



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 12:52 AM UTC

PDB ID : 5TQR / pdb_00005tqr
Title : ctPRC2 in an autoinhibited conformation bound to S-adenosylmethionine
Authors : Bratkowski, M.A.; Liu, X.
Deposited on : 2016-10-24
Resolution : 2.57 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

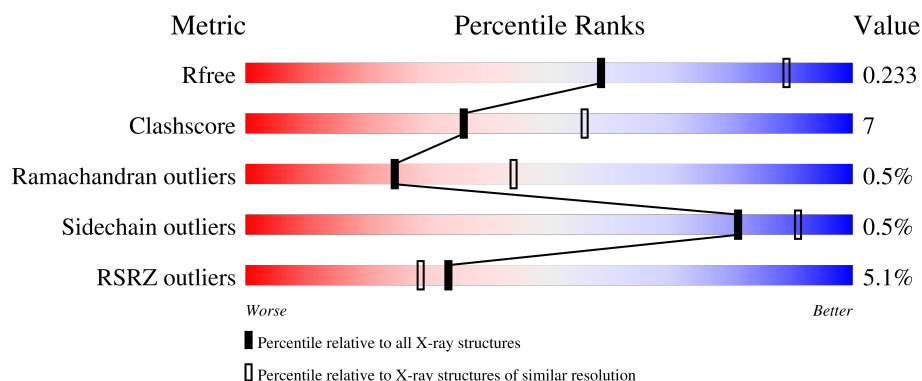
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.57 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}	180053	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (2.60-2.56)

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	3% 65% 12% 22%
2	B	937	5% 72% 14% 14%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10500 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 Polycomb Protein EED.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	470	3706	2366	639	682	19	0	2	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 Histone-lysine N-methyltransferase EZH2, Polycomb protein SUZ12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	809	Total	C	N	O	S	0	0	0
			6515	4096	1185	1193	41			

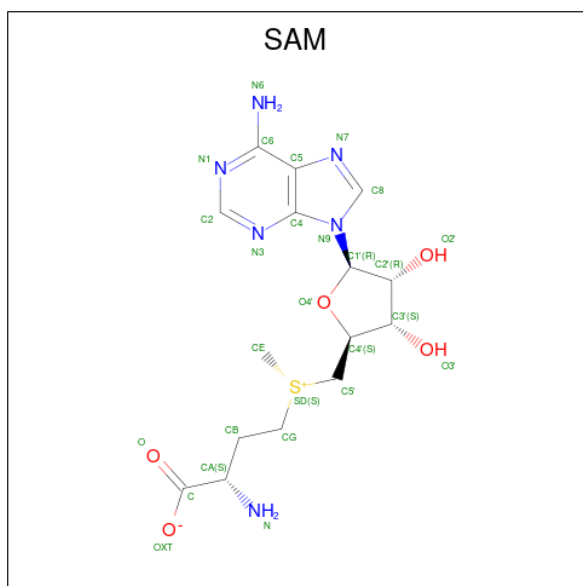
There are 15 discrepancies between the modelled and reference sequences:

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	-	linker	UNP G0SDW4
B	2525	VAL	-	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 (CCD ID: ZN) (formula: Zn).

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

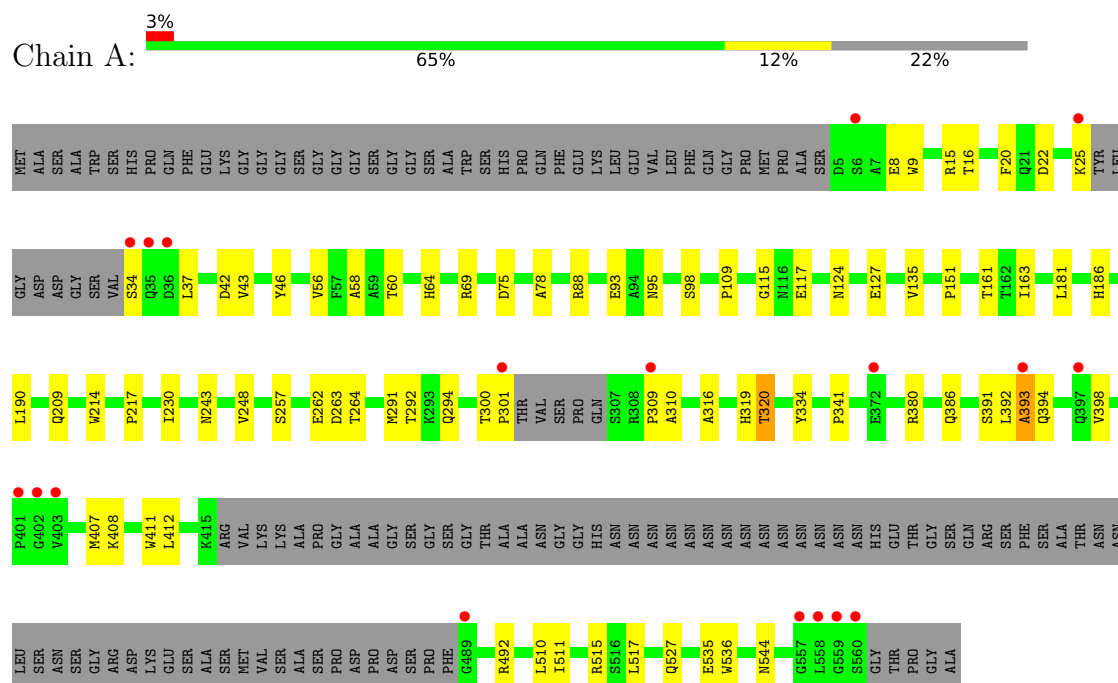
- Molecule 4 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



