Full wwPDB X-ray Structure Validation Report (i)

Jun 13, 2024 – 12:30 PM EDT

PDB ID	:	1NU7
Title	:	Staphylocoagulase-Thrombin Complex
Authors	:	Friedrich, R.; Bode, W.; Fuentes-Prior, P.; Panizzi, P.; Bock, P.E.
Deposited on	:	2003-01-31
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 (i) 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 (1)) were used in the production of this report:

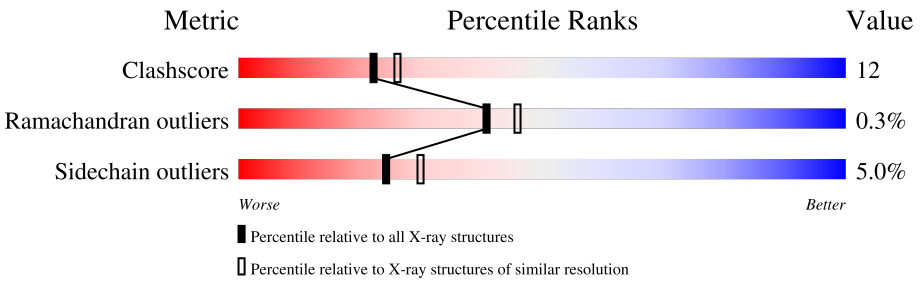
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

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	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	28	86% 14%
1	E	28	54% 43% .
2	B	259	75% 21% .
2	F	259	70% 28% .
3	D	282	80% 17% .
3	H	282	75% 22% .

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

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	0ZJ	B	299	X	-	-	-
4	0ZJ	F	299	X	-	-	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 10160 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 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	28	228	141	37	49	1	8	0	0
1	E	27	224	139	36	48	1	7	0	0

- Molecule 2 is a protein called Thrombin heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	258	2083	1329	369	371	14	13	0	0
2	F	258	2083	1329	369	371	14	19	0	0

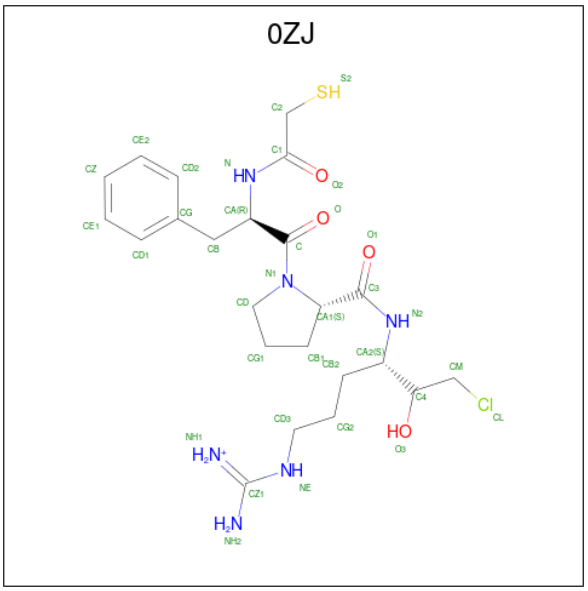
- Molecule 3 is a protein called Staphylocoagulase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	D	282	2346	1482	387	471	6	84	0	0
3	H	282	2346	1482	387	471	6	88	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	0	MET	-	INITIATING METHIONINE	UNP Q846V4
H	0	MET	-	INITIATING METHIONINE	UNP Q846V4

- Molecule 4 is N-(sulfanylacetyl)-D-phenylalanyl-N-[(2S,3S)-6-{[amino(iminio)methyl]amino}-1-chloro-2-hydroxyhexan-3-yl]-L-prolinamide (three-letter code: 0ZJ) (formula: $C_{23}H_{36}ClN_6O_4S$).

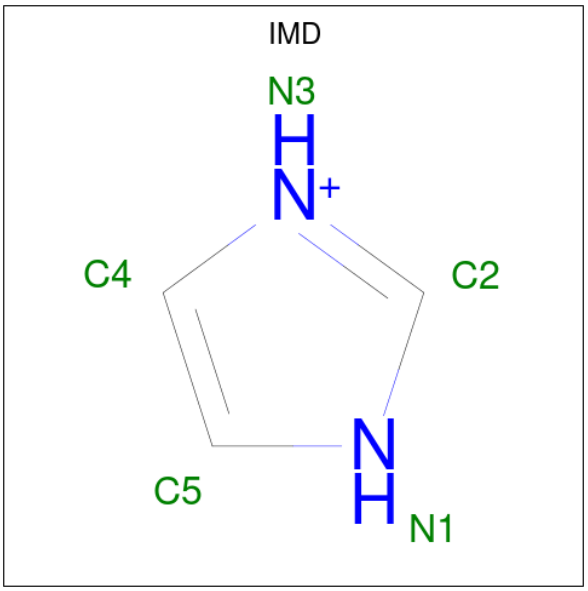


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
4	B	1	34	23	6	4	1	0	0
			Total	C	N	O	S		
4	F	1	34	23	6	4	1	0	0

- Molecule 5 is MERCURY (II) ION (three-letter code: HG) (formula: Hg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Hg		
5	D	2	2	2	0	0
			Total	Hg		
5	H	2	2	2	0	0

- Molecule 6 is IMIDAZOLE (three-letter code: IMD) (formula: $C_3H_5N_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	D	1	Total C N 5 3 2	0	0
6	D	1	Total C N 5 3 2	0	0
6	D	1	Total C N 5 3 2	0	0
6	H	1	Total C N 5 3 2	0	0
6	H	1	Total C N 5 3 2	0	0
6	H	1	Total C N 5 3 2	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	9	Total O 9 9	0	0
7	B	158	Total O 158 158	0	0
7	D	212	Total O 212 212	0	0
7	E	8	Total O 8 8	0	0
7	F	150	Total O 150 150	0	0
7	H	211	Total O 211 211	0	0

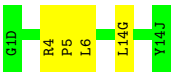
3 Residue-property plots (i)

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.

