



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 20, 2023 – 12:56 PM EDT

PDB ID : 5KJI
Title : Crystal structure of an active polycomb repressive complex 2 in the basal state
Authors : Jiao, L.; Liu, X.
Deposited on : 2016-06-20
Resolution : 2.71 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

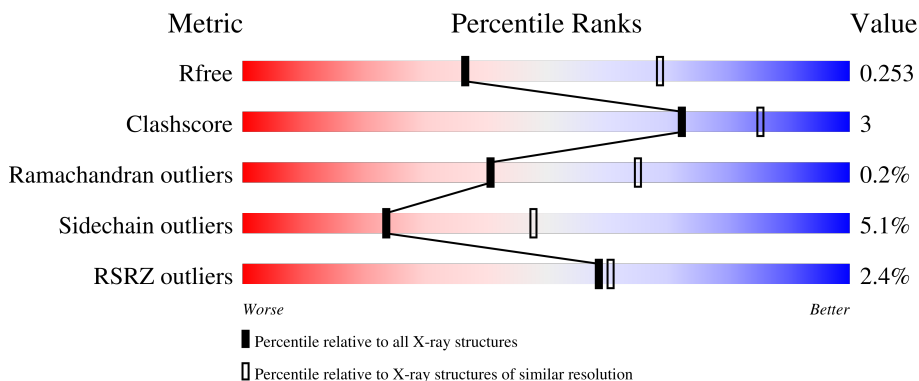
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


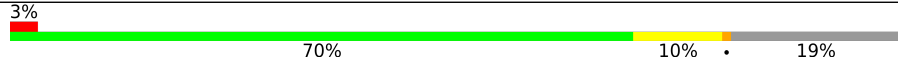
The reported resolution of this entry is 2.71 Å.

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))
R_{free}	130704	3359 (2.74-2.70)
Clashscore	141614	3686 (2.74-2.70)
Ramachandran outliers	138981	3622 (2.74-2.70)
Sidechain outliers	138945	3623 (2.74-2.70)
RSRZ outliers	127900	3276 (2.74-2.70)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	605	 70% 9% 21%
2	B	937	 70% 10% 19%

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 10028 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 putative polycomb protein Eed.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	479	3762	2403	645	694	20	0	0	0

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-39	MET	-	expression tag	UNP G0S8H7
A	-38	ALA	-	expression tag	UNP G0S8H7
A	-37	SER	-	expression tag	UNP G0S8H7
A	-36	ALA	-	expression tag	UNP G0S8H7
A	-35	TRP	-	expression tag	UNP G0S8H7
A	-34	SER	-	expression tag	UNP G0S8H7
A	-33	HIS	-	expression tag	UNP G0S8H7
A	-32	PRO	-	expression tag	UNP G0S8H7
A	-31	GLN	-	expression tag	UNP G0S8H7
A	-30	PHE	-	expression tag	UNP G0S8H7
A	-29	GLU	-	expression tag	UNP G0S8H7
A	-28	LYS	-	expression tag	UNP G0S8H7
A	-27	GLY	-	expression tag	UNP G0S8H7
A	-26	GLY	-	expression tag	UNP G0S8H7
A	-25	GLY	-	expression tag	UNP G0S8H7
A	-24	SER	-	expression tag	UNP G0S8H7
A	-23	GLY	-	expression tag	UNP G0S8H7
A	-22	GLY	-	expression tag	UNP G0S8H7
A	-21	GLY	-	expression tag	UNP G0S8H7
A	-20	SER	-	expression tag	UNP G0S8H7
A	-19	GLY	-	expression tag	UNP G0S8H7
A	-18	GLY	-	expression tag	UNP G0S8H7
A	-17	SER	-	expression tag	UNP G0S8H7
A	-16	ALA	-	expression tag	UNP G0S8H7
A	-15	TRP	-	expression tag	UNP G0S8H7
A	-14	SER	-	expression tag	UNP G0S8H7
A	-13	HIS	-	expression tag	UNP G0S8H7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	PRO	-	expression tag	UNP G0S8H7
A	-11	GLN	-	expression tag	UNP G0S8H7
A	-10	PHE	-	expression tag	UNP G0S8H7
A	-9	GLU	-	expression tag	UNP G0S8H7
A	-8	LYS	-	expression tag	UNP G0S8H7
A	-7	LEU	-	expression tag	UNP G0S8H7
A	-6	GLU	-	expression tag	UNP G0S8H7
A	-5	VAL	-	expression tag	UNP G0S8H7
A	-4	LEU	-	expression tag	UNP G0S8H7
A	-3	PHE	-	expression tag	UNP G0S8H7
A	-2	GLN	-	expression tag	UNP G0S8H7
A	-1	GLY	-	expression tag	UNP G0S8H7
A	0	PRO	-	expression tag	UNP G0S8H7

