WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Aug 20, 2023 – 10:46 AM EDT

PDB ID	:	2OIC
Title	:	Crystal structure of IRAK4 kinase domain complexed with staurosporine
Authors	:	Kuglstatter, A.; Villasenor, A.G.; Browner, M.F.
Deposited on	:	2007-01-10
Resolution	:	2.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i)) were used in the production of this report:

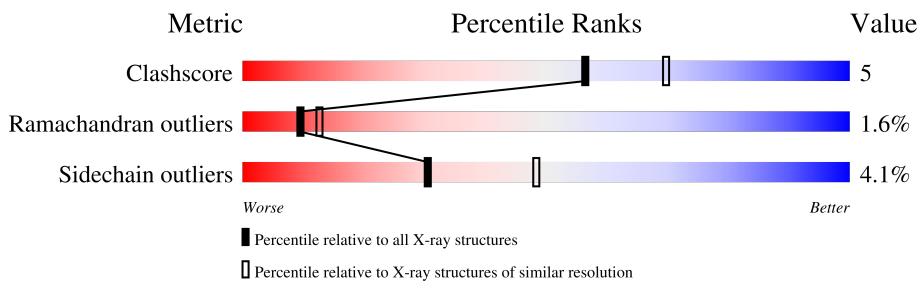|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.40 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	Percentile Ranks	Value
Clashscore		5
Ramachandran outliers		1.6%
Sidechain outliers		4.1%

Worse   *Better*

▮ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

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	301	78% 13% • 7%
1	B	301	77% 13% • 8%
1	C	301	80% 13% 7%
1	D	301	85% 10% • 5%

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	STU	A	1	X	-	-	-
2	STU	B	2	X	-	-	-
2	STU	C	3	X	-	-	-
2	STU	D	4	X	-	-	-

2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 9302 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.
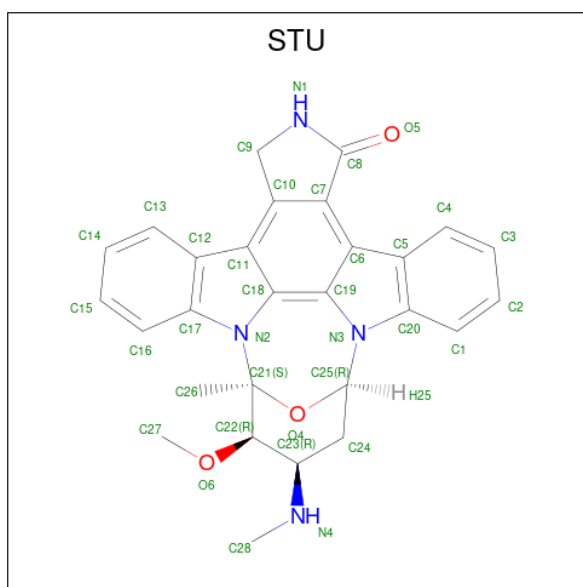
- Molecule 1 is a protein called Interleukin-1 receptor-associated kinase 4.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	279	Total	C	N	O	P	S	0	0	0
			2210	1385	373	435	3	14			
1	B	278	Total	C	N	O	P	S	0	0	0
			2196	1378	372	430	2	14			
1	C	280	Total	C	N	O	P	S	0	0	0
			2221	1390	371	443	3	14			
1	D	287	Total	C	N	O	P	S	0	0	0
			2266	1417	382	450	3	14			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	342	TPO	THR	modified residue	UNP Q9NWZ3
A	345	TPO	THR	modified residue	UNP Q9NWZ3
A	346	SEP	SER	modified residue	UNP Q9NWZ3
B	342	TPO	THR	modified residue	UNP Q9NWZ3
B	345	TPO	THR	modified residue	UNP Q9NWZ3
B	346	SEP	SER	modified residue	UNP Q9NWZ3
C	342	TPO	THR	modified residue	UNP Q9NWZ3
C	345	TPO	THR	modified residue	UNP Q9NWZ3
C	346	SEP	SER	modified residue	UNP Q9NWZ3
D	342	TPO	THR	modified residue	UNP Q9NWZ3
D	345	TPO	THR	modified residue	UNP Q9NWZ3
D	346	SEP	SER	modified residue	UNP Q9NWZ3

- Molecule 2 is STAUROSPORINE (three-letter code: STU) (formula: $C_{28}H_{26}N_4O_3$).