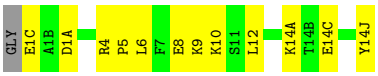
• Molecule 1: Thrombin light chain

Chain A: 86% 14%



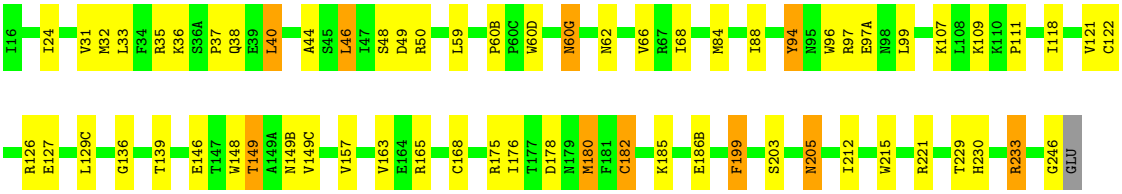
• Molecule 1: Thrombin light chain

Chain E: 54% 43% •



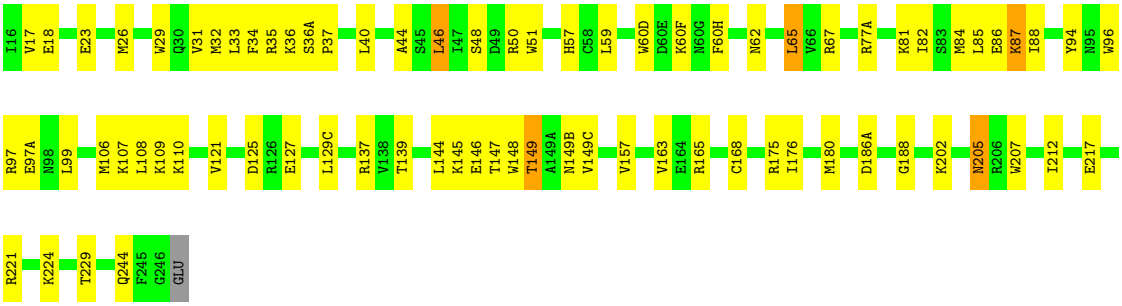
• Molecule 2: Thrombin heavy chain

Chain B: 75% 21% •



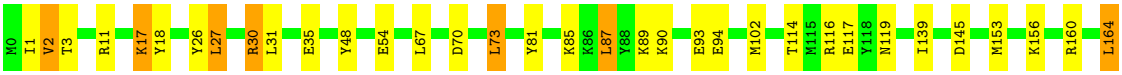
• Molecule 2: Thrombin heavy chain

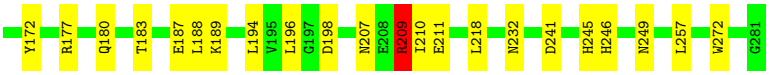
Chain F: 70% 28% •



- Molecule 3: Staphylocoagulase

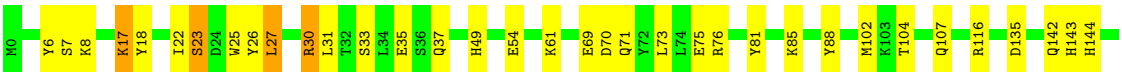
Chain D:

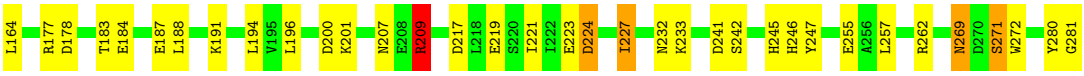




- Molecule 3: Staphylocoagulase

Chain H:





4 Data and refinement statistics (i)

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	180.17Å 102.00Å 135.30Å 90.00° 130.08° 90.00°	Depositor
Resolution (Å)	14.99 – 2.20	Depositor
% Data completeness (in resolution range)	95.6 (14.99-2.20)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.209 , 0.249	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10160	wwPDB-VP
Average B, all atoms (Å^2)	37.0	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: HG, 0ZJ, IMD

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	0.57	0/230	0.71	0/304
1	E	0.56	0/226	0.77	0/299
2	B	0.53	0/2138	0.80	1/2891 (0.0%)
2	F	0.53	0/2138	0.78	0/2891
3	D	0.55	0/2388	0.70	2/3204 (0.1%)
3	H	0.54	0/2388	0.69	2/3204 (0.1%)
All	All	0.54	0/9508	0.74	5/12793 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	209	ARG	NE-CZ-NH1	-6.69	116.95	120.30
3	D	2	VAL	N-CA-C	6.42	128.34	111.00
3	H	209	ARG	NE-CZ-NH1	-6.18	117.21	120.30
2	B	199	PHE	N-CA-C	-5.47	96.24	111.00
3	H	224	ASP	CB-CG-OD2	5.22	123.00	118.30

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	228	0	223	2	0
1	E	224	0	220	9	0
2	B	2083	0	2057	54	0
2	F	2083	0	2057	72	0
3	D	2346	0	2312	37	0
3	H	2346	0	2312	56	0
4	B	34	0	31	2	0
4	F	34	0	31	3	0
5	D	2	0	0	0	0
5	H	2	0	0	0	0
6	D	15	0	15	0	0
6	H	15	0	15	1	0
7	A	9	0	0	0	0
7	B	158	0	0	7	0
7	D	212	0	0	3	0
7	E	8	0	0	1	0
7	F	150	0	0	5	0
7	H	211	0	0	6	0
All	All	10160	0	9273	212	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 12.

