Full wwPDB X-ray Structure Validation Report ⓘ

Sep 20, 2023 – 12:35 AM EDT

PDB ID	:	5KKL
Title	:	Structure of ctPRC2 in complex with H3K27me3 and H3K27M
Authors	:	Jiao, L.; Liu, X.
Deposited on	:	2016-06-21
Resolution	:	2.94 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:

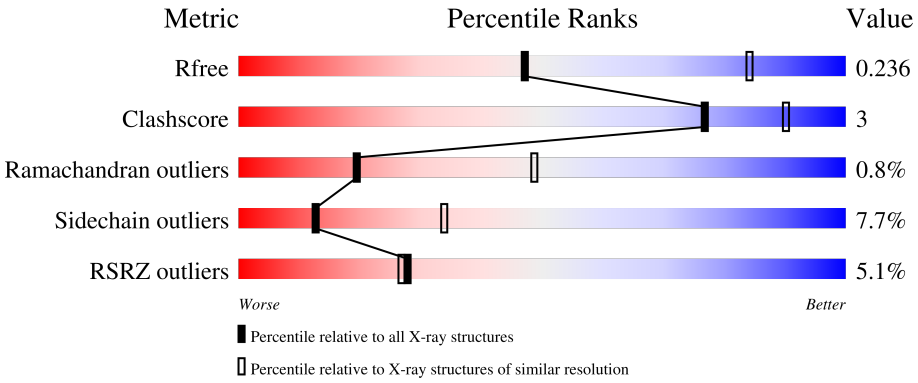
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh &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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.94 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	2969 (2.98-2.90)
Clashscore	141614	3218 (2.98-2.90)
Ramachandran outliers	138981	3122 (2.98-2.90)
Sidechain outliers	138945	3124 (2.98-2.90)
RSRZ outliers	127900	2902 (2.98-2.90)

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% 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	% 68% 11% 20%
2	B	938	7% 75% 13% · 11%
3	D	11	64% 9% 27%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 10614 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	481	3785	2419	646	700	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,Histone H3.1 peptide,Zinc finger domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	839	Total	C	N	O	S	0	0	0
			6738	4241	1219	1235	43			

There are 18 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	2014	LEU	-	linker	UNP G0SDW4
B	2015	VAL	-	linker	UNP G0SDW4
B	2016	PRO	-	linker	UNP G0SDW4
B	2017	ALA	-	linker	UNP G0SDW4
B	2018	GLY	-	linker	UNP G0SDW4
B	2019	SER	-	linker	UNP G0SDW4
B	2020	GLU	-	linker	UNP G0SDW4
B	2021	VAL	-	linker	UNP G0SDW4
B	2027	MET	LYS	engineered mutation	UNP P68431

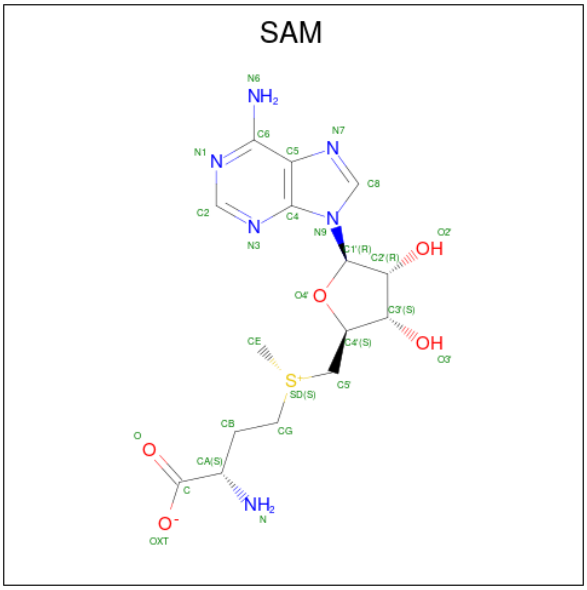
- Molecule 3 is a protein called ALA-ALA-ARG-M3L-SER-ALA-PRO-ALA.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	8	Total	C	N	O	0	0	0
			56	35	12	9			

