WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 3, 2025 – 04:05 PM EST

PDB ID	:	8SCV
Title	:	Crystal structure of IRAK4-HSA complexed with BMS-986126; 6-((5-CYAN O-2-PYRIMIDINYL)AMINO)-N-((2R)-2-FLUORO-3-HYDROXHYLBUTY L)-4-(ISOPROPYLAMINO)NICOTINAMIDE
Authors	:	Muckelbauer, J.K.; Ghosh, K.
Deposited on	:	2023-04-05
Resolution	:	2.69 Å(reported)

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 2.69 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
Rfree		0.608
Clashscore		5
Ramachandran outliers		1.3%
Sidechain outliers		6.5%
RSRZ outliers		97.6%

Worse — *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution
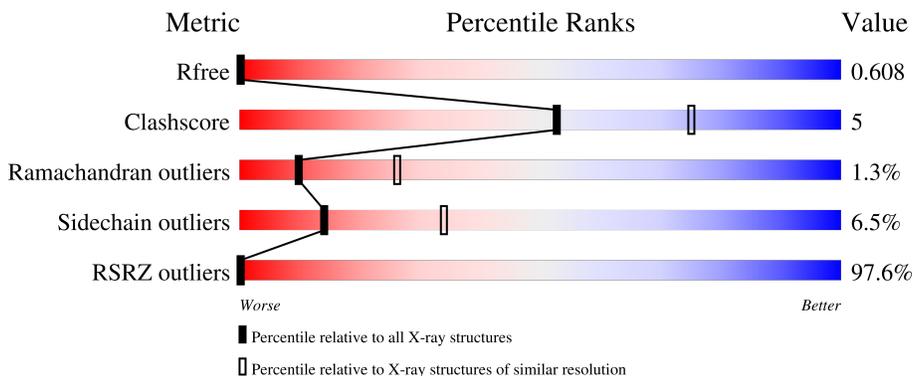
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	3333 (2.70-2.70)
Clashscore	180529	3684 (2.70-2.70)
Ramachandran outliers	177936	3633 (2.70-2.70)
Sidechain outliers	177891	3633 (2.70-2.70)
RSRZ outliers	164620	3333 (2.70-2.70)

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%

Mol	Chain	Length	Quality of chain
1	A	305	91% / 80% 13% · 5%
2	B	305	84% / 78% 7% · 14%

2 Entry composition ⓘ

There are 5 unique types of molecules in this entry. The entry contains 4214 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	290	Total 2203	C 1385	N 369	O 431	P 3	S 15	0	1	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	156	GLY	-	expression tag	UNP Q9NWZ3
A	157	ALA	-	expression tag	UNP Q9NWZ3
A	158	MET	-	expression tag	UNP Q9NWZ3
A	159	GLY	-	expression tag	UNP Q9NWZ3

- Molecule 2 is a protein called Interleukin-1 receptor-associated kinase 4.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	263	Total 1879	C 1180	N 316	O 368	P 2	S 13	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	156	GLY	-	expression tag	UNP Q9NWZ3
B	157	ALA	-	expression tag	UNP Q9NWZ3
B	158	MET	-	expression tag	UNP Q9NWZ3
B	159	GLY	-	expression tag	UNP Q9NWZ3

- Molecule 3 is 6-[(5-cyanopyrimidin-2-yl)amino]-N-[(2R)-2-fluoro-3-hydroxy-3-methylbutyl]-4-[(propan-2-yl)amino]pyridine-3-carboxamide (three-letter code: ZVG) (formula: $C_{19}H_{24}FN_7O_2$) (labeled as "Ligand of Interest" by depositor).
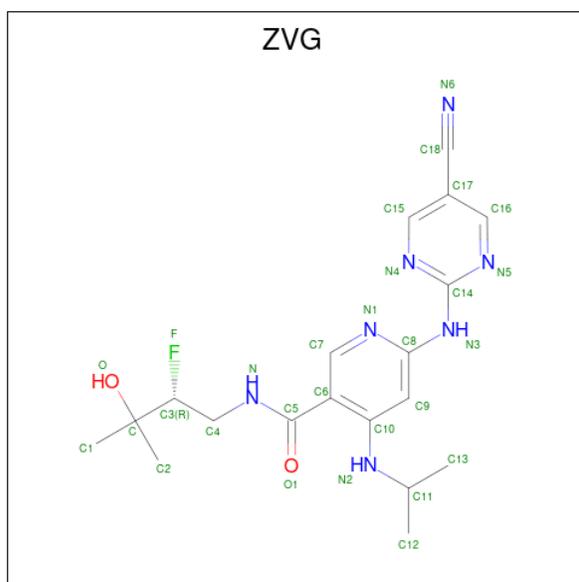
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	0	0
			29	19	1	7	2		
3	B	1	Total	C	F	N	O	0	0
			29	19	1	7	2		

• Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).
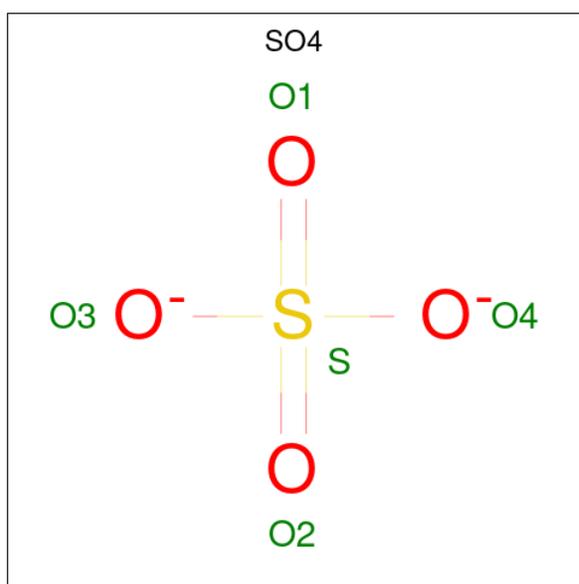
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	38	Total O 38 38	0	0
5	B	26	Total O 26 26	0	0

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.

- Molecule 1: Interleukin-1 receptor-associated kinase 4
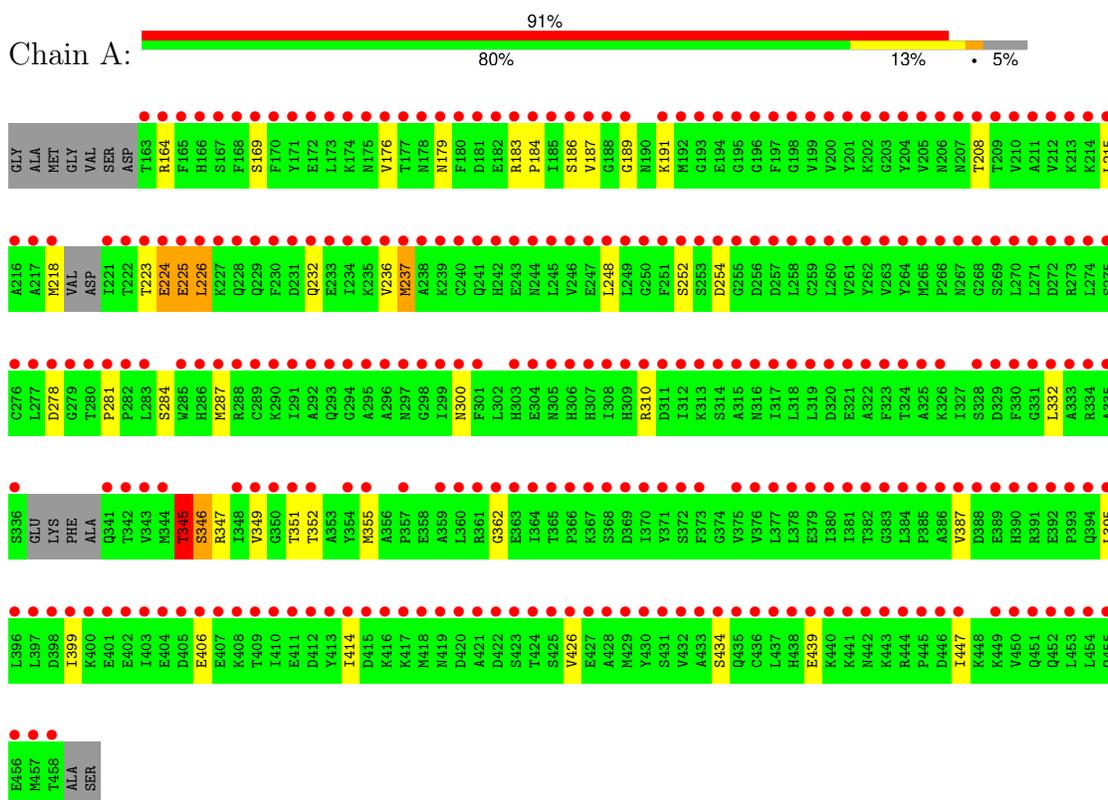
- Molecule 2: Interleukin-1 receptor-associated kinase 4