- Molecule 2 is a protein called Putative uncharacterized protein,Zinc finger domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	761	6121	3858	1107	1114	42	0	0	0

There are 15 discrepancies between the modelled and reference sequences:

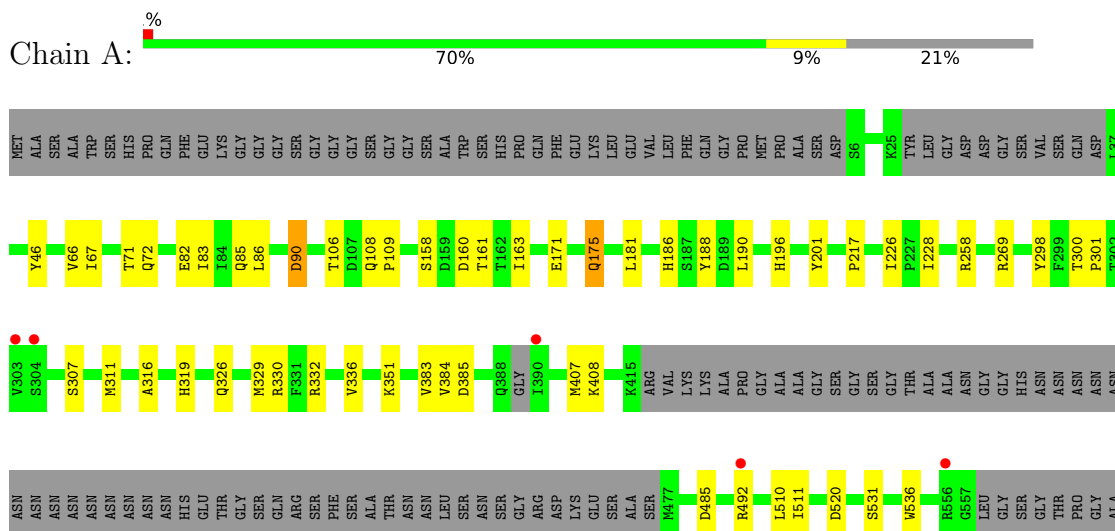
Chain	Residue	Modelled	Actual	Comment	Reference
B	182	SER	-	expression tag	UNP G0SDW4
B	183	ASN	-	expression tag	UNP G0SDW4
B	184	HIS	-	expression tag	UNP G0SDW4
B	185	HIS	-	expression tag	UNP G0SDW4
B	186	HIS	-	expression tag	UNP G0SDW4
B	187	HIS	-	expression tag	UNP G0SDW4
B	188	HIS	-	expression tag	UNP G0SDW4
B	189	HIS	-	expression tag	UNP G0SDW4
B	190	ALA	-	expression tag	UNP G0SDW4
B	2524	LEU	ALA	linker	UNP G0SDW4
B	2525	VAL	ALA	linker	UNP G0SDW4
B	2526	PRO	-	linker	UNP G0SDW4
B	2527	ARG	-	linker	UNP G0SDW4
B	2528	GLY	-	linker	UNP G0SDW4
B	2529	SER	-	linker	UNP G0SDW4