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	8	Total	Zn	0	0
			8	8		

- Molecule 5 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



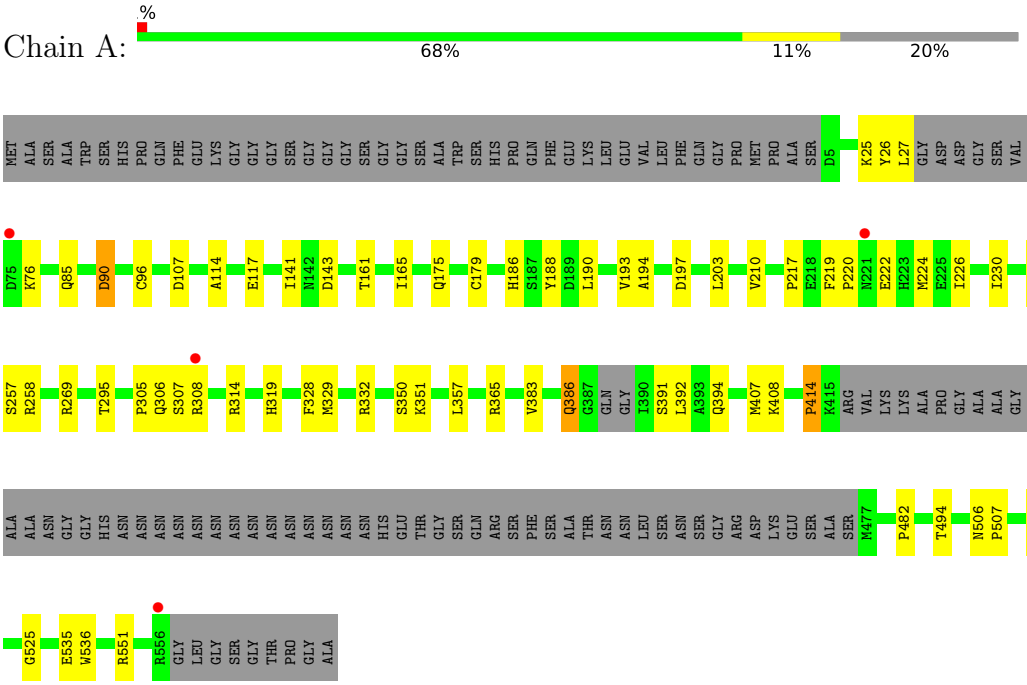
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	S	0	0
			27	15	6	5	1		

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.

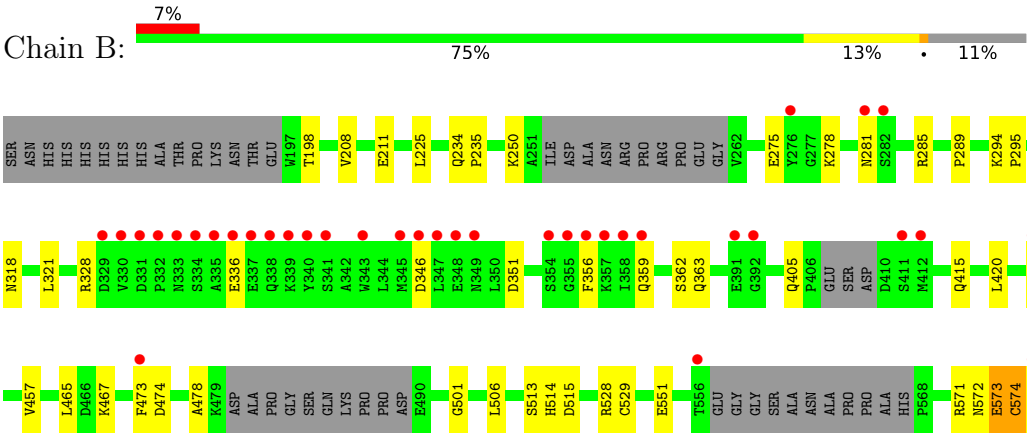
• Molecule 1: putative polycomb protein Eed