STU

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 35	C 28	N 4	O 3	0	0
2	B	1	Total 35	C 28	N 4	O 3	0	0
2	C	1	Total 35	C 28	N 4	O 3	0	0
2	D	1	Total 35	C 28	N 4	O 3	0	0

- Molecule 3 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	78	Total 78	O 78	0	0
3	B	58	Total 58	O 58	0	0
3	C	59	Total 59	O 59	0	0
3	D	74	Total 74	O 74	0	0

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3 Residue-property plots ⓘ

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.
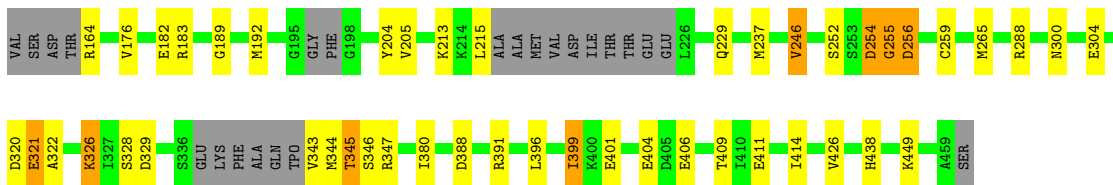
Note EDS was not executed.

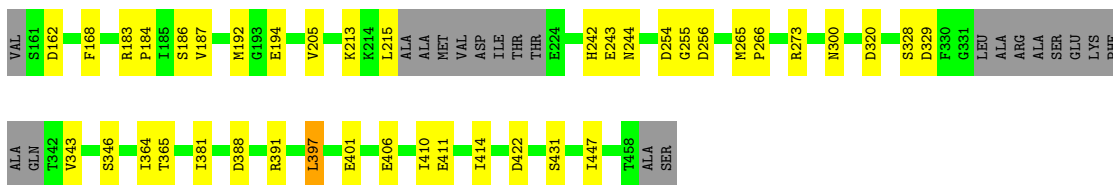• Molecule 1: Interleukin-1 receptor-associated kinase 4

Chain A:
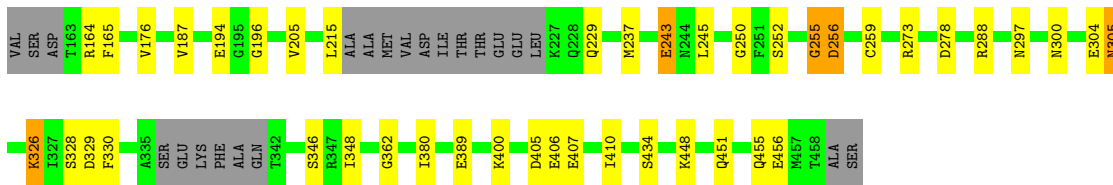
• Molecule 1: Interleukin-1 receptor-associated kinase 4

Chain B:

• Molecule 1: Interleukin-1 receptor-associated kinase 4

Chain C:

• Molecule 1: Interleukin-1 receptor-associated kinase 4

Chain D:
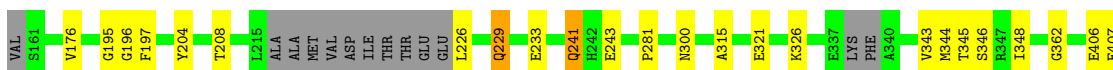
4 Data and refinement statistics ⓘ

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	153.89Å 141.32Å 88.26Å 90.00° 122.27° 90.00°	Depositor
Resolution (Å)	48.17 – 2.40	Depositor
% Data completeness (in resolution range)	99.9 (48.17-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	7.10	Depositor
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.223 , 0.278	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9302	wwPDB-VP
Average B, all atoms (Å^2)	64.0	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: STU, SEP, TPO

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	0.55	0/2214	0.62	0/2981
1	B	0.50	0/2209	0.61	0/2973
1	C	0.50	0/2225	0.61	1/2996 (0.0%)
1	D	0.52	0/2269	0.59	0/3054
All	All	0.52	0/8917	0.61	1/12004 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	397	LEU	CA-CB-CG	5.74	128.50	115.30

There are no chirality outliers.