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

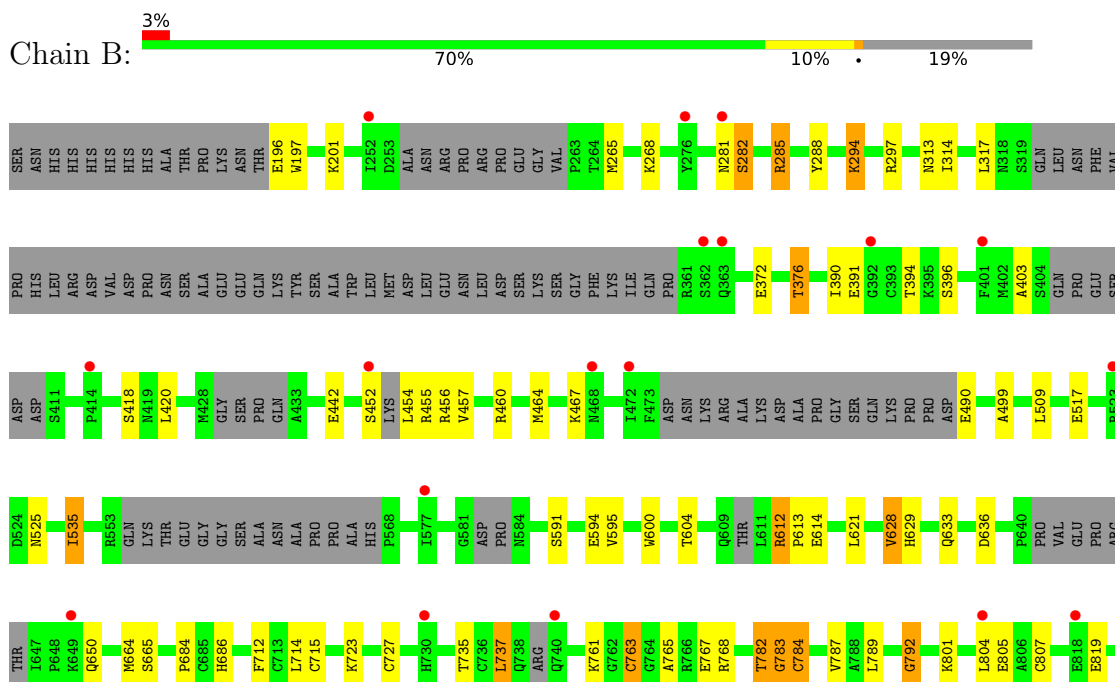
3 Residue-property plots [i](#)

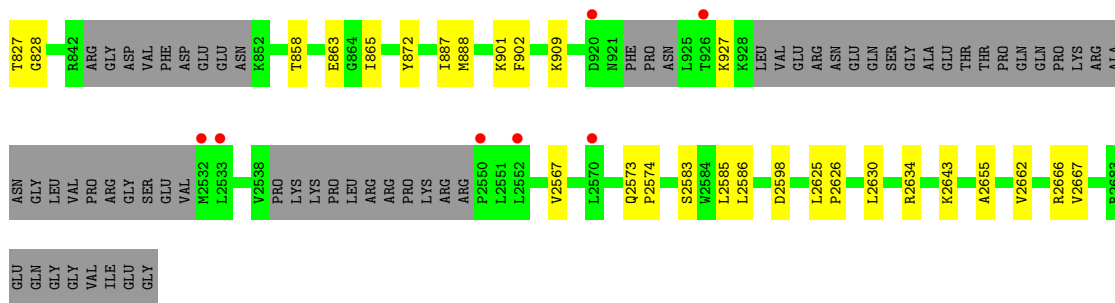
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: putative polycomb protein Eed



- Molecule 2: Putative uncharacterized protein, Zinc finger domain-containing protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.33Å 74.62Å 127.03Å 90.00° 105.63° 90.00°	Depositor
Resolution (Å)	47.31 – 2.71 47.31 – 2.71	Depositor EDS
% Data completeness (in resolution range)	91.2 (47.31-2.71) 90.9 (47.31-2.71)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.63 (at 2.69Å)	Xtrriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.179 , 0.249 0.181 , 0.253	Depositor DCC
R_{free} test set	1827 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	43.0	Xtrriage
Anisotropy	0.093	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 63.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10028	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: SAH, ZN

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	0.51	0/3873	0.69	0/5276
2	B	0.52	0/6251	0.71	3/8430 (0.0%)
All	All	0.51	0/10124	0.70	3/13706 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	784	CYS	C-N-CA	5.95	136.57	121.70
2	B	737	LEU	C-N-CA	5.43	135.27	121.70
2	B	792	GLY	C-N-CA	5.36	135.09	121.70

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	3762	0	3619	23	1
2	B	6121	0	6031	47	2
3	B	8	0	0	0	0
4	B	26	0	19	1	0
5	A	48	0	0	0	0
5	B	63	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	10028	0	9669	66	2

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 3.