All (212) 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:F:97:ARG:HG3	7:F:386:HOH:O	1.62	0.99
3:H:104:THR:H	3:H:107:GLN:HE21	1.13	0.95
2:B:50:ARG:NH1	2:B:107:LYS:HE2	1.87	0.88
2:F:99:LEU:HD11	4:F:299:0ZJ:HB21	1.56	0.87
2:F:36:LYS:HD3	2:F:65:LEU:HD13	1.58	0.86
1:E:4:ARG:HD3	1:E:8:GLU:OE1	1.76	0.85
3:D:241:ASP:H	3:D:245:HIS:HD2	1.24	0.83
2:F:84:MET:HG2	3:H:187:GLU:HG2	1.61	0.81
2:F:149:THR:HG22	2:F:149(C):VAL:HG23	1.62	0.80
3:D:232:ASN:HD22	3:D:272:TRP:HE1	1.29	0.79
2:B:99:LEU:HD11	4:B:299:0ZJ:HB21	1.64	0.79
3:H:232:ASN:HD22	3:H:272:TRP:HE1	1.33	0.77
3:D:177:ARG:HD3	7:D:2211:HOH:O	1.88	0.74
2:B:139:THR:HG22	2:B:157:VAL:HG22	1.70	0.73
2:B:32:MET:HG2	2:B:40:LEU:HD21	1.71	0.72
2:F:97(A):GLU:CD	2:F:175:ARG:HH12	1.92	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:178:ASP:O	2:B:233:ARG:HD2	1.88	0.71
3:H:241:ASP:H	3:H:245:HIS:HD2	1.37	0.70
2:F:50:ARG:HD2	2:F:108:LEU:O	1.91	0.69
3:D:54:GLU:CD	3:D:209:ARG:HH12	1.96	0.68
2:F:88:ILE:HD12	2:F:106:MET:HG2	1.75	0.68
3:H:178:ASP:HB2	3:H:262:ARG:NH2	2.08	0.68
3:H:104:THR:H	3:H:107:GLN:NE2	1.91	0.67
2:F:36:LYS:HD3	2:F:65:LEU:CD1	2.25	0.67
2:B:149:THR:HG22	2:B:149(C):VAL:H	1.60	0.67
3:H:81:TYR:CE2	3:H:85:LYS:HD2	2.30	0.66
3:H:269:ASN:C	3:H:269:ASN:HD22	1.98	0.66
2:F:145:LYS:HG3	2:F:146:GLU:O	1.96	0.65
2:F:202:LYS:CE	2:F:205:ASN:ND2	2.60	0.65
2:B:149:THR:HG23	2:B:149(B):ASN:H	1.60	0.65
2:F:149:THR:HG22	2:F:149(C):VAL:H	1.60	0.65
2:B:163:VAL:HG22	2:B:168:CYS:SG	2.38	0.64
2:F:36(A):SER:HA	2:F:37:PRO:C	2.18	0.63
3:D:160:ARG:NH2	3:D:211:GLU:OE1	2.30	0.63
1:E:14(A):LYS:HG2	2:F:23:GLU:OE1	1.98	0.63
3:H:178:ASP:HB2	3:H:262:ARG:HH21	1.64	0.62
3:H:54:GLU:CD	3:H:209:ARG:HH12	2.02	0.62
2:F:244:GLN:HB2	7:F:284:HOH:O	2.00	0.62
2:B:203:SER:O	2:B:205:ASN:HA	2.00	0.61
1:E:5:PRO:HA	1:E:9:LYS:HD2	1.83	0.61
1:A:14(G):LEU:HG	7:B:396:HOH:O	2.00	0.61
2:F:125:ASP:OD2	2:F:127:GLU:HG3	2.02	0.60
2:B:50:ARG:HG3	7:B:349:HOH:O	2.01	0.60
2:B:149:THR:HG21	3:D:35:GLU:OE2	2.01	0.60
3:D:232:ASN:ND2	3:D:272:TRP:HE1	1.98	0.60
3:H:269:ASN:HD21	3:H:271:SER:HB2	1.67	0.59
2:F:149:THR:HG22	2:F:149(C):VAL:N	2.18	0.58
2:B:84:MET:CE	2:B:109:LYS:HG3	2.33	0.58
3:H:227:ILE:HD13	3:H:280:TYR:CZ	2.39	0.58
3:D:54:GLU:OE2	3:D:209:ARG:NH1	2.36	0.57
2:F:202:LYS:HE3	2:F:205:ASN:ND2	2.20	0.56
2:B:50:ARG:HH11	2:B:107:LYS:HE2	1.68	0.56
2:F:224:LYS:HE3	7:F:332:HOH:O	2.05	0.56
3:H:54:GLU:OE2	3:H:209:ARG:NH1	2.36	0.56
3:D:27:LEU:HD22	3:D:31:LEU:HG	1.88	0.56
3:D:17:LYS:HD3	3:D:18:TYR:CE1	2.41	0.55
2:F:149:THR:HG23	2:F:149(B):ASN:N	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:36:LYS:HE2	2:F:62:ASN:O	2.07	0.55
3:H:232:ASN:ND2	3:H:272:TRP:HE1	2.03	0.55
2:F:81:LYS:HD3	2:F:82:ILE:N	2.20	0.55
3:D:30:ARG:N	3:D:30:ARG:HD2	2.22	0.55
2:B:46:LEU:HD22	2:B:48:SER:O	2.07	0.55
3:H:269:ASN:ND2	3:H:271:SER:HB2	2.23	0.54
2:F:57:HIS:CD2	4:F:299:0ZJ:HB31	2.43	0.54
3:D:87:LEU:HD13	3:H:25:TRP:CZ2	2.43	0.54
2:F:97(A):GLU:CD	2:F:175:ARG:NH1	2.60	0.54
1:E:14(C):GLU:OE2	2:F:202:LYS:NZ	2.33	0.54
3:H:30:ARG:N	3:H:30:ARG:HD2	2.23	0.53
2:B:163:VAL:HG22	2:B:182:CYS:SG	2.48	0.53
2:F:149:THR:HG21	3:H:35:GLU:OE1	2.08	0.53
2:B:165:ARG:HH12	2:B:176:ILE:HD12	1.75	0.52
2:F:148:TRP:HD1	3:H:70:ASP:OD2	1.93	0.52