SER GLU LYS PHE ALA GLN T342 V343 M344 T345 S346 R347 I348 V349 GLY THR T352 A353 Y354 M355 A356 P357 E358 A359 L360 R361 G362 E363 I364 T365 P366 K367 S368 D369 I370 Y371 S372 F373 G374 V375 V376 L377 L378 E379 I380 I381 T382 G383 L384 P385 A386 V387 D388 E389 H390 R391 E392 P393 Q394 L395

L396 L397 D398 I399 K400 E401 E402 I403 E404 D405 E406 E407 K408 T409 I410 E411 D412 Y413 I414 D415 K416 K417 M418 N419 D420 A421 D422 S423 T424 S425 V426 E427 A428 M429 Y430 S431 V432 A433 S434 Q435 C436 L437 H438 E439 K440 K441 N442 K443 R444 P445 D446 I447 K448 K449 V450 Q451 Q452 L453 L454 Q455

E456 M457 T458 A459 SER

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	86.29Å 103.75Å 139.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.11 – 2.69 48.11 – 2.69	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.11-2.69) 99.8 (48.11-2.69)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.93 (at 2.69Å)	Xtriage
Refinement program	BUSTER 2.11.1	Depositor
R, R_{free}	0.220 , 0.261 0.583 , 0.608	Depositor DCC
R_{free} test set	870 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å^2)	57.0	Xtriage
Anisotropy	0.590	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.47 , 218.9	EDS
L-test for twinning[2]	$< |L| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.39	EDS
Total number of atoms	4214	wwPDB-VP
Average B, all atoms (Å^2)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.13% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SEP, SO4, TPO, ZVG

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	0.56	0/2211	0.73	0/2996
2	B	0.48	0/1882	0.69	0/2561
All	All	0.53	0/4093	0.71	0/5557

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	345	TPO	Peptide

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.

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2203	0	2081	30	0
2	B	1879	0	1695	11	0
3	A	29	0	0	0	0
3	B	29	0	0	0	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
5	A	38	0	0	2	0
5	B	26	0	0	0	0
All	All	4214	0	3776	39	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 39 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:224:GLU:HA	1:A:226:LEU:H	1.17	1.07
1:A:224:GLU:HA	1:A:226:LEU:N	1.96	0.80
1:A:223:THR:O	1:A:224:GLU:CG	2.30	0.80
1:A:224:GLU:CA	1:A:226:LEU:H	1.99	0.74
1:A:345:TPO:HG22	1:A:346:SEP:N	2.09	0.68

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	282/305 (92%)	266 (94%)	11 (4%)	5 (2%)	7	18
2	B	247/305 (81%)	232 (94%)	13 (5%)	2 (1%)	16	38
All	All	529/610 (87%)	498 (94%)	24 (4%)	7 (1%)	10	26

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	224	GLU
1	A	406	GLU
2	B	406	GLU
1	A	254	ASP
1	A	347	ARG

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	225/260 (86%)	209 (93%)	16 (7%)	12	30
2	B	177/261 (68%)	167 (94%)	10 (6%)	17	41
All	All	402/521 (77%)	376 (94%)	26 (6%)	14	34

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	434	SER
2	B	215	LEU
2	B	439	GLU
2	B	176	VAL
2	B	332	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3   RNA ⓘ

There are no RNA molecules in this entry.