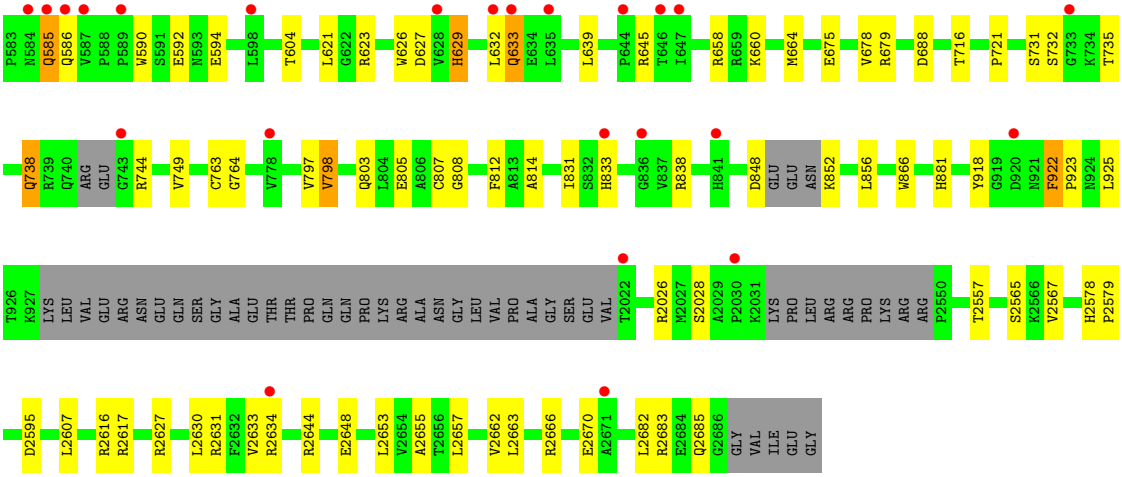
Chain A:



• Molecule 2: Putative uncharacterized protein,Histone H3.1 peptide,Zinc finger domain-containing protein

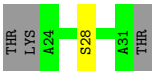
Chain B:





• Molecule 3: ALA-ALA-ARG-M3L-SER-ALA-PRO-ALA

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	86.25Å 80.56Å 133.22Å 90.00° 107.42° 90.00°	Depositor
Resolution (Å)	48.74 – 2.94 44.29 – 2.94	Depositor EDS
% Data completeness (in resolution range)	83.0 (48.74-2.94) 83.3 (44.29-2.94)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.84 (at 2.96Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.186 , 0.234 0.193 , 0.236	Depositor DCC
R_{free} test set	1517 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å^2)	53.2	Xtriage
Anisotropy	0.136	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 58.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.017 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	10614	wwPDB-VP
Average B, all atoms (Å^2)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.37% of the height of the origin peak. No significant pseudotranslation is detected.*

[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: ZN, SAM, M3L

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	0.45	0/3897	0.66	0/5310
2	B	0.44	0/6892	0.65	1/9313 (0.0%)
3	D	0.54	0/44	0.62	0/59
All	All	0.44	0/10833	0.65	1/14682 (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})
2	B	429	GLY	C-N-CA	5.18	134.66	121.70