There are no planarity outliers.

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	2210	0	2175	22	0
1	B	2196	0	2168	26	0
1	C	2221	0	2173	17	0
1	D	2266	0	2222	16	0
2	A	35	0	26	6	0
2	B	35	0	26	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	35	0	26	2	0
2	D	35	0	26	2	0
3	A	78	0	0	2	0
3	B	58	0	0	1	0
3	C	59	0	0	2	0
3	D	74	0	0	0	0
All	All	9302	0	8842	90	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 5.

The worst 5 of 90 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:B:265:MET:HE1	1:B:320:ASP:HB3	1.52	0.90
2:A:1:STU:H261	2:A:1:STU:H16	1.60	0.83
1:D:411:GLU:HA	1:D:414:ILE:HD12	1.62	0.81
1:D:176:VAL:HG21	1:D:204:TYR:O	1.83	0.79
1:C:242:HIS:HE1	3:C:2240:HOH:O	1.69	0.74

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	271/301 (90%)	253 (93%)	12 (4%)	6 (2%)	6	7
1	B	268/301 (89%)	251 (94%)	12 (4%)	5 (2%)	8	10
1	C	272/301 (90%)	257 (94%)	11 (4%)	4 (2%)	10	14
1	D	278/301 (92%)	265 (95%)	11 (4%)	2 (1%)	22	32
All	All	1089/1204 (90%)	1026 (94%)	46 (4%)	17 (2%)	9	13

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	255	GLY
1	A	256	ASP
1	A	406	GLU
1	B	254	ASP
1	B	255	GLY

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	241/259 (93%)	232 (96%)	9 (4%)	34	53
1	B	241/259 (93%)	226 (94%)	15 (6%)	18	29
1	C	244/259 (94%)	235 (96%)	9 (4%)	34	53
1	D	247/259 (95%)	240 (97%)	7 (3%)	43	63
All	All	973/1036 (94%)	933 (96%)	40 (4%)	30	48

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	328	SER
1	D	229	GLN
1	C	365	THR
1	C	431	SER
1	D	321	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	229	GLN
1	B	455	GLN
1	D	241	GLN
1	C	242	HIS
1	D	206	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

11 non-standard protein/DNA/RNA residues are 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	#$|Z| > 2$
1	SEP	D	346	1	8,9,10	1.58	1 (12%)	8,12,14	2.05	2 (25%)
1	SEP	C	346	1	8,9,10	1.62	1 (12%)	8,12,14	1.96	2 (25%)
1	TPO	D	345	1	8,10,11	0.77	0	10,14,16	0.99	1 (10%)
1	TPO	A	345	1	8,10,11	0.79	0	10,14,16	0.92	0
1	TPO	D	342	1	8,10,11	0.77	0	10,14,16	1.00	0
1	TPO	B	345	1	8,10,11	0.76	0	10,14,16	1.09	1 (10%)
1	TPO	C	345	1	8,10,11	0.80	0	10,14,16	0.93	0
1	SEP	B	346	1	8,9,10	1.57	1 (12%)	8,12,14	2.04	2 (25%)
1	TPO	C	342	1	8,10,11	0.81	0	10,14,16	1.04	0
1	SEP	A	346	1	8,9,10	1.62	1 (12%)	8,12,14	1.71	2 (25%)
1	TPO	A	342	1	8,10,11	0.86	0	10,14,16	0.97	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
1	SEP	D	346	1	-	1/5/8/10	-
1	SEP	C	346	1	-	0/5/8/10	-
1	TPO	D	345	1	-	4/9/11/13	-
1	TPO	A	345	1	-	3/9/11/13	-
1	TPO	D	342	1	-	1/9/11/13	-
1	TPO	B	345	1	-	3/9/11/13	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	TPO	C	345	1	-	<mark>2/9/11/13</mark>	-
1	SEP	B	346	1	-	0/5/8/10	-
1	TPO	C	342	1	-	<mark>3/9/11/13</mark>	-
1	SEP	A	346	1	-	1/5/8/10	-
1	TPO	A	342	1	-	0/9/11/13	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	346	SEP	P-O1P	3.50	1.61	1.50
1	C	346	SEP	P-O1P	3.44	1.61	1.50
1	D	346	SEP	P-O1P	3.41	1.61	1.50
1	B	346	SEP	P-O1P	3.36	1.61	1.50