2:B:60(D):TRP:CH2	4:B:299:0ZJ:HG3	2.45	0.52
2:B:230:HIS:HE1	7:B:294:HOH:O	1.91	0.52
2:F:165:ARG:NH2	2:F:180:MET:O	2.40	0.52
2:B:38:GLN:HG3	3:D:198:ASP:OD1	2.10	0.51
2:F:87:LYS:HD3	2:F:88:ILE:H	1.75	0.51
3:D:207:ASN:OD1	3:D:210:ILE:HG12	2.11	0.51
2:F:77(A):ARG:HB2	7:F:249:HOH:O	2.10	0.51
3:D:145:ASP:OD1	3:D:209:ARG:HD3	2.11	0.51
2:B:97(A):GLU:CD	2:B:175:ARG:NH1	2.64	0.50
3:D:81:TYR:CE2	3:D:85:LYS:HD2	2.46	0.50
2:B:94:TYR:CZ	2:B:96:TRP:HB3	2.47	0.50
2:B:84:MET:HE1	2:B:109:LYS:HG3	1.92	0.50
2:F:86:GLU:HB2	2:F:109:LYS:HD3	1.93	0.50
2:B:99:LEU:HD12	2:B:215:TRP:HB3	1.93	0.50
2:F:60(D):TRP:CH2	4:F:299:0ZJ:HG3	2.46	0.50
3:H:61:LYS:HE3	3:H:135:ASP:OD1	2.11	0.50
2:F:217:GLU:OE1	2:F:224:LYS:NZ	2.44	0.50
2:B:97:ARG:HG2	7:B:263:HOH:O	2.12	0.49
3:D:90:LYS:O	3:D:94:GLU:HG3	2.11	0.49
2:F:149:THR:CG2	2:F:149(C):VAL:H	2.24	0.49
3:H:241:ASP:N	3:H:245:HIS:HD2	2.08	0.49
3:H:116:ARG:HD2	7:H:2185:HOH:O	2.12	0.49
3:H:33:SER:O	3:H:37:GLN:HG3	2.12	0.49
2:F:17:VAL:HG22	2:F:145:LYS:HA	1.94	0.49
3:H:177:ARG:HD3	7:H:2159:HOH:O	2.13	0.48
3:H:233:LYS:HZ2	6:H:2004:IMD:H2	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:146:GLU:OE2	2:B:221:ARG:HD2	2.13	0.48
3:D:102:MET:HE1	7:D:2102:HOH:O	2.13	0.48
2:F:212:ILE:HB	2:F:229:THR:HB	1.94	0.48
3:H:49:HIS:CE1	3:H:207:ASN:HD22	2.30	0.48
2:B:60(G):ASN:HD22	2:B:60(G):ASN:C	2.14	0.48
2:F:149(B):ASN:O	2:F:149(C):VAL:C	2.51	0.48
2:B:31:VAL:HB	2:B:44:ALA:HB3	1.96	0.48
3:H:76:ARG:HD3	7:H:2045:HOH:O	2.14	0.48
2:B:24:ILE:HD12	2:B:24:ILE:N	2.29	0.48
1:E:1(C):GLU:OE2	1:E:1(A):ASP:HB3	2.13	0.48
3:H:219:GLU:O	3:H:223:GLU:HG3	2.13	0.48
3:D:172:TYR:CE2	3:D:189:LYS:HD2	2.49	0.47
3:H:6:TYR:CE1	3:H:75:GLU:HB3	2.50	0.47
2:F:60(F):LYS:HD3	2:F:60(H):PHE:CE2	2.50	0.47
2:B:149:THR:HG22	2:B:149(C):VAL:N	2.27	0.47
3:D:54:GLU:O	3:D:139:ILE:HD12	2.15	0.47
2:F:146:GLU:OE2	2:F:221:ARG:HD2	2.15	0.47
3:H:191:LYS:HE3	7:H:2102:HOH:O	2.15	0.47
2:B:59:LEU:HD13	2:B:88:ILE:HG21	1.97	0.47
3:H:144:HIS:HB3	7:H:2202:HOH:O	2.15	0.46
3:D:194:LEU:C	3:D:194:LEU:HD13	2.36	0.46
3:D:17:LYS:HD3	3:D:18:TYR:CZ	2.51	0.46
3:D:89:LYS:O	3:D:93:GLU:HG3	2.15	0.46
2:F:87:LYS:HD3	2:F:88:ILE:N	2.30	0.46
2:F:149:THR:HG23	2:F:149(B):ASN:H	1.80	0.46
3:H:26:TYR:CE2	3:H:30:ARG:HD3	2.51	0.46
2:F:33:LEU:HD21	2:F:59:LEU:HD21	1.97	0.46
2:F:94:TYR:CZ	2:F:96:TRP:HB3	2.50	0.46
3:H:269:ASN:ND2	3:H:271:SER:H	2.13	0.46
2:F:17:VAL:HG12	2:F:18:GLU:HG2	1.98	0.45
2:B:107:LYS:NZ	2:B:246:GLY:CA	2.80	0.45
2:F:163:VAL:HG22	2:F:168:CYS:SG	2.56	0.45
1:E:14(J):TYR:OXT	7:E:756:HOH:O	2.21	0.45
2:B:31:VAL:CG1	2:B:66:VAL:HG13	2.46	0.45
3:D:153:MET:HA	3:D:153:MET:CE	2.46	0.45
2:B:107:LYS:NZ	2:B:246:GLY:HA3	2.32	0.45
2:F:18:GLU:HB2	2:F:188:GLY:HA2	1.98	0.45
2:B:33:LEU:HD21	2:B:59:LEU:HD21	1.99	0.45
2:B:185:LYS:HB2	2:B:186(B):GLU:HG3	1.99	0.44
2:B:31:VAL:HG13	2:B:66:VAL:HG13	1.99	0.44
2:F:37:PRO:HG2	7:F:251:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:27:LEU:HD22	3:H:31:LEU:HG	1.99	0.44
3:H:242:SER:O	3:H:246:HIS:HB2	2.16	0.44
3:D:246:HIS:HB3	3:D:249:ASN:HB2	2.00	0.44
2:B:165:ARG:NH2	2:B:180:MET:O	2.51	0.44
3:D:183:THR:O	3:D:187:GLU:HG3	2.18	0.44
2:B:221:ARG:HB2	7:B:374:HOH:O	2.17	0.44
2:F:110:LYS:HD3	3:H:184:GLU:OE2	2.17	0.44