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	3785	0	3636	26	1
2	B	6738	0	6629	40	2
3	D	56	0	62	0	0
4	B	8	0	0	0	0
5	B	27	0	22	0	0
All	All	10614	0	10349	62	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 (62) 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:881:HIS:HD2	2:B:918:TYR:H	1.26	0.81
2:B:881:HIS:CD2	2:B:918:TYR:H	2.07	0.71
2:B:831:ILE:HD11	2:B:856:LEU:HD21	1.75	0.68
2:B:604:THR:HG21	2:B:2655:ALA:HB1	1.81	0.63
1:A:219:PHE:HB3	1:A:224:MET:HE1	1.81	0.62
2:B:763:CYS:H	2:B:764:GLY:HA2	1.63	0.62
2:B:582:ASP:HB3	2:B:585:GLN:HB2	1.83	0.59
2:B:318:ASN:HB3	2:B:838:ARG:HH12	1.67	0.58
1:A:391:SER:HB3	1:A:394:GLN:HB2	1.86	0.58
2:B:658:ARG:HD3	2:B:721:PRO:HA	1.84	0.57
2:B:234:GLN:HE21	2:B:235:PRO:HD2	1.69	0.56
2:B:763:CYS:N	2:B:764:GLY:HA2	2.21	0.55
1:A:307:SER:HB2	2:B:467:LYS:HA	1.88	0.55
2:B:359:GLN:HE21	2:B:363:GLN:HE21	1.52	0.55
1:A:220:PRO:HB2	1:A:222:GLU:HG2	1.87	0.55
2:B:731:SER:HB3	2:B:735:THR:HB	1.90	0.54
2:B:301:PRO:HB3	2:B:808:GLY:HA2	1.88	0.53
1:A:237:SER:HB2	1:A:295:THR:HG23	1.90	0.53
1:A:165:ILE:HB	1:A:179:CYS:HB3	1.91	0.52
1:A:186:HIS:CG	1:A:190:LEU:HD21	2.45	0.52
2:B:2644:ARG:HH12	2:B:2648:GLU:HB2	1.75	0.51
1:A:194:ALA:HB3	1:A:203:LEU:HB2	1.91	0.51
1:A:203:LEU:HD13	1:A:248:VAL:HG22	1.93	0.51
2:B:738:GLN:HA	2:B:749:VAL:HG11	1.93	0.50
2:B:2630:LEU:HA	2:B:2633:VAL:HG12	1.94	0.49
1:A:217:PRO:HD3	1:A:230:ILE:HD11	1.94	0.49
2:B:250:LYS:HB3	2:B:289:PRO:HD2	1.95	0.48
2:B:798:VAL:HG22	2:B:814:ALA:HB2	1.94	0.48
1:A:319:HIS:HB2	1:A:510:LEU:HB3	1.96	0.46
1:A:210:VAL:HG22	1:A:238:SER:HB3	1.97	0.46
1:A:305:PRO:HG2	1:A:306:GLN:HE21	1.81	0.46
1:A:350:SER:HB3	1:A:519:ILE:HB	1.98	0.46
2:B:675:GLU:O	2:B:679:ARG:HG3	2.16	0.46
2:B:922:PHE:HB3	2:B:925:LEU:HD11	1.97	0.45
1:A:535:GLU:HG2	1:A:536:TRP:CD1	2.51	0.45
2:B:573:GLU:HG3	2:B:626:TRP:HD1	1.81	0.45
1:A:85:GLN:HA	2:B:250:LYS:HE2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:386:GLN:HE22	1:A:407:MET:HB3	1.81	0.45
1:A:414:PRO:HA	1:A:494:THR:HG23	1.98	0.45
2:B:831:ILE:HD11	2:B:856:LEU:CD2	2.46	0.44
2:B:803:GLN:HE21	2:B:812:PHE:HE2	1.66	0.44
1:A:506:ASN:HA	1:A:507:PRO:HD2	1.85	0.44
1:A:90:ASP:O	2:B:295:PRO:HD3	2.17	0.43
2:B:2578:HIS:HA	2:B:2579:PRO:HD3	1.91	0.43
2:B:478:ALA:HB1	2:B:506:LEU:HD21	2.00	0.43
2:B:514:HIS:CG	2:B:2607:LEU:HD22	2.54	0.42
2:B:594:GLU:HG2	2:B:621:LEU:HD22	2.01	0.42
1:A:114:ALA:HB1	1:A:141:ILE:HB	2.01	0.42
1:A:143:ASP:HB3	1:A:193:VAL:HG12	2.02	0.42
2:B:2565:SER:OG	2:B:2567:VAL:HG12	2.20	0.42
1:A:248:VAL:HG23	1:A:257:SER:HB3	2.01	0.41
1:A:383:VAL:CG1	1:A:408:LYS:HB2	2.49	0.41
1:A:329:MET:HG2	1:A:525:GLY:O	2.21	0.41
2:B:208:VAL:O	2:B:211:GLU:HG2	2.20	0.41
2:B:2657:LEU:HB3	2:B:2663:LEU:HB2	2.02	0.41
2:B:675:GLU:HB3	2:B:678:VAL:HG22	2.02	0.41
2:B:573:GLU:HG3	2:B:626:TRP:CD1	2.55	0.41
2:B:2627:ARG:HG2	2:B:2631:ARG:HD2	2.03	0.41
1:A:357:LEU:HD23	2:B:225:LEU:HD22	2.03	0.41
2:B:590:TRP:HZ2	2:B:627:ASP:HB3	1.86	0.40
2:B:866:TRP:CZ2	2:B:2026:ARG:HD3	2.56	0.40
2:B:629:HIS:HD2	2:B:633:GLN:HE22	1.69	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)
2:B:732:SER:OG	2:B:805:GLU:OE2[2_9510]	1.85	0.35
1:A:391:SER:OG	2:B:592:GLU:OE1[2_949]	2.10	0.10