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	346	SEP	OG-CB-CA	4.50	112.52	108.14
1	B	346	SEP	OG-CB-CA	4.49	112.52	108.14
1	C	346	SEP	OG-CB-CA	4.34	112.37	108.14
1	A	346	SEP	OG-CB-CA	3.59	111.64	108.14
1	D	346	SEP	P-OG-CB	-3.09	109.77	118.30

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	345	TPO	N-CA-CB-OG1
1	A	346	SEP	N-CA-CB-OG
1	B	345	TPO	N-CA-CB-OG1
1	B	345	TPO	O-C-CA-CB
1	B	345	TPO	CB-OG1-P-O1P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	345	TPO	1	0

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 ligands are 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	#$|Z| > 2$
2	STU	B	2	-	30,42,42	2.14	8 (26%)	31,68,68	2.54	7 (22%)
2	STU	A	1	-	30,42,42	2.11	7 (23%)	31,68,68	2.29	10 (32%)
2	STU	C	3	-	30,42,42	2.01	6 (20%)	31,68,68	2.61	8 (25%)
2	STU	D	4	-	30,42,42	2.27	7 (23%)	31,68,68	2.15	5 (16%)

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
2	STU	B	2	-	1/1/5/7	2/4/42/42	-
2	STU	A	1	-	1/1/5/7	1/4/42/42	-
2	STU	C	3	-	1/1/5/7	1/4/42/42	-
2	STU	D	4	-	1/1/5/7	1/4/42/42	-

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	4	STU	C9-C10	-8.28	1.44	1.50
2	B	2	STU	C9-C10	-6.38	1.45	1.50
2	A	1	STU	C9-C10	-6.27	1.45	1.50
2	C	3	STU	C7-C8	-6.19	1.39	1.49
2	B	2	STU	C7-C8	-6.16	1.39	1.49

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	3	STU	C7-C8-N1	7.86	114.33	106.37
2	C	3	STU	C9-N1-C8	-7.79	106.36	113.85
2	B	2	STU	C7-C8-N1	7.62	114.08	106.37
2	B	2	STU	C9-N1-C8	-7.43	106.71	113.85
2	A	1	STU	C9-N1-C8	-6.72	107.39	113.85

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1	STU	C23
2	B	2	STU	C23
2	C	3	STU	C23
2	D	4	STU	C23

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1	STU	C22-C23-N4-C28
2	B	2	STU	C22-C23-N4-C28
2	C	3	STU	C24-C23-N4-C28
2	D	4	STU	C24-C23-N4-C28
2	B	2	STU	C24-C23-N4-C28

