:HG3	1:A:178:GLN:H	1.51	0.46
1:A:188:GLU:O	1:A:189:ASP:HB2	2.15	0.46
1:A:185:TYR:CD2	1:A:186:LYS:HB3	2.51	0.46
1:A:239:ASP:O	1:A:240:ARG:C	2.55	0.46
1:A:122:CYS:SG	2:L:132:CYS:C	2.94	0.46
1:A:99:TYR:HD1	1:A:215:TRP:CG	2.34	0.45
2:L:103:GLU:O	2:L:105:ASN:N	2.39	0.45
1:A:232:THR:HA	1:A:235:LEU:CD1	2.46	0.45
1:A:58:CYS:HA	1:A:61:GLN:OE1	2.17	0.45
1:A:145:HIS:ND1	1:A:147:GLU:N	2.65	0.45
1:A:30:GLN:HG2	1:A:155:LEU:HD11	1.99	0.45
1:A:185:TYR:CG	1:A:186:LYS:HB3	2.52	0.45
1:A:96:LYS:N	1:A:96:LYS:HD3	2.07	0.45
1:A:191:CYS:SG	1:A:192:GLN:N	2.87	0.44
1:A:33:LEU:HD22	1:A:64:PHE:CE2	2.53	0.44
2:L:88:LEU:C	2:L:90:SER:N	2.70	0.44
1:A:240:ARG:CD	1:A:245:ARG:HD3	2.44	0.44
1:A:203:PHE:O	1:A:204:LYS:HB2	2.18	0.44
1:A:71:ARG:CB	1:A:71:ARG:NH1	2.80	0.44
1:A:217:GLU:OE2	1:A:224:LYS:NZ	2.40	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:215:TRP:CH2	1:A:227:ILE:HG13	2.52	0.44
1:A:201:THR:OG1	1:A:210:THR:HG21	2.18	0.44
1:A:243:LYS:O	1:A:244:THR:HB	2.18	0.43
1:A:143:ARG:CZ	1:A:192:GLN:OE1	2.66	0.43
2:L:88:LEU:HD23	2:L:91:LEU:CD2	2.47	0.43
1:A:36:GLU:HG2	1:A:37:GLU:HG3	2.00	0.43
2:L:113:ARG:NH1	2:L:113:ARG:N	2.52	0.43
1:A:234:PHE:O	1:A:235:LEU:C	2.55	0.43
2:L:125:ILE:HA	2:L:126:PRO:HD3	1.85	0.43
1:A:161:PRO:HG2	1:A:185:TYR:CE1	2.53	0.43
1:A:185:TYR:CE2	1:A:186:LYS:HD3	2.54	0.43
1:A:150:ARG:NH2	1:A:150:ARG:HG3	2.33	0.43
1:A:76:GLU:HG3	1:A:78:GLY:H	1.84	0.43
1:A:115:ARG:HD3	1:A:118:VAL:HG21	2.00	0.42
1:A:179:ASN:HB3	1:A:234:PHE:HE2	1.84	0.42
1:A:101:PHE:CD2	1:A:234:PHE:HE1	2.38	0.42
2:L:125:ILE:N	2:L:125:ILE:HD13	2.35	0.42
1:A:128:ALA:HA	1:A:131(A):LEU:HB2	2.02	0.42
1:A:55:ALA:N	1:A:196:GLY:HA2	2.27	0.41
1:A:73:THR:C	1:A:74:GLU:HG3	2.40	0.41
1:A:124:PRO:HA	2:L:99:PHE:HE1	1.82	0.41
1:A:123:LEU:HD23	2:L:113:ARG:HH21	1.82	0.41
1:A:101:PHE:CD2	1:A:234:PHE:CE1	3.08	0.41
1:A:235:LEU:O	1:A:237:TRP:N	2.53	0.41
1:A:41:PHE:O	1:A:193:GLY:HA2	2.20	0.41
1:A:94:PHE:CG	1:A:95:THR:N	2.89	0.41
1:A:164:ASP:C	1:A:166:ASN:N	2.74	0.41
1:A:189:ASP:OD1	4:A:401:XMD:H10	2.21	0.41
1:A:137:ILE:HD13	1:A:159:GLU:HA	2.02	0.41
1:A:206:THR:HA	2:L:133:GLY:O	2.20	0.41
1:A:51:TYR:CE1	1:A:107:ARG:HB2	2.55	0.41
1:A:61:GLN:N	1:A:61:GLN:CD	2.75	0.41
2:L:115:TYR:CE2	2:L:126:PRO:HG3	2.55	0.41
1:A:166:ASN:O	1:A:167:SER:C	2.60	0.40
1:A:163:VAL:CB	1:A:182:CYS:HB3	2.49	0.40
1:A:35:ASN:CG	1:A:37:GLU:H	2.24	0.40
1:A:92:ASN:O	1:A:94:PHE:N	2.52	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	233/235 (99%)	178 (76%)	44 (19%)	11 (5%)	2	17
2	L	49/96 (51%)	37 (76%)	10 (20%)	2 (4%)	3	21
All	All	282/331 (85%)	215 (76%)	54 (19%)	13 (5%)	2	18