All (66) 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:B:452:SER:H	2:B:454:LEU:HD22	1.42	0.83
2:B:452:SER:HB3	2:B:454:LEU:HD13	1.67	0.75
1:A:160:ASP:O	1:A:161:THR:HB	1.86	0.75
2:B:460:ARG:O	2:B:464:MET:HG2	1.87	0.75
2:B:454:LEU:HD23	2:B:456:ARG:HH21	1.52	0.74
2:B:763:CYS:HB3	2:B:765:ALA:H	1.55	0.71
2:B:2630:LEU:O	2:B:2634:ARG:HG3	1.94	0.68
2:B:2625:LEU:HD23	2:B:2662:VAL:CG1	2.29	0.62
2:B:768:ARG:HH21	2:B:782:THR:HB	1.66	0.61
1:A:316:ALA:HB1	1:A:511:ILE:HD11	1.82	0.61
2:B:2625:LEU:HD23	2:B:2662:VAL:HG12	1.83	0.61
2:B:887:ILE:HD12	2:B:902:PHE:CD1	2.38	0.59
1:A:326:GLN:HB2	1:A:329:MET:HE1	1.85	0.59
2:B:735:THR:H	2:B:783:GLY:HA2	1.70	0.56
2:B:314:ILE:HG21	2:B:2585:LEU:HD21	1.87	0.56
1:A:66:VAL:HG22	1:A:86:LEU:HD13	1.87	0.56
1:A:384:VAL:HG13	1:A:407:MET:SD	2.46	0.55
2:B:454:LEU:N	2:B:455:ARG:HA	2.21	0.55
1:A:67:ILE:HB	1:A:85:GLN:HB3	1.88	0.55
2:B:452:SER:N	2:B:454:LEU:HD22	2.18	0.55
1:A:186:HIS:CG	1:A:190:LEU:HD21	2.43	0.54
2:B:768:ARG:HD3	2:B:784:CYS:O	2.07	0.54
2:B:2583:SER:HA	2:B:2586:LEU:HD12	1.90	0.53
1:A:258:ARG:NH2	1:A:329:MET:HE3	2.24	0.53
1:A:326:GLN:HB2	1:A:329:MET:CE	2.38	0.53
2:B:763:CYS:HB3	2:B:765:ALA:N	2.23	0.52
1:A:90:ASP:HB3	2:B:294:LYS:HG3	1.94	0.50
2:B:789:LEU:HD21	2:B:901:LYS:HB3	1.94	0.50
2:B:372:GLU:O	2:B:376:THR:HG23	2.11	0.50
2:B:612:ARG:HE	2:B:613:PRO:HD2	1.77	0.49
2:B:604:THR:HG21	2:B:2655:ALA:HB1	1.95	0.49
2:B:2573:GLN:HG2	2:B:2574:PRO:HD2	1.95	0.48
2:B:313:ASN:OD1	2:B:827:THR:HA	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:828:GLY:HA2	2:B:872:TYR:O	2.14	0.48
2:B:317:LEU:HD22	2:B:525:ASN:HB3	1.96	0.47
1:A:217:PRO:HG3	1:A:228:ILE:HG21	1.97	0.47
2:B:614:GLU:HA	2:B:628:VAL:CG2	2.45	0.46
1:A:300:THR:HB	1:A:311:MET:HG2	1.97	0.46
2:B:281:ASN:CG	2:B:282:SER:H	2.19	0.46
2:B:197:TRP:CE2	2:B:390:ILE:HG12	2.51	0.45
2:B:594:GLU:HG2	2:B:621:LEU:HD22	1.99	0.45
2:B:403:ALA:HB2	2:B:420:LEU:HD23	1.98	0.45
2:B:314:ILE:CG2	2:B:2585:LEU:HD21	2.47	0.45
1:A:83:ILE:HB	2:B:288:TYR:CE2	2.52	0.45
1:A:300:THR:HA	1:A:301:PRO:HD3	1.90	0.44
2:B:2626:PRO:HB3	2:B:2667:VAL:HG21	2.00	0.44
2:B:686:HIS:HA	2:B:714:LEU:HD12	1.99	0.43
2:B:499:ALA:HB1	2:B:600:TRP:CE3	2.54	0.42
2:B:612:ARG:NE	2:B:613:PRO:HD2	2.34	0.42
1:A:175:GLN:HG2	2:B:2567:VAL:HG21	2.00	0.42
2:B:535:ILE:HD11	2:B:684:PRO:HB2	2.00	0.42
1:A:531:SER:HB3	1:A:536:TRP:HB2	2.00	0.42
1:A:163:ILE:HB	1:A:181:LEU:HB2	2.01	0.41
1:A:307:SER:HB2	2:B:467:LYS:HA	2.02	0.41
2:B:629:HIS:O	2:B:633:GLN:HG2	2.20	0.41
1:A:196:HIS:HB2	1:A:201:TYR:HB2	2.02	0.41
2:B:509:LEU:HB3	2:B:712:PHE:CE1	2.56	0.41
2:B:715:CYS:O	2:B:723:LYS:HE3	2.20	0.41
1:A:106:THR:HG23	1:A:108:GLN:HB2	2.03	0.41
1:A:383:VAL:CG1	1:A:408:LYS:HB2	2.51	0.41
2:B:268:LYS:HB2	2:B:285:ARG:HG3	2.02	0.41
2:B:591:SER:O	2:B:595:VAL:HG13	2.22	0.40
1:A:46:TYR:CE1	1:A:109:PRO:HB3	2.56	0.40
2:B:863:GLU:HG3	2:B:865:ILE:HD12	2.02	0.40
1:A:319:HIS:HB2	1:A:510:LEU:HB3	2.02	0.40
2:B:927:LYS:HG3	4:B:8009:SAH:H2	2.03	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:485:ASP:OD2	2:B:394:THR:OG1[2_949]	2.12	0.08
2:B:418:SER:OG	2:B:636:ASP:OD2[2_849]	2.18	0.02