There are no ring outliers.
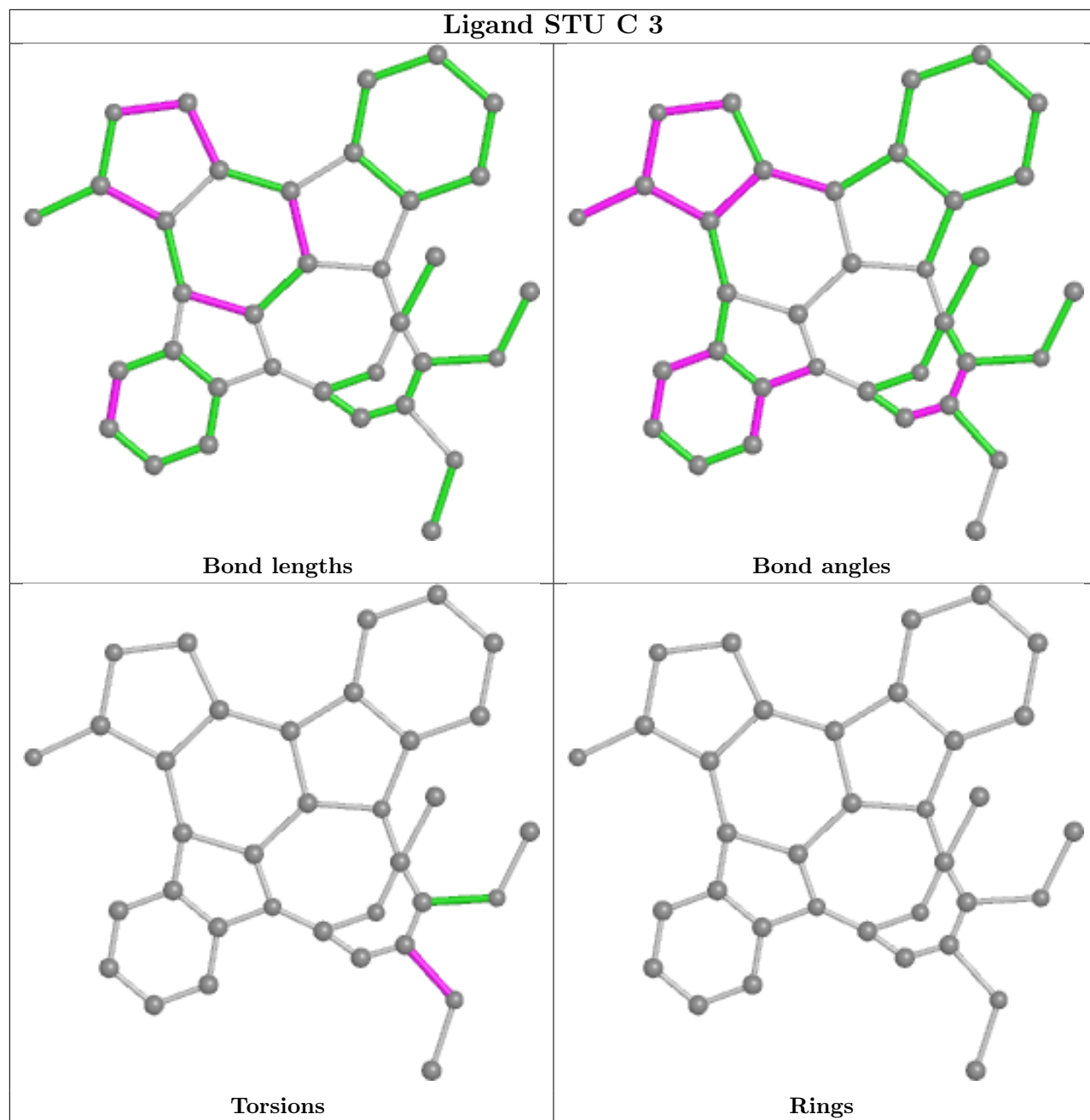
4 monomers are involved in 14 short contacts:

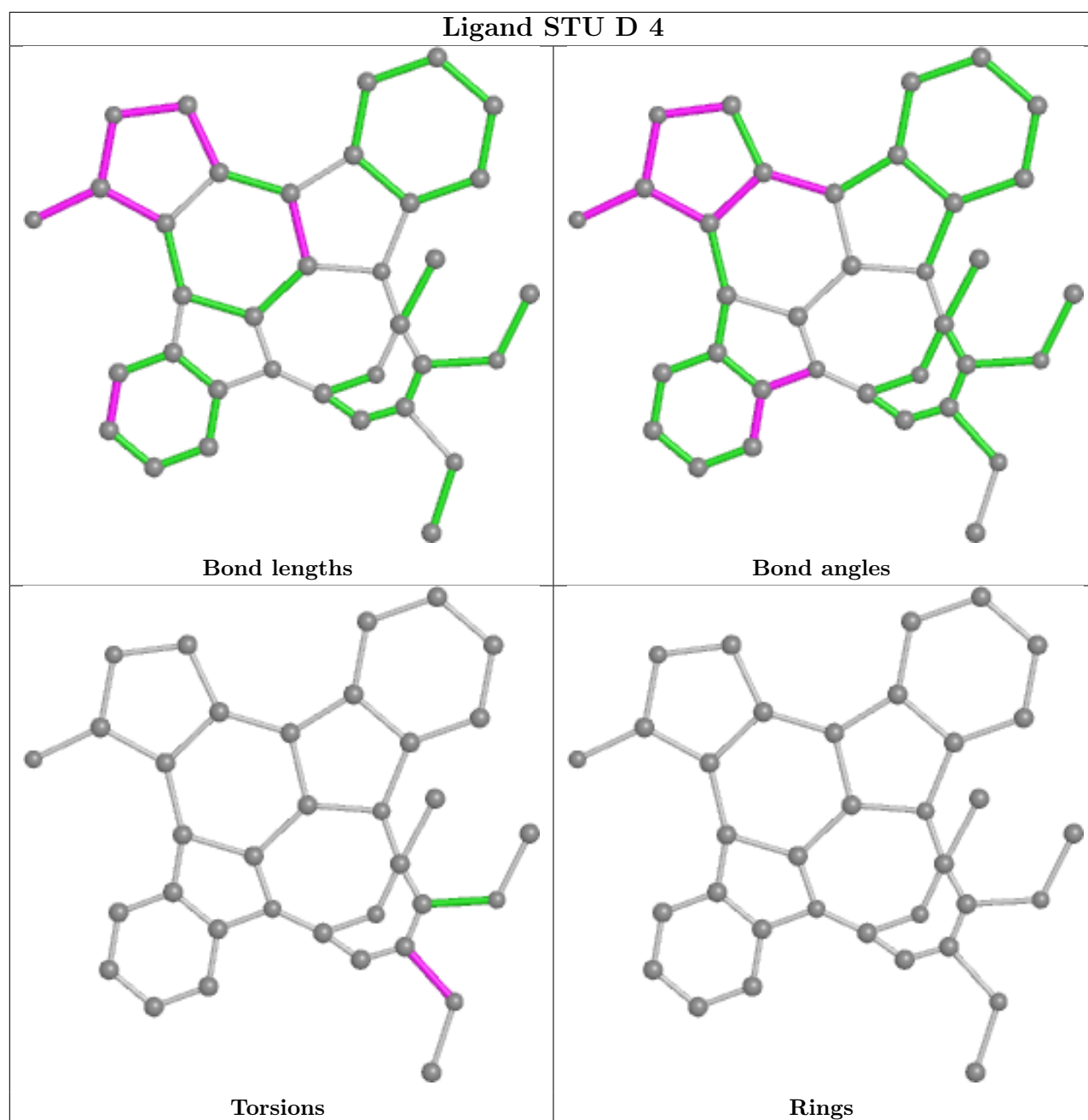| Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2	STU	4	0
2	A	1	STU	6	0
2	C	3	STU	2	0
2	D	4	STU	2	0