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	74	GLU
1	A	93	ARG
1	A	80	GLU
1	A	125	ARG
1	A	22	CYS
1	A	92	ASN
1	A	172	SER
1	A	235	LEU
1	A	236	LYS
2	L	104	GLN
1	A	244	THR
2	L	136	THR
1	A	81	ALA

### 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	A	200/200 (100%)	180 (90%)	20 (10%)	7	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	L	43/82 (52%)	38 (88%)	5 (12%)	5	24
All	All	243/282 (86%)	218 (90%)	25 (10%)	7	29

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	VAL
1	A	74	GLU
1	A	77	GLU
1	A	92	ASN
1	A	95	THR
1	A	96	LYS
1	A	97	GLU
1	A	109	LYS
1	A	115	ARG
1	A	116	MET
1	A	124(A)	GLU
1	A	131(A)	LEU
1	A	133	GLN
1	A	134	LYS
1	A	158	LEU
1	A	178	GLN
1	A	181	PHE
1	A	187	GLN
1	A	231	VAL
1	A	235	LEU
2	L	89	CYS
2	L	91	LEU
2	L	101	HIS
2	L	113	ARG
2	L	125	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	30	GLN
1	A	35	ASN
1	A	133	GLN
2	L	104	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is 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
4	XMD	A	401	-	43,43,43	4.08	30 (69%)	55,62,62	1.86	14 (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	XMD	A	401	-	-	12/27/53/53	0/4/5/5

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	401	XMD	O13-S12	10.46	1.55	1.43
4	A	401	XMD	O26-S12	9.76	1.54	1.43
4	A	401	XMD	S12-N21	6.86	1.73	1.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	401	XMD	C22-N25	6.39	1.45	1.35
4	A	401	XMD	C5-C2	6.30	1.48	1.38
4	A	401	XMD	C14-N25	5.81	1.54	1.47
4	A	401	XMD	C10-C11	5.21	1.47	1.38
4	A	401	XMD	C1-C2	5.18	1.46	1.36
4	A	401	XMD	C33-C30	5.06	1.49	1.39
4	A	401	XMD	C6-C3	5.04	1.53	1.42
4	A	401	XMD	C31-C30	4.79	1.48	1.39
4	A	401	XMD	C30-N29	4.74	1.51	1.38
4	A	401	XMD	C9-C11	4.61	1.45	1.36
4	A	401	XMD	C20-C14	4.59	1.57	1.53
4	A	401	XMD	C32-N29	3.78	1.52	1.46
4	A	401	XMD	C34-N29	3.60	1.52	1.46
4	A	401	XMD	C4-C5	3.55	1.44	1.36
4	A	401	XMD	C8-C10	3.36	1.43	1.36
4	A	401	XMD	C24-C22	3.23	1.57	1.51
4	A	401	XMD	C33-C38	2.89	1.44	1.38
4	A	401	XMD	C39-C35	2.88	1.60	1.52
4	A	401	XMD	C20-N21	2.83	1.50	1.47
4	A	401	XMD	C31-C28	2.72	1.44	1.38
4	A	401	XMD	C4-C3	2.60	1.48	1.41
4	A	401	XMD	C36-C35	2.58	1.59	1.52
4	A	401	XMD	C27-N25	2.56	1.51	1.47
4	A	401	XMD	O16-C15	2.53	1.38	1.33
4	A	401	XMD	C8-C6	2.46	1.47	1.41
4	A	401	XMD	C9-C3	2.36	1.47	1.42
4	A	401	XMD	C1-C6	2.09	1.46	1.42

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	401	XMD	O26-S12-O13	-6.99	108.20	119.52
4	A	401	XMD	C15-C14-N25	4.55	120.53	112.05
4	A	401	XMD	C2-S12-N21	3.47	111.44	107.30
4	A	401	XMD	C39-C35-C36	3.35	117.52	109.33
4	A	401	XMD	C22-C24-N21	3.06	119.58	115.12
4	A	401	XMD	O13-S12-C2	2.55	111.27	108.05
4	A	401	XMD	C10-C11-C9	-2.41	119.13	121.99
4	A	401	XMD	O23-C22-N25	2.34	124.67	121.92
4	A	401	XMD	C5-C2-C1	-2.32	118.21	121.05
4	A	401	XMD	C8-C10-C11	2.29	121.87	119.21
4	A	401	XMD	C11-C9-C3	2.16	121.44	119.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	401	XMD	C36-C32-N29	2.13	115.50	111.10
4	A	401	XMD	C39-C34-N29	2.09	115.41	111.10
4	A	401	XMD	C32-C36-C35	2.05	117.19	111.99

There are no chirality outliers.