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

5 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	#$|Z| > 2$
2	TPO	B	345	2	8,10,11	0.93	0	10,14,16	1.33	1 (10%)
2	SEP	B	346	2	8,9,10	1.05	1 (12%)	7,12,14	3.13	3 (42%)
1	SEP	A	284	1	8,9,10	2.50	3 (37%)	7,12,14	8.33	4 (57%)
1	TPO	A	345	1	8,10,11	0.85	0	10,14,16	1.32	1 (10%)
1	SEP	A	346	1	8,9,10	0.79	0	7,12,14	2.69	1 (14%)

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	TPO	B	345	2	-	3/9/11/13	-
2	SEP	B	346	2	-	2/6/8/10	-
1	SEP	A	284	1	-	3/6/8/10	-
1	TPO	A	345	1	-	4/9/11/13	-
1	SEP	A	346	1	-	2/6/8/10	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	284	SEP	P-OG	5.01	1.76	1.60
1	A	284	SEP	CB-CA	3.72	1.62	1.52
1	A	284	SEP	OG-CB	2.48	1.54	1.44
2	B	346	SEP	P-OG	-2.12	1.53	1.60

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	284	SEP	OG-CB-CA	21.09	128.66	108.14
2	B	346	SEP	OG-CB-CA	6.91	114.87	108.14
1	A	346	SEP	OG-CB-CA	6.65	114.62	108.14
1	A	284	SEP	O2P-P-OG	5.01	119.74	106.67
2	B	346	SEP	O3P-P-O1P	-3.17	98.50	110.83

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	284	SEP	CB-OG-P-O3P
1	A	345	TPO	N-CA-CB-OG1
1	A	345	TPO	CA-CB-OG1-P
1	A	346	SEP	N-CA-CB-OG
1	A	346	SEP	C-CA-CB-OG

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	345	TPO	5	0
1	A	346	SEP	3	0

5.5 Carbohydrates ⓘ

There are no oligosaccharides 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	#$|Z| > 2$
3	ZVG	B	501	-	28,30,30	1.94	6 (21%)	37,42,42	1.25	6 (16%)
3	ZVG	A	501	-	28,30,30	1.61	6 (21%)	37,42,42	1.12	3 (8%)
4	SO4	B	502	-	4,4,4	0.34	0	6,6,6	0.14	0
4	SO4	A	502	-	4,4,4	0.25	0	6,6,6	0.09	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ZVG	B	501	-	-	2/22/25/25	0/2/2/2
3	ZVG	A	501	-	-	3/22/25/25	0/2/2/2

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	501	ZVG	C14-N5	5.47	1.42	1.34
3	B	501	ZVG	C14-N4	4.41	1.40	1.34
3	A	501	ZVG	C14-N5	3.90	1.40	1.34
3	B	501	ZVG	C9-C10	3.85	1.45	1.39
3	A	501	ZVG	C5-N	3.38	1.41	1.33

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	501	ZVG	F-C3-C4	3.28	111.11	108.06
3	A	501	ZVG	C15-C17-C16	2.96	117.59	115.57
3	B	501	ZVG	C10-N2-C11	2.92	128.81	124.66
3	B	501	ZVG	C15-C17-C16	2.53	117.30	115.57
3	A	501	ZVG	N3-C14-N4	2.38	123.04	116.29

There are no chirality outliers.

All (5) torsion outliers are listed below:

| Mol	Chain	Res	Type	Atoms
3	A	501	ZVG	O1-C5-C6-C7
3	B	501	ZVG	O1-C5-C6-C7
3	B	501	ZVG	N-C5-C6-C7
3	A	501	ZVG	N-C5-C6-C7
3	A	501	ZVG	N5-C14-N3-C8

There are no ring outliers.

No monomer is involved in short contacts.