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	471/605 (78%)	453 (96%)	18 (4%)	0	100	100
2	B	729/937 (78%)	689 (94%)	37 (5%)	3 (0%)	34	58
All	All	1200/1542 (78%)	1142 (95%)	55 (5%)	3 (0%)	41	65

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	783	GLY
2	B	792	GLY
2	B	665	SER

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	404/495 (82%)	386 (96%)	18 (4%)	27	53
2	B	664/816 (81%)	627 (94%)	37 (6%)	21	43
All	All	1068/1311 (82%)	1013 (95%)	55 (5%)	24	48

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	THR
1	A	72	GLN
1	A	82	GLU

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Mol	Chain	Res	Type
1	A	90	ASP
1	A	158	SER
1	A	171	GLU
1	A	175	GLN
1	A	188	TYR
1	A	226	ILE
1	A	269	ARG
1	A	298	TYR
1	A	330	ARG
1	A	332	ARG
1	A	336	VAL
1	A	351	LYS
1	A	385	ASP
1	A	492	ARG
1	A	520	ASP
2	B	196	GLU
2	B	201	LYS
2	B	265	MET
2	B	282	SER
2	B	285	ARG
2	B	294	LYS
2	B	297	ARG
2	B	376	THR
2	B	391	GLU
2	B	396	SER
2	B	442	GLU
2	B	457	VAL
2	B	490	GLU
2	B	517	GLU
2	B	535	ILE
2	B	612	ARG
2	B	628	VAL
2	B	650	GLN
2	B	664	MET
2	B	727	CYS
2	B	737	LEU
2	B	761	LYS
2	B	763	CYS
2	B	767	GLU
2	B	782	THR
2	B	787	VAL
2	B	801	LYS

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Mol	Chain	Res	Type
2	B	804	LEU
2	B	805	GLU
2	B	807	CYS
2	B	819	GLU
2	B	858	THR
2	B	888	MET
2	B	909	LYS
2	B	2598	ASP
2	B	2643	LYS
2	B	2666	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	221	ASN
2	B	740	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 8 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SAH	B	8009	-	24,28,28	0.64	0	25,40,40	0.89	1 (4%)

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	SAH	B	8009	-	-	3/11/31/31	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	8009	SAH	C5-C6-N6	2.29	123.83	120.35

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	8009	SAH	OXT-C-CA-CB
4	B	8009	SAH	C3'-C4'-C5'-SD
4	B	8009	SAH	O-C-CA-CB