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	473/605 (78%)	454 (96%)	15 (3%)	4 (1%)	19 49
2	B	821/938 (88%)	762 (93%)	53 (6%)	6 (1%)	22 52
3	D	5/11 (46%)	5 (100%)	0	0	100 100
All	All	1299/1554 (84%)	1221 (94%)	68 (5%)	10 (1%)	19 49

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	574	CYS
2	B	923	PRO
2	B	501	GLY
2	B	281	ASN
1	A	328	PHE
1	A	482	PRO
1	A	96	CYS
1	A	414	PRO
2	B	573	GLU
2	B	457	VAL

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	407/495 (82%)	385 (95%)	22 (5%)	22 51
2	B	733/815 (90%)	668 (91%)	65 (9%)	9 27
3	D	3/6 (50%)	2 (67%)	1 (33%)	0 0
All	All	1143/1316 (87%)	1055 (92%)	88 (8%)	13 34

All (88) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	LYS

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Mol	Chain	Res	Type
1	A	26	TYR
1	A	27	LEU
1	A	76	LYS
1	A	90	ASP
1	A	107	ASP
1	A	117	GLU
1	A	161	THR
1	A	175	GLN
1	A	188	TYR
1	A	197	ASP
1	A	226	ILE
1	A	258	ARG
1	A	269	ARG
1	A	308	ARG
1	A	314	ARG
1	A	332	ARG
1	A	351	LYS
1	A	365	ARG
1	A	386	GLN
1	A	392	LEU
1	A	551	ARG
2	B	198	THR
2	B	275	GLU
2	B	278	LYS
2	B	285	ARG
2	B	294	LYS
2	B	311	ARG
2	B	321	LEU
2	B	328	ARG
2	B	336	GLU
2	B	346	ASP
2	B	351	ASP
2	B	356	PHE
2	B	362	SER
2	B	405	GLN
2	B	415	GLN
2	B	420	LEU
2	B	446	ARG
2	B	454	LEU
2	B	465	LEU
2	B	473	PHE
2	B	474	ASP