3:H:255:GLU:HA	3:H:255:GLU:OE1	2.18	0.44
2:F:51:TRP:CZ3	2:F:107:LYS:HB2	2.53	0.44
2:F:84:MET:CG	3:H:187:GLU:HG2	2.39	0.44
1:E:4:ARG:HA	1:E:5:PRO:HD3	1.87	0.44
2:B:37:PRO:HG2	7:B:275:HOH:O	2.17	0.43
2:B:212:ILE:HB	2:B:229:THR:HB	2.00	0.43
3:D:67:LEU:HD23	3:D:67:LEU:HA	1.80	0.43
3:H:142:GLN:HG2	3:H:143:HIS:CD2	2.54	0.43
2:B:68:ILE:HG22	2:B:118:ILE:HG12	2.01	0.43
2:B:107:LYS:CE	2:B:246:GLY:HA3	2.47	0.43
3:D:153:MET:HE2	3:D:156:LYS:HD2	1.99	0.43
1:E:4:ARG:HD2	2:F:207:TRP:CD1	2.53	0.43
2:F:88:ILE:CD1	2:F:106:MET:HG2	2.46	0.43
2:B:107:LYS:HE3	2:B:246:GLY:HA3	2.00	0.43
3:H:7:SER:HB2	7:H:2052:HOH:O	2.18	0.43
1:A:4:ARG:HA	1:A:5:PRO:HD3	1.93	0.43
2:F:81:LYS:HD3	2:F:81:LYS:C	2.39	0.43
2:F:149:THR:CG2	2:F:149(C):VAL:N	2.82	0.43
3:D:241:ASP:H	3:D:245:HIS:CD2	2.17	0.42
3:H:191:LYS:NZ	3:H:224:ASP:OD1	2.51	0.42
3:H:88:TYR:CE2	3:H:102:MET:HB2	2.54	0.42
2:B:36:LYS:HE2	2:B:62:ASN:O	2.19	0.42
2:B:97(A):GLU:OE1	2:B:175:ARG:NH1	2.47	0.42
2:F:32:MET:HE2	2:F:67:ARG:HD3	2.00	0.42
3:D:11:ARG:HA	3:D:11:ARG:HD3	1.90	0.42
2:B:149(B):ASN:O	2:B:149(C):VAL:C	2.58	0.42
2:F:31:VAL:HB	2:F:44:ALA:HB3	2.02	0.42
2:F:50:ARG:NH1	2:F:107:LYS:NZ	2.67	0.42
2:F:144:LEU:O	2:F:145:LYS:HB3	2.19	0.42
2:F:202:LYS:CE	2:F:205:ASN:HD21	2.30	0.42
3:H:22:ILE:HG22	3:H:23:SER:O	2.19	0.42
2:B:49:ASP:O	2:B:111:PRO:HA	2.20	0.42
2:F:46:LEU:HD22	2:F:48:SER:O	2.20	0.42
2:F:29:TRP:CG	2:F:121:VAL:HB	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:145:LYS:NZ	3:H:70:ASP:OD1	2.49	0.42
3:H:69:GLU:OE2	3:H:69:GLU:HA	2.19	0.41
2:B:24:ILE:HD12	2:B:24:ILE:H	1.84	0.41
2:B:35:ARG:HD3	7:B:275:HOH:O	2.19	0.41
3:D:119:ASN:ND2	7:D:2180:HOH:O	2.48	0.41
2:B:32:MET:HG2	2:B:40:LEU:CD2	2.47	0.41
2:F:36:LYS:CE	2:F:62:ASN:O	2.67	0.41
3:H:17:LYS:HD3	3:H:18:TYR:CZ	2.56	0.41
3:D:48:TYR:HE2	3:D:210:ILE:HD12	1.84	0.41
2:F:149:THR:HG22	2:F:149(C):VAL:CG2	2.42	0.41
3:H:200:ASP:OD1	3:H:201:LYS:HG2	2.21	0.41
2:F:26:MET:HE2	2:F:137:ARG:NH1	2.35	0.41
2:F:77(A):ARG:HD3	3:H:217:ASP:OD2	2.20	0.41
3:H:280:TYR:O	3:H:281:GLY:C	2.59	0.41
3:D:164:LEU:HD13	3:D:218:LEU:CB	2.51	0.41
2:F:40:LEU:HD23	2:F:40:LEU:C	2.41	0.41
2:F:147:THR:HA	3:H:70:ASP:OD1	2.21	0.41
3:H:22:ILE:CG2	3:H:26:TYR:HD2	2.34	0.41
3:D:26:TYR:CE2	3:D:30:ARG:HD3	2.55	0.41
3:D:114:THR:OG1	3:D:117:GLU:HG3	2.21	0.41
3:D:73:LEU:HD12	3:D:73:LEU:HA	1.96	0.41
1:E:10:LYS:HE2	1:E:12:LEU:HD11	2.02	0.41
2:F:34:PHE:CE2	3:H:194:LEU:HD23	2.55	0.41
2:B:59:LEU:HD13	2:B:88:ILE:CG2	2.51	0.40
2:F:145:LYS:HE2	3:H:71:GLN:HB2	2.03	0.40
2:F:110:LYS:HG3	3:H:183:THR:HG21	2.03	0.40
3:H:188:LEU:HD12	3:H:221:ILE:HG22	2.03	0.40
2:B:121:VAL:HG22	2:B:122:CYS:N	2.37	0.40
3:H:22:ILE:HG21	3:H:26:TYR:HD2	1.86	0.40
2:F:139:THR:HG22	2:F:157:VAL:HB	2.04	0.40
2:B:136:GLY:HA3	2:B:199:PHE:CE1	2.56	0.40
2:B:148:TRP:HD1	3:D:70:ASP:OD2	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	A	26/28 (93%)	25 (96%)	1 (4%)	0	100	100
1	E	25/28 (89%)	24 (96%)	1 (4%)	0	100	100
2	B	256/259 (99%)	243 (95%)	13 (5%)	0	100	100
2	F	256/259 (99%)	240 (94%)	16 (6%)	0	100	100
3	D	280/282 (99%)	272 (97%)	5 (2%)	3 (1%)	14	12
3	H	280/282 (99%)	273 (98%)	7 (2%)	0	100	100
All	All	1123/1138 (99%)	1077 (96%)	43 (4%)	3 (0%)	41	46