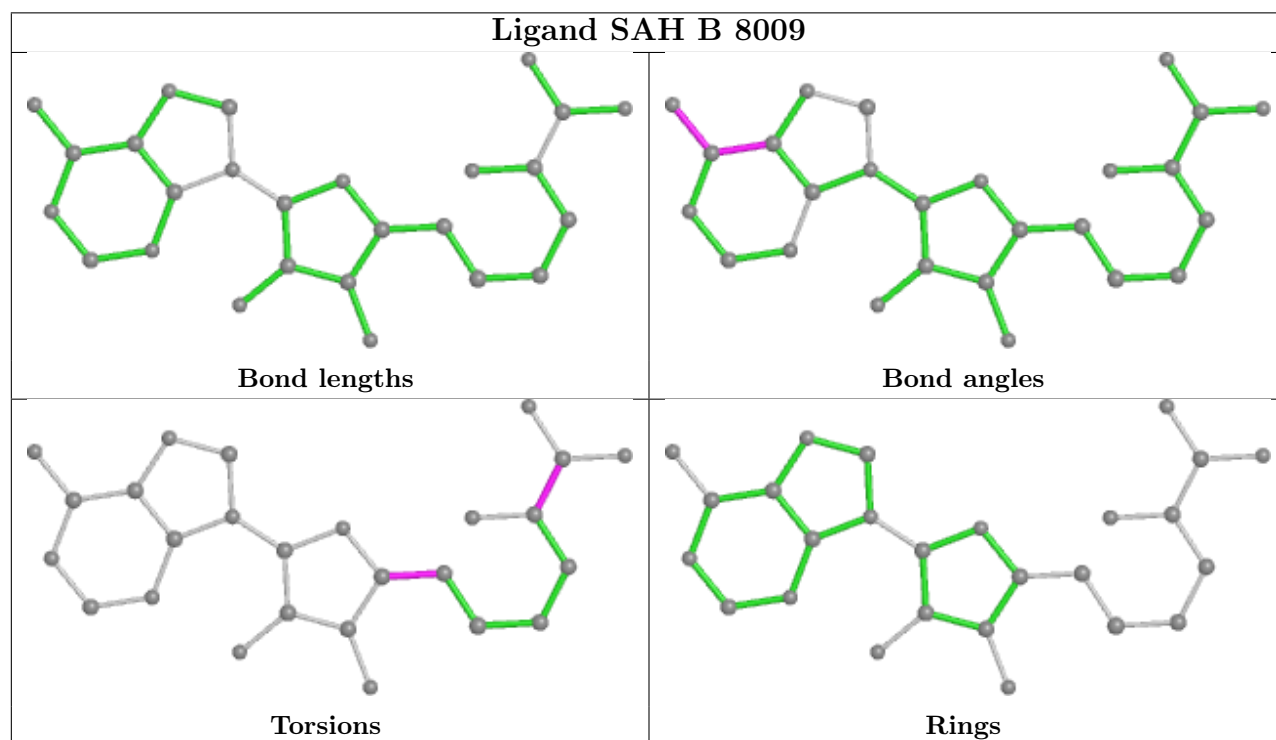
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	8009	SAH	1	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

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	479/605 (79%)	-0.12	5 (1%) 82 83	16, 38, 72, 96	0
2	B	761/937 (81%)	0.06	25 (3%) 46 47	17, 50, 86, 115	0
All	All	1240/1542 (80%)	-0.01	30 (2%) 59 60	16, 46, 81, 115	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	2533	LEU	4.4
2	B	276	TYR	4.3
2	B	577	ILE	3.7
2	B	363	GLN	3.7
2	B	2532	MET	3.4
2	B	362	SER	3.1
1	A	492	ARG	3.0
2	B	804	LEU	2.9
2	B	523	ARG	2.9
2	B	401	PHE	2.8
2	B	252	ILE	2.8
2	B	472	ILE	2.8
2	B	452	SER	2.7
2	B	414	PRO	2.7
2	B	392	GLY	2.5
2	B	468	ASN	2.5
2	B	2550	PRO	2.4
1	A	390	ILE	2.4
2	B	649	LYS	2.4
2	B	920	ASP	2.4
2	B	730	HIS	2.3
1	A	304	SER	2.3
2	B	926	THR	2.3
1	A	556	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	740	GLN	2.1
2	B	818	GLU	2.1
2	B	2570	LEU	2.0
2	B	2552	LEU	2.0
2	B	281	ASN	2.0
1	A	303	VAL	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