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 STU B 2

Bond lengths

Bond angles

Torsions

Rings

Ligand STU A 1

Bond lengths

Bond angles

Torsions

Rings

Ligand STU C 3

Bond lengths

Bond angles

Torsions

Rings

Ligand STU D 4

Bond lengths

Bond angles

Torsions

Rings
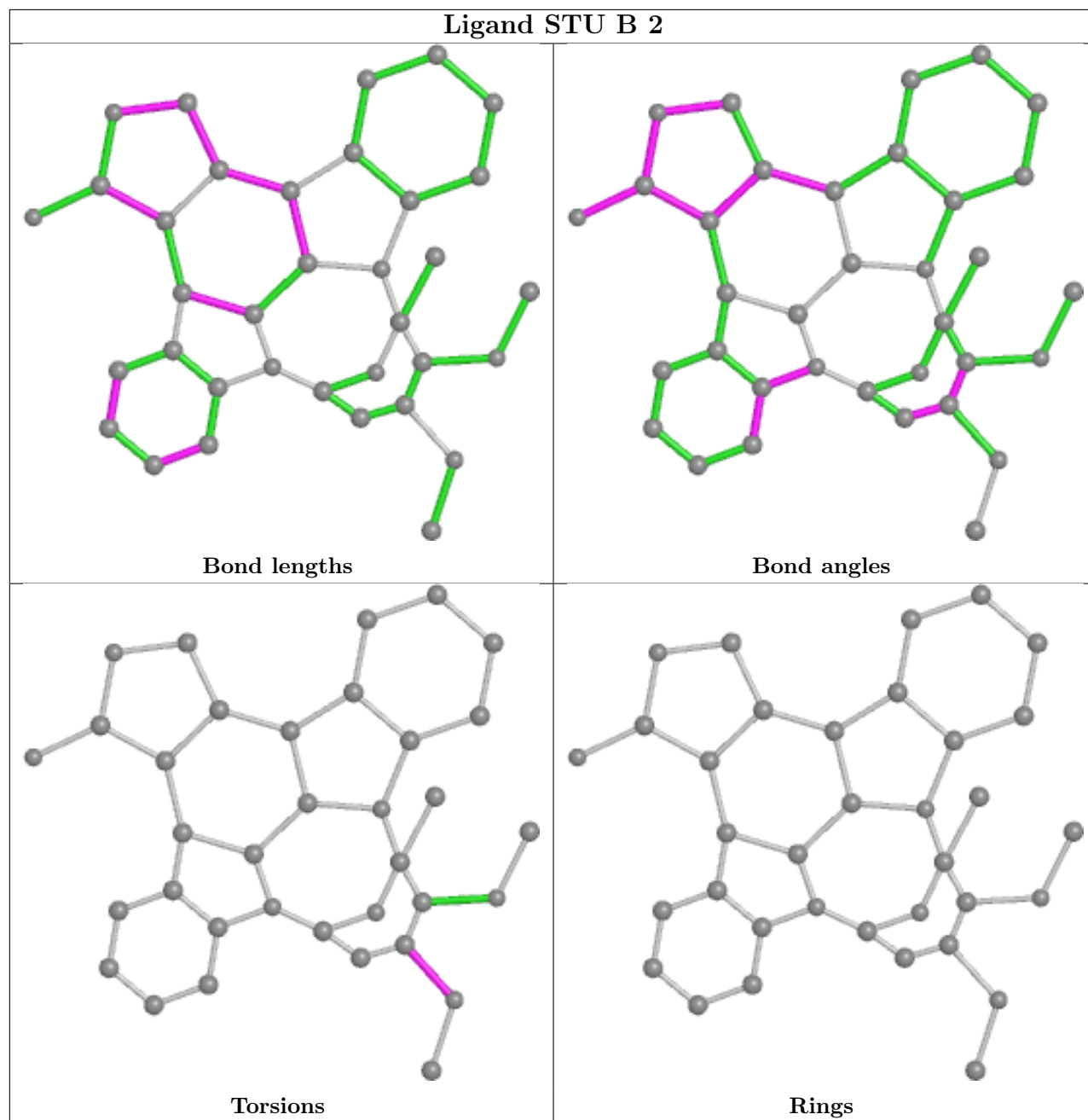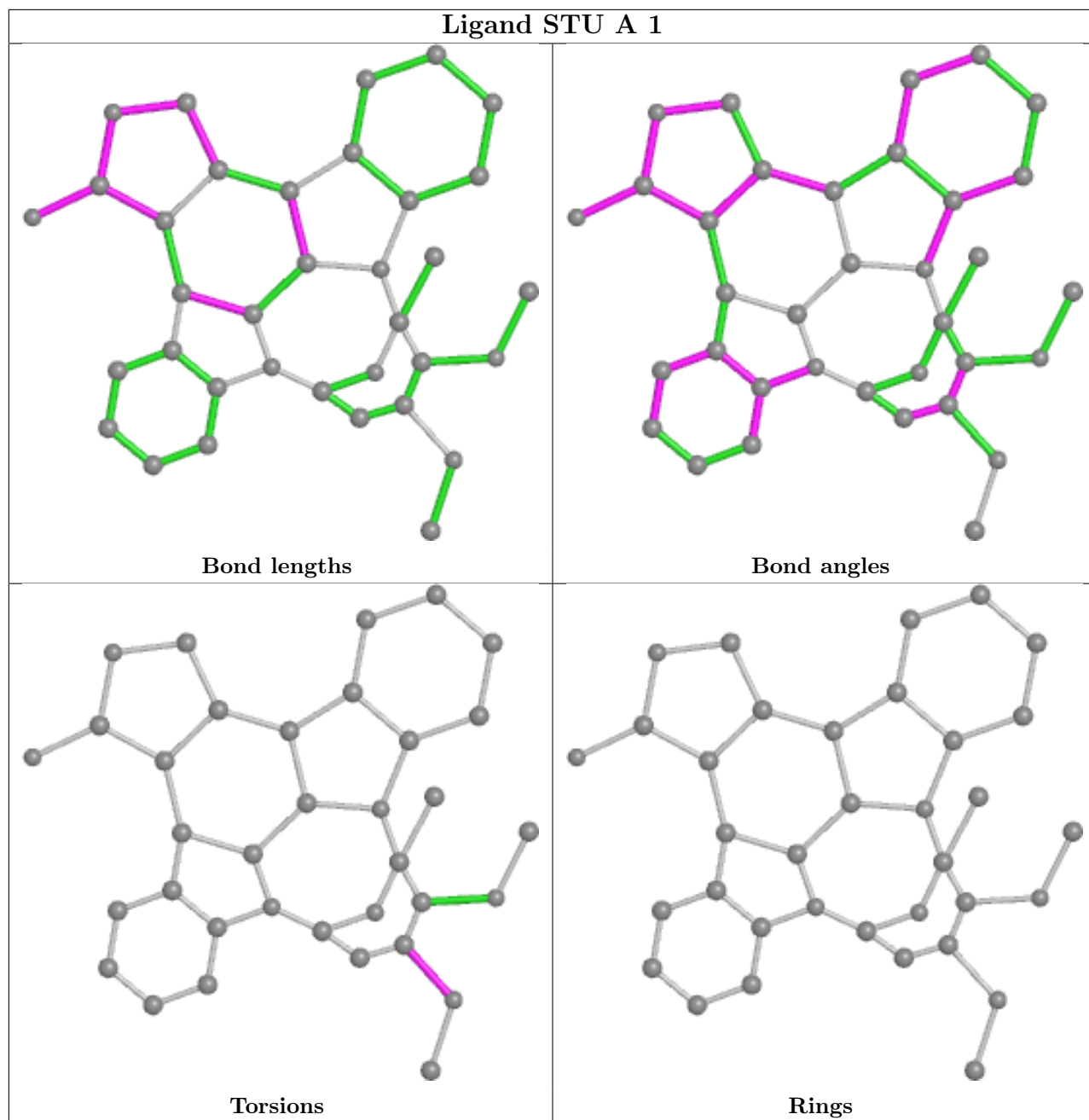
5.7 Other polymers ⓘ

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.