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	2	VAL
3	D	3	THR
3	D	1	ILE

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	25/25 (100%)	24 (96%)	1 (4%)	31	40
1	E	25/25 (100%)	24 (96%)	1 (4%)	31	40
2	B	224/225 (100%)	211 (94%)	13 (6%)	20	23
2	F	224/225 (100%)	214 (96%)	10 (4%)	27	34
3	D	260/260 (100%)	248 (95%)	12 (5%)	27	34
3	H	260/260 (100%)	246 (95%)	14 (5%)	22	26
All	All	1018/1020 (100%)	967 (95%)	51 (5%)	24	30

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LEU
2	B	40	LEU
2	B	46	LEU
2	B	60(B)	PRO
2	B	60(G)	ASN
2	B	94	TYR
2	B	126	ARG
2	B	127	GLU
2	B	129(C)	LEU
2	B	149	THR
2	B	180	MET
2	B	182	CYS
2	B	205	ASN
2	B	233	ARG
3	D	17	LYS
3	D	27	LEU
3	D	30	ARG
3	D	73	LEU
3	D	87	LEU
3	D	116	ARG
3	D	164	LEU
3	D	180	GLN
3	D	188	LEU
3	D	196	LEU
3	D	209	ARG
3	D	257	LEU
1	E	6	LEU
2	F	35	ARG
2	F	46	LEU
2	F	65	LEU
2	F	85	LEU
2	F	87	LYS
2	F	129(C)	LEU
2	F	149	THR
2	F	176	ILE
2	F	186(A)	ASP
2	F	205	ASN
3	H	8	LYS
3	H	17	LYS
3	H	23	SER
3	H	27	LEU
3	H	30	ARG
3	H	73	LEU