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 ZVG B 501

Bond lengths

Bond angles

Torsions

Rings

Ligand ZVG A 501

Bond lengths

Bond angles

Torsions

Rings
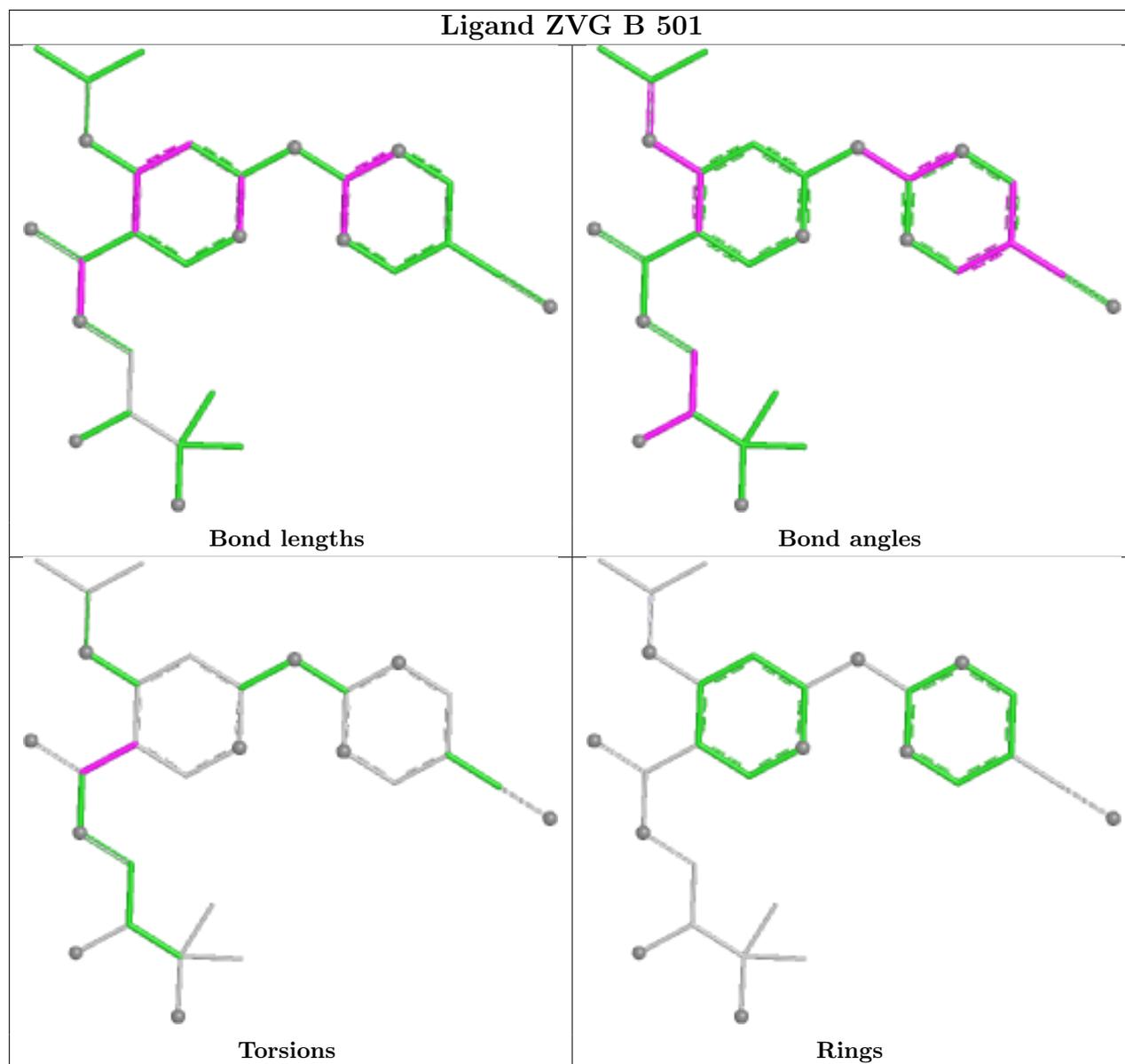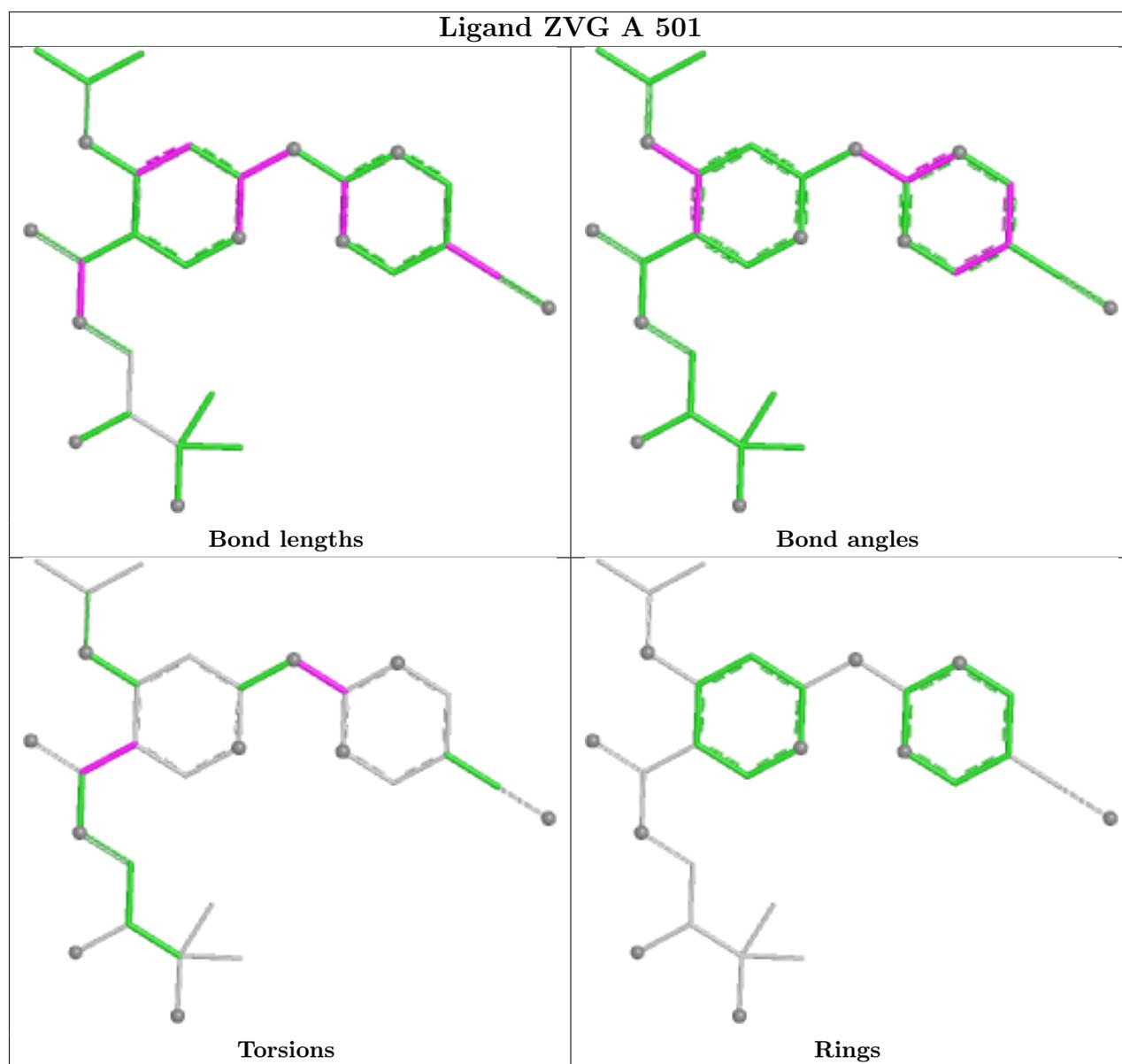
5.7 Other polymers ⓘ