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Mol	Chain	Res	Type
2	B	513	SER
2	B	515	ASP
2	B	528	ARG
2	B	529	CYS
2	B	551	GLU
2	B	571	ARG
2	B	572	ASN
2	B	574	CYS
2	B	575	TYR
2	B	576	ARG
2	B	585	GLN
2	B	586	GLN
2	B	623	ARG
2	B	629	HIS
2	B	632	LEU
2	B	633	GLN
2	B	639	LEU
2	B	645	ARG
2	B	660	LYS
2	B	664	MET
2	B	688	ASP
2	B	716	THR
2	B	738	GLN
2	B	744	ARG
2	B	797	VAL
2	B	798	VAL
2	B	807	CYS
2	B	833	HIS
2	B	848	ASP
2	B	852	LYS
2	B	922	PHE
2	B	2028	SER
2	B	2557	THR
2	B	2595	ASP
2	B	2616	ARG
2	B	2617	ARG
2	B	2634	ARG
2	B	2653	LEU
2	B	2662	VAL
2	B	2666	ARG
2	B	2670	GLU
2	B	2682	LEU

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Mol	Chain	Res	Type
2	B	2683	ARG
2	B	2685	GLN
3	D	28	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	ASN
1	A	207	HIS
1	A	386	GLN
2	B	234	GLN
2	B	359	GLN
2	B	363	GLN
2	B	609	GLN
2	B	633	GLN
2	B	803	GLN
2	B	833	HIS
2	B	880	ASN
2	B	881	HIS
2	B	2558	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)

1 non-standard protein/DNA/RNA residue is 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	M3L	D	27	3	10,11,12	0.57	0	9,14,16	0.40	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	M3L	D	27	3	-	0/9/10/12	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	$\#\|Z\| > 2$
5	SAM	B	8009	-	24,29,29	0.73	0	23,42,42	0.85	2 (8%)

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
5	SAM	B	8009	-	-	6/12/33/33	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	8009	SAM	CG-SD-C5'	-2.28	97.60	103.40
5	B	8009	SAM	C5-C6-N6	2.17	123.65	120.35

There are no chirality outliers.

All (6) torsion outliers are listed below:

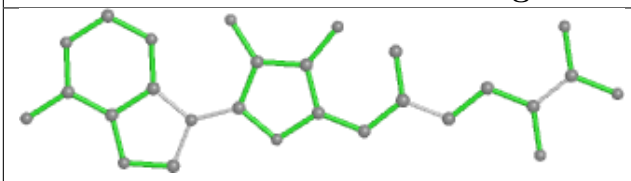
Mol	Chain	Res	Type	Atoms
5	B	8009	SAM	CB-CG-SD-CE
5	B	8009	SAM	CB-CG-SD-C5'
5	B	8009	SAM	C3'-C4'-C5'-SD
5	B	8009	SAM	O4'-C4'-C5'-SD
5	B	8009	SAM	OXT-C-CA-CB
5	B	8009	SAM	O-C-CA-CB

There are no ring outliers.

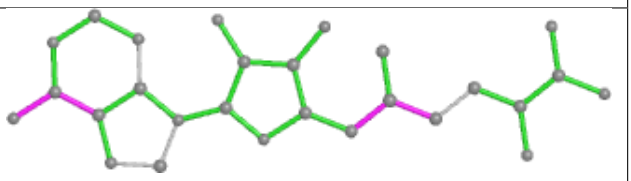
No monomer is involved in short contacts.

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.