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Mol	Chain	Res	Type
3	H	164	LEU
3	H	196	LEU
3	H	209	ARG
3	H	227	ILE
3	H	247	TYR
3	H	257	LEU
3	H	269	ASN
3	H	271	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	60(G)	ASN
2	B	71	HIS
2	B	230	HIS
2	B	239	GLN
2	B	244	GLN
3	D	15	ASN
3	D	119	ASN
3	D	142	GLN
3	D	166	ASN
3	D	232	ASN
3	D	245	HIS
2	F	62	ASN
2	F	205	ASN
2	F	239	GLN
3	H	107	GLN
3	H	119	ASN
3	H	180	GLN
3	H	232	ASN
3	H	245	HIS
3	H	269	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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	$\#\|Z\| > 2$
6	IMD	H	2002	-	3,5,5	0.54	0	4,5,5	0.50	0
4	0ZJ	B	299	5,2	33,35,36	1.53	3 (9%)	40,46,47	0.96	1 (2%)
6	IMD	D	2001	-	3,5,5	0.58	0	4,5,5	0.47	0
6	IMD	D	2003	-	3,5,5	0.72	0	4,5,5	0.43	0
6	IMD	H	2004	-	3,5,5	0.61	0	4,5,5	0.43	0
4	0ZJ	F	299	5,2	33,35,36	1.48	2 (6%)	40,46,47	1.01	2 (5%)
6	IMD	H	2000	-	3,5,5	0.61	0	4,5,5	0.47	0
6	IMD	D	2005	-	3,5,5	0.64	0	4,5,5	0.55	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
6	IMD	H	2002	-	-	-	0/1/1/1
4	0ZJ	B	299	5,2	1/1/9/12	2/35/47/49	0/2/2/2
6	IMD	D	2001	-	-	-	0/1/1/1
6	IMD	D	2003	-	-	-	0/1/1/1
6	IMD	H	2004	-	-	-	0/1/1/1
4	0ZJ	F	299	5,2	1/1/9/12	3/35/47/49	0/2/2/2
6	IMD	H	2000	-	-	-	0/1/1/1
6	IMD	D	2005	-	-	-	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	299	0ZJ	O3-C4	-6.97	1.24	1.43
4	F	299	0ZJ	O3-C4	-6.54	1.25	1.43
4	F	299	0ZJ	CZ-CE2	2.15	1.43	1.38
4	B	299	0ZJ	CZ-CE2	2.05	1.43	1.38
4	B	299	0ZJ	CD2-CG	2.04	1.43	1.38

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	F	299	0ZJ	O3-C4-CM	4.27	122.39	109.74
4	B	299	0ZJ	O3-C4-CM	3.94	121.42	109.74
4	F	299	0ZJ	C-CA-N	-2.60	102.74	108.81

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	B	299	0ZJ	C4
4	F	299	0ZJ	C4

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	299	0ZJ	CM-C4-CA2-N2
4	B	299	0ZJ	CM-C4-CA2-CB2
4	F	299	0ZJ	CM-C4-CA2-N2
4	F	299	0ZJ	CM-C4-CA2-CB2
4	F	299	0ZJ	O-C-N1-CD

There are no ring outliers.

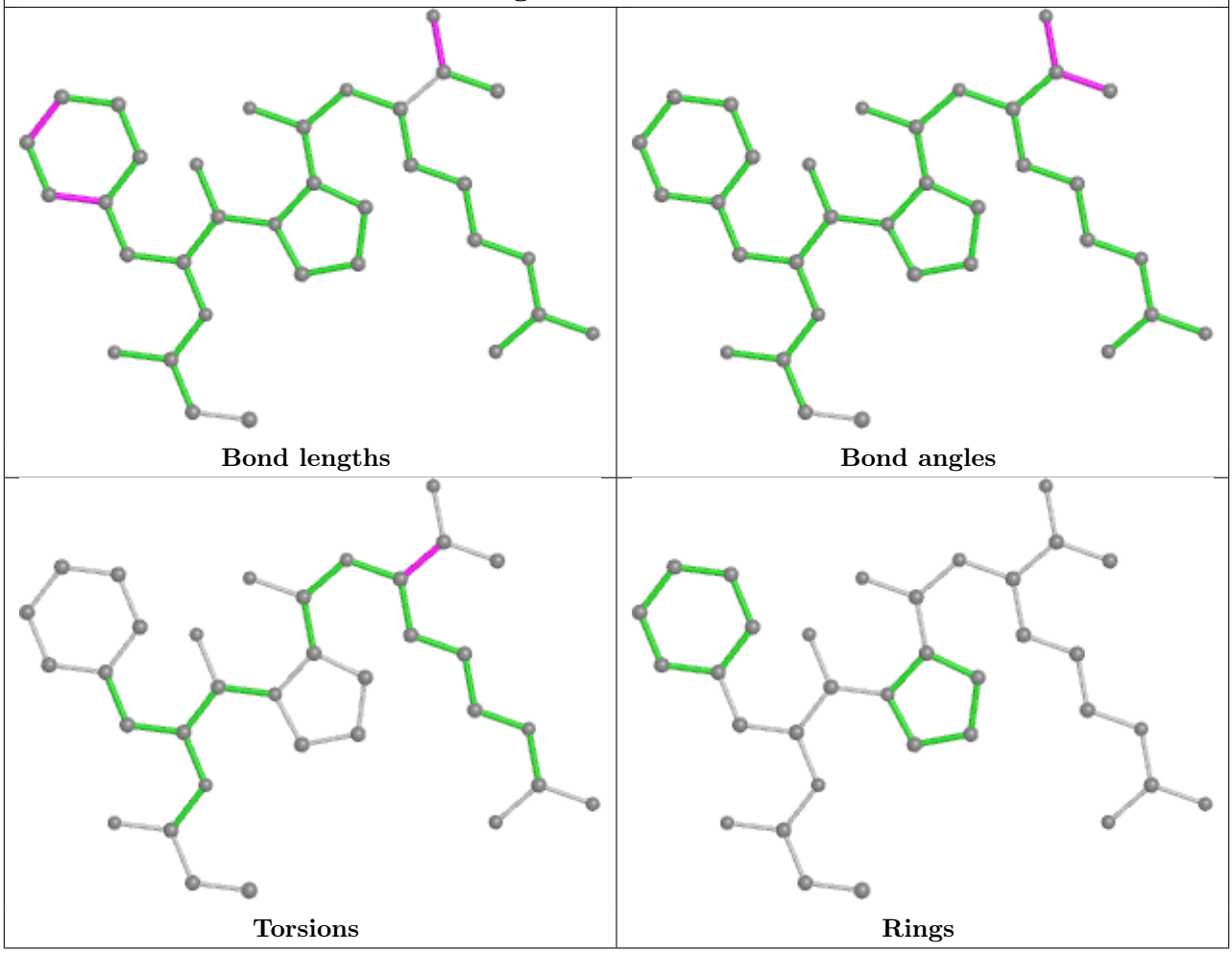
3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	299	0ZJ	2	0
6	H	2004	IMD	1	0
4	F	299	0ZJ	3	0