All (12) torsion outliers are listed below:

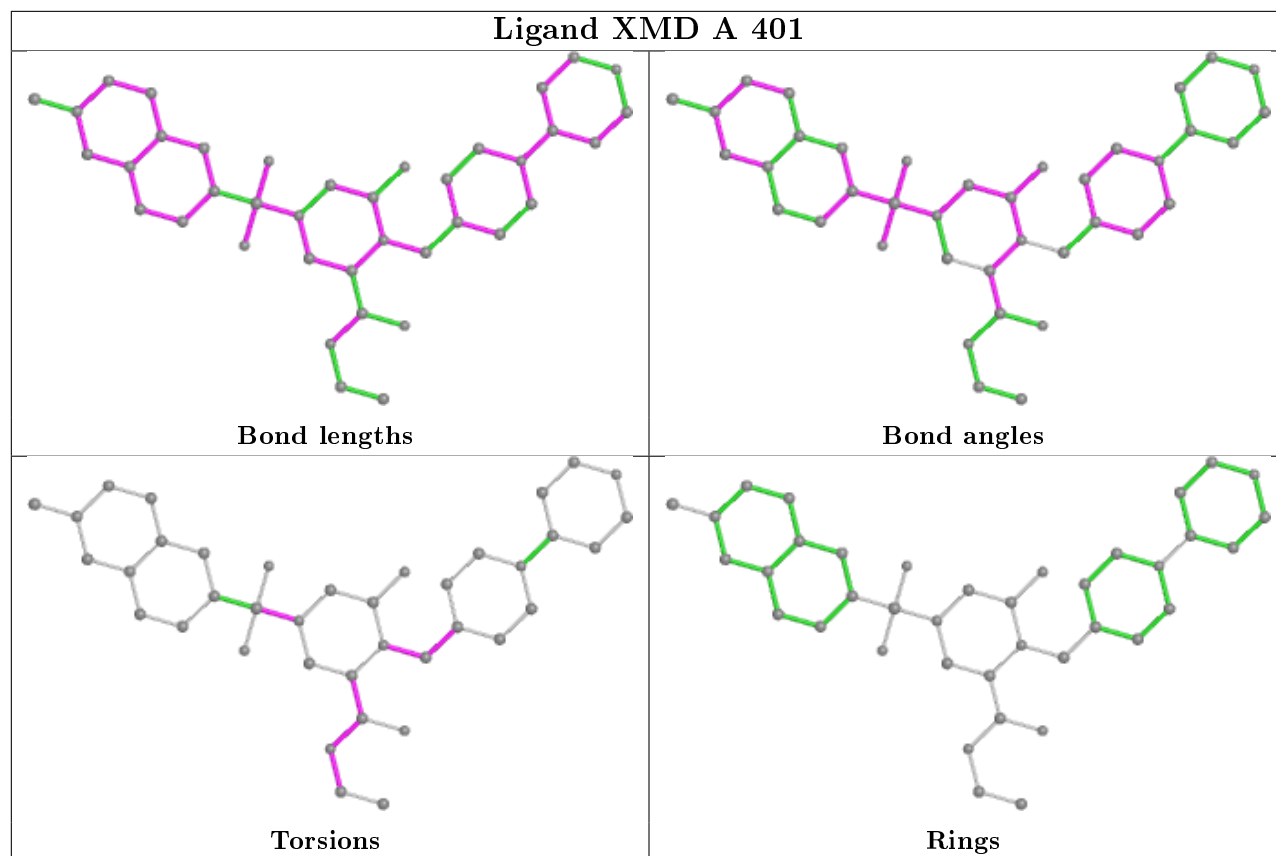
Mol	Chain	Res	Type	Atoms
4	A	401	XMD	C14-C15-O16-C17
4	A	401	XMD	O19-C15-O16-C17
4	A	401	XMD	C20-N21-S12-O13
4	A	401	XMD	C24-N21-S12-O13
4	A	401	XMD	N25-C27-C35-C39
4	A	401	XMD	C24-N21-S12-C2
4	A	401	XMD	N25-C14-C15-O16
4	A	401	XMD	C20-N21-S12-C2
4	A	401	XMD	C24-N21-S12-O26
4	A	401	XMD	N25-C14-C15-O19
4	A	401	XMD	C35-C27-N25-C14
4	A	401	XMD	C18-C17-O16-C15

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	401	XMD	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.