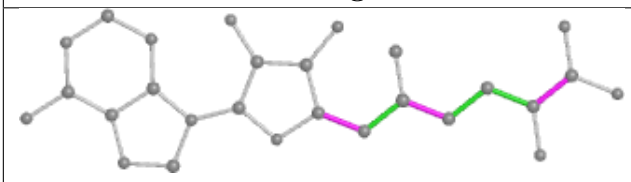
Ligand SAM B 8009



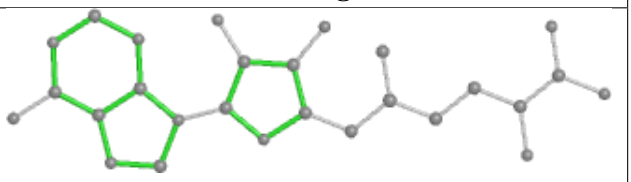
Bond lengths



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

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, 95^{th} 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	481/605 (79%)	-0.19	6 (1%) 79 80	21, 59, 111, 164	0
2	B	839/938 (89%)	0.23	62 (7%) 14 12	20, 84, 145, 184	0
3	D	7/11 (63%)	0.52	0 100 100	79, 93, 105, 118	0
All	All	1327/1554 (85%)	0.08	68 (5%) 28 27	20, 74, 137, 184	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	586	GLN	6.5
2	B	356	PHE	5.4
2	B	358	ILE	5.3
2	B	335	ALA	5.3
2	B	349	ASN	5.1
2	B	575	TYR	4.7
2	B	2022	THR	4.7
2	B	576	ARG	4.4
2	B	647	ILE	4.4
2	B	355	GLY	4.3
2	B	346	ASP	4.2
2	B	587	VAL	4.1
2	B	354	SER	4.0
2	B	646	THR	3.9
2	B	330	VAL	3.9
2	B	833	HIS	3.9
2	B	392	GLY	3.9
2	B	635	LEU	3.8
2	B	585	GLN	3.7
2	B	333	ASN	3.6
1	A	74	THR	3.4
2	B	334	SER	3.4
2	B	556	THR	3.4

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Mol	Chain	Res	Type	RSRZ
2	B	841	HIS	3.4
2	B	577	ILE	3.3
2	B	359	GLN	3.3
2	B	340	TYR	3.2
2	B	633	GLN	3.1
2	B	628	VAL	3.1
2	B	348	GLU	3.0
2	B	2671	ALA	2.9
2	B	276	TYR	2.9
2	B	281	ASN	2.9
2	B	632	LEU	2.8
2	B	282	SER	2.8
2	B	347	LEU	2.8
2	B	589	PRO	2.7
2	B	337	GLU	2.7
2	B	338	GLN	2.7
2	B	391	GLU	2.6
2	B	778	VAL	2.6
2	B	2634	ARG	2.6
2	B	343	TRP	2.6
2	B	341	SER	2.6
2	B	473	PHE	2.6
2	B	339	LYS	2.6
2	B	329	ASP	2.6
2	B	584	ASN	2.5
2	B	332	PRO	2.4
2	B	331	ASP	2.4
1	A	308	ARG	2.4
2	B	357	LYS	2.4
2	B	743	GLY	2.4
2	B	412	MET	2.4
1	A	556	ARG	2.3
2	B	920	ASP	2.3
2	B	429	GLY	2.2
1	A	221	ASN	2.2
1	A	522	ALA	2.2
2	B	345	MET	2.2
2	B	644	PRO	2.2
2	B	733	GLY	2.1
2	B	411	SER	2.1
1	A	75	ASP	2.1
2	B	598	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	336	GLU	2.1
2	B	2030	PRO	2.0
2	B	836	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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, 95^{th} 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	M3L	D	27	12/13	0.94	0.25	70,74,88,88	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