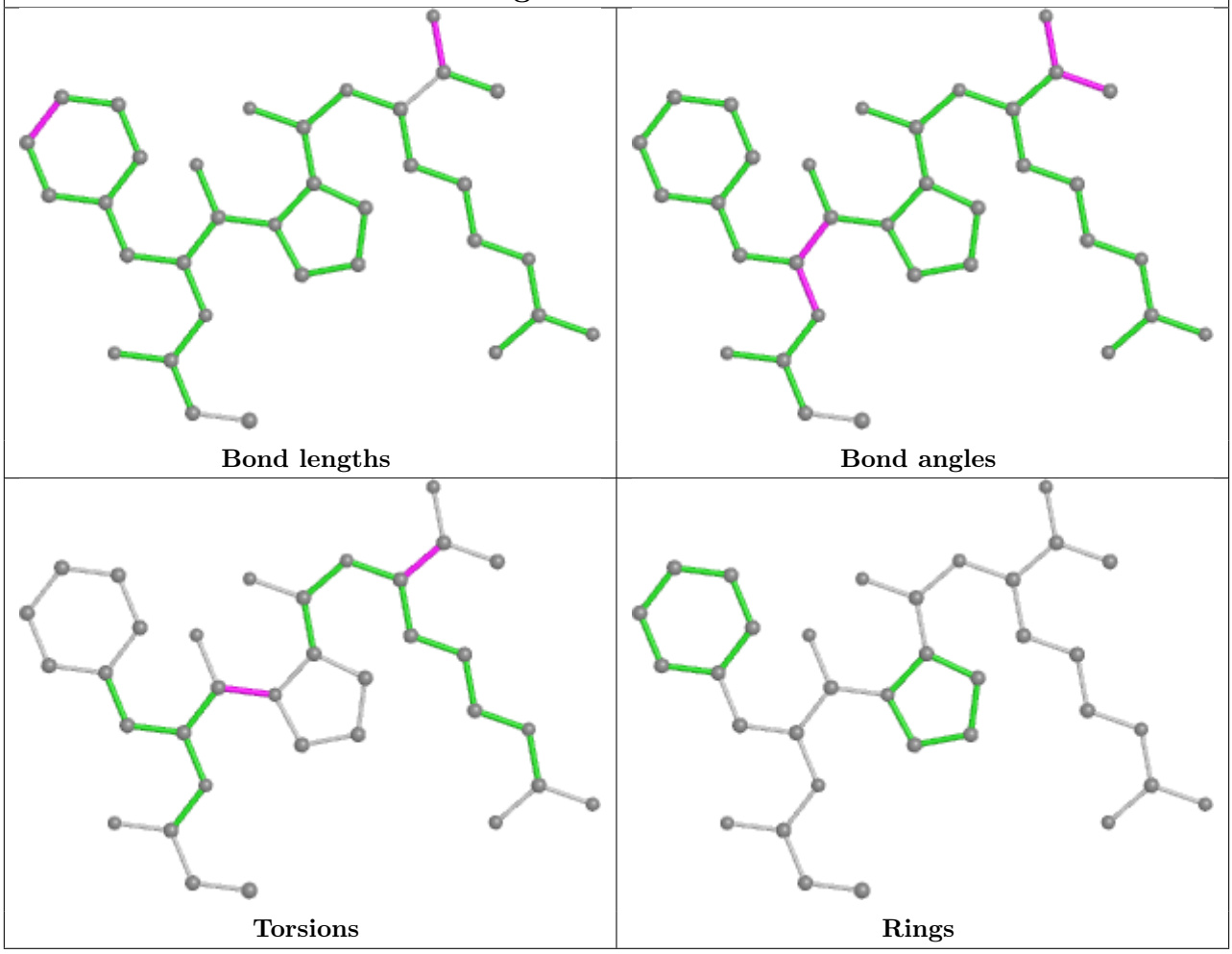
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.

Ligand 0ZJ B 299



Ligand 0ZJ F 299



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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.