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 ⓘ

Warning: The R factor obtained from EDS is 0.5938, which does not match the depositor's R factor of 0.22. Please interpret the results in this section carefully.

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	287/305 (94%)	6.28	278 (96%)	0	0	31, 59, 91, 111	1 (0%)
2	B	261/305 (85%)	6.85	257 (98%)	0	0	44, 78, 142, 159	0
All	All	548/610 (89%)	6.55	535 (97%)	0	0	31, 67, 114, 159	1 (0%)

The worst 5 of 535 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	212	VAL	31.1
2	B	181	ASP	29.2
1	A	436	CYS	26.2
2	B	342	THR	25.9
1	A	450	VAL	25.5

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

| Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	SEP	A	284	10/11	0.34	0.30	57,64,71,73	0
2	TPO	B	345	11/12	0.54	0.27	73,75,87,87	0
1	SEP	A	346	10/11	0.66	0.30	95,97,101,102	0
2	SEP	B	346	10/11	0.70	0.19	69,71,74,74	0
1	TPO	A	345	11/12	0.73	0.20	79,93,95,113	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	ZVG	B	501	29/29	0.36	0.27	55,68,76,80	0
4	SO4	A	502	5/5	0.39	0.35	144,148,149,150	0
3	ZVG	A	501	29/29	0.53	0.36	24,31,44,55	0
4	SO4	B	502	5/5	0.56	0.30	66,70,71,72	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around ZVG B 501:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative) and green (positive)

Electron density around ZVG A 501:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

6.5 Other polymers ⓘ

There are no such residues in this entry.