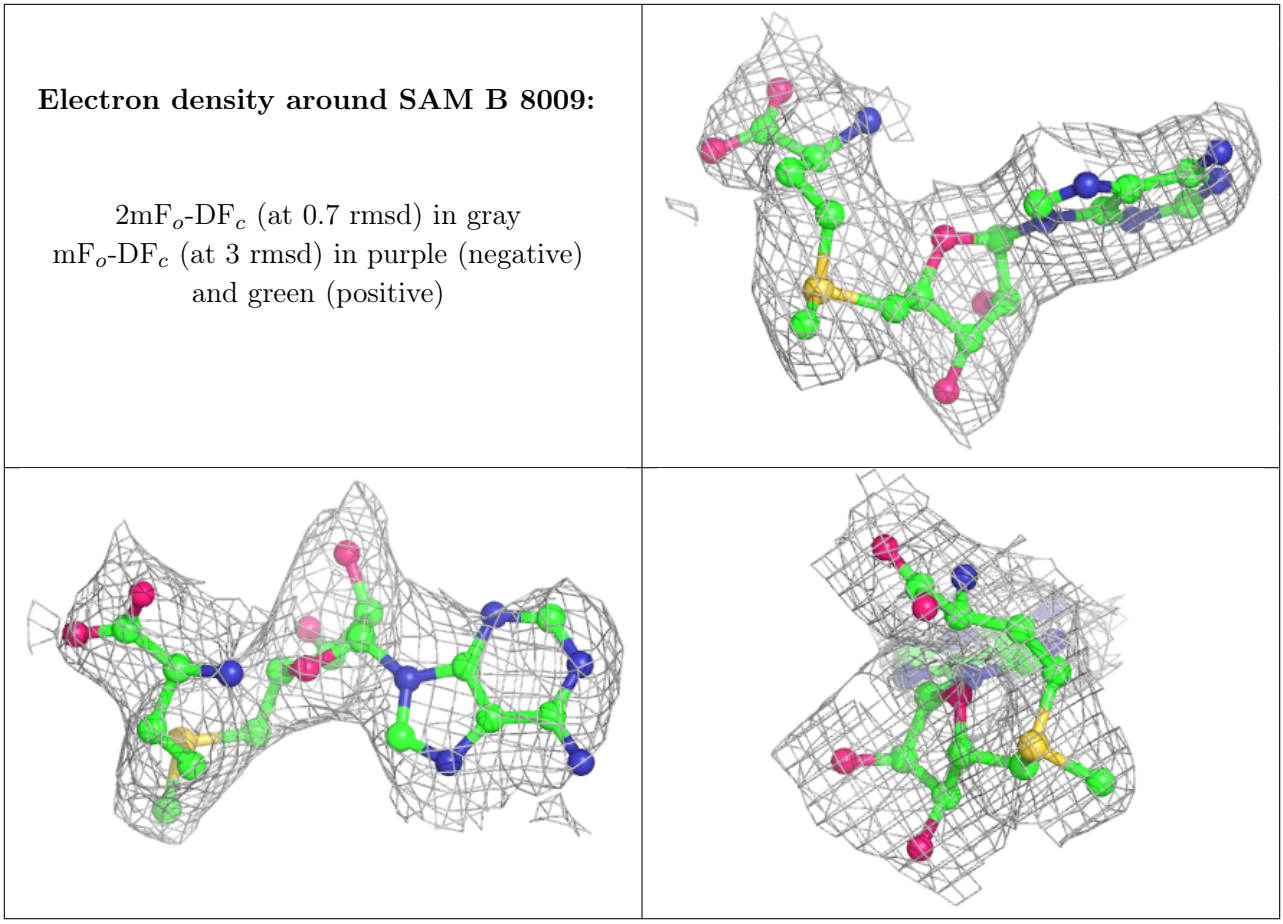
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
5	SAM	B	8009	27/27	0.94	0.18	71,87,93,95	0
4	ZN	B	8008	1/1	0.95	0.06	142,142,142,142	0
4	ZN	B	8004	1/1	0.99	0.14	72,72,72,72	0
4	ZN	B	8002	1/1	0.99	0.11	75,75,75,75	0
4	ZN	B	8003	1/1	0.99	0.10	86,86,86,86	0
4	ZN	B	8006	1/1	1.00	0.12	66,66,66,66	0
4	ZN	B	8007	1/1	1.00	0.17	40,40,40,40	0
4	ZN	B	8001	1/1	1.00	0.11	80,80,80,80	0
4	ZN	B	8005	1/1	1.00	0.11	69,69,69,69	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 SAM B 8009:

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



6.5 Other polymers (i)

There are no such residues in this entry.