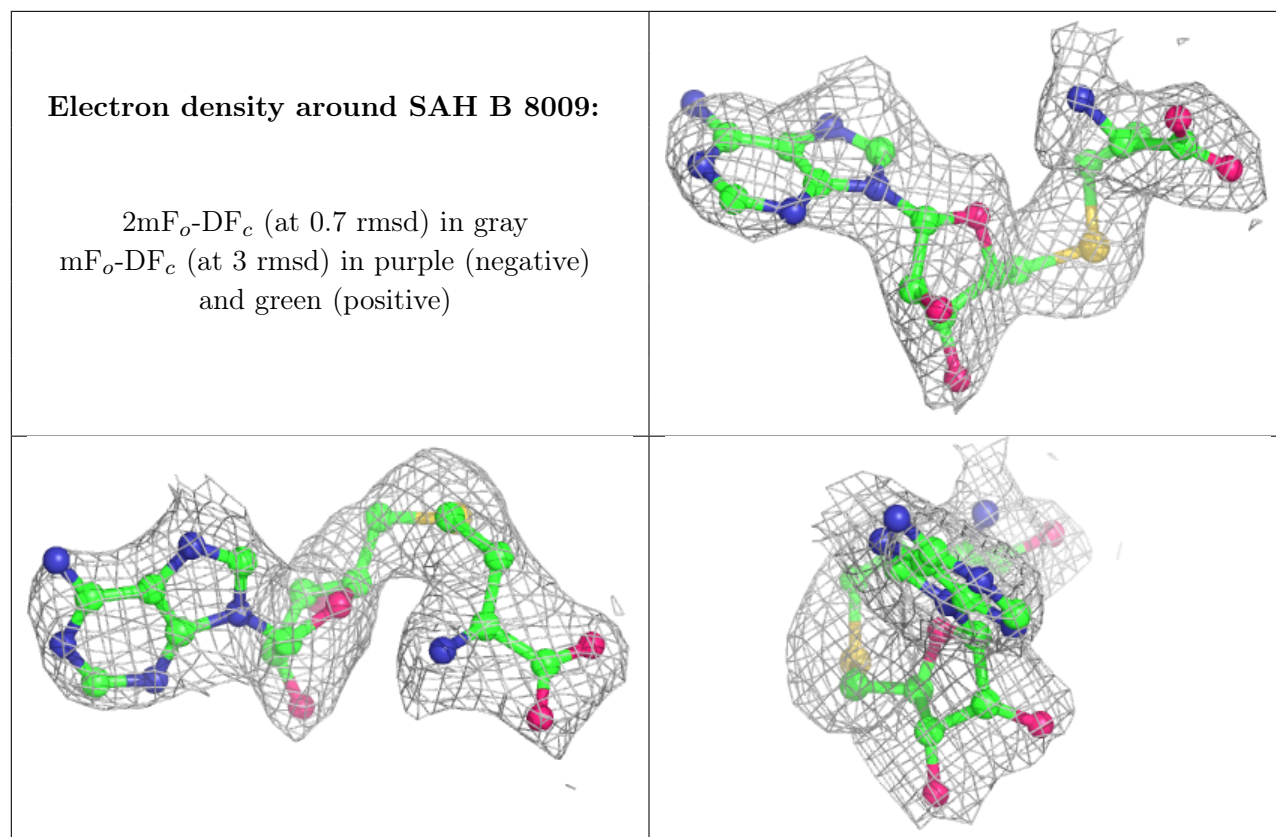
There are no monosaccharides in this entry.

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
4	SAH	B	8009	26/26	0.95	0.19	44,57,64,67	0
3	ZN	B	8003	1/1	0.99	0.14	51,51,51,51	0
3	ZN	B	8004	1/1	0.99	0.11	48,48,48,48	0
3	ZN	B	8005	1/1	0.99	0.14	46,46,46,46	0
3	ZN	B	8006	1/1	0.99	0.17	41,41,41,41	0
3	ZN	B	8008	1/1	0.99	0.07	52,52,52,52	0
3	ZN	B	8002	1/1	0.99	0.14	45,45,45,45	0
3	ZN	B	8001	1/1	1.00	0.15	41,41,41,41	0
3	ZN	B	8007	1/1	1.00	0.18	31,31,31,31	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.