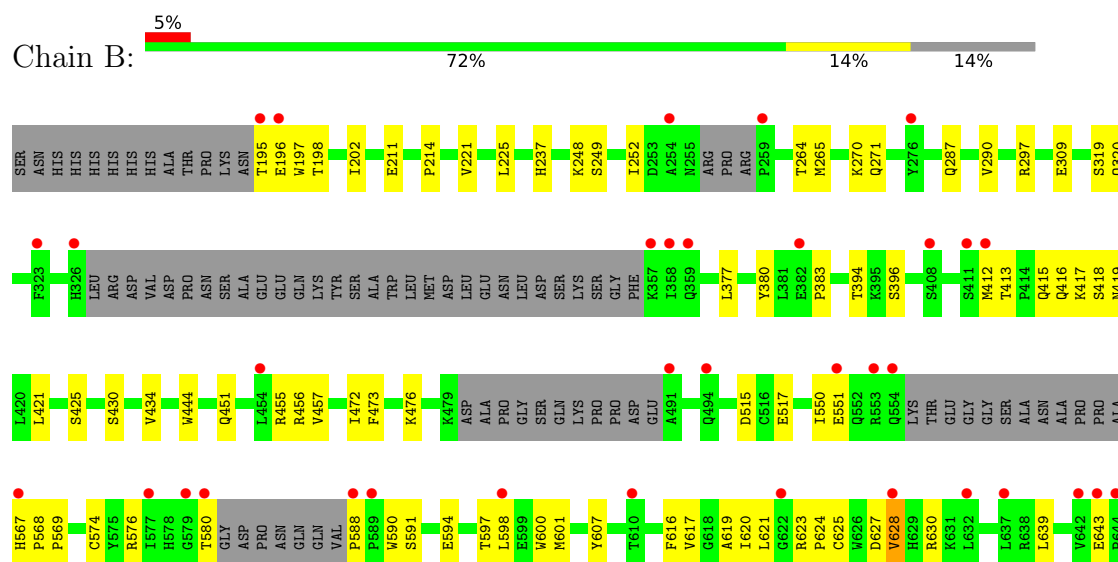
3 Residue-property plots [i](#)

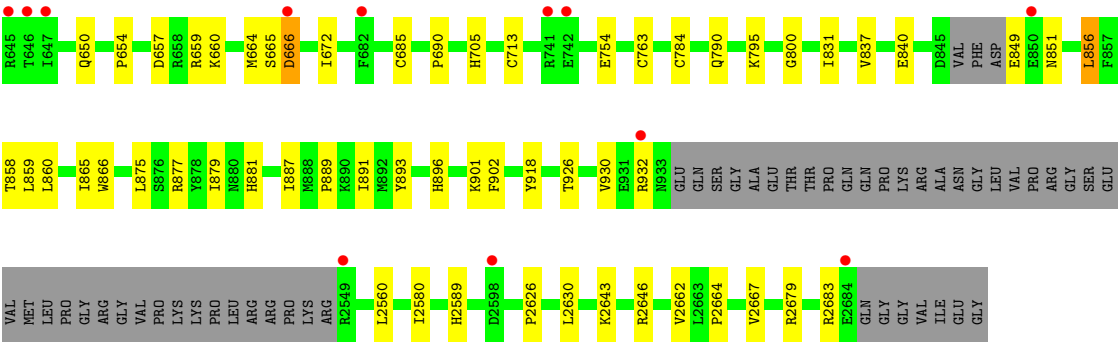
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Polycomb Protein EED



• Molecule 2: Histone-lysine N-methyltransferase EZH2, Polycomb protein SUZ12





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	117.45Å 138.01Å 223.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.32 – 2.57 47.32 – 2.57	Depositor EDS
% Data completeness (in resolution range)	95.4 (47.32-2.57) 95.4 (47.32-2.57)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 2.58Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.174 , 0.233 0.174 , 0.233	Depositor DCC
R_{free} test set	2733 reflections (4.72%)	wwPDB-VP
Wilson B-factor (Å ²)	44.0	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10500	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% 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: ZN, SAM

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	0.38	0/3818	0.60	0/5195
2	B	0.37	0/6664	0.57	0/9006
All	All	0.37	0/10482	0.58	0/14201

There are no bond length outliers.

There are no bond angle outliers.

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	3706	0	3574	54	0
2	B	6515	0	6403	101	0
3	B	8	0	0	0	0
4	B	27	0	22	1	0
5	A	92	0	0	2	0
5	B	152	0	0	5	0
All	All	10500	0	9999	148	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 7.

All (148) 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	1.07	1.00
2:B:881:HIS:CD2	2:B:918:TYR:H	1.95	0.84
2:B:591:SER:HB3	2:B:594:GLU:HG3	1.63	0.80
2:B:837:VAL:HG13	2:B:926:THR:HG22	1.67	0.76
2:B:550:ILE:HG13	2:B:551:GLU:OE1	1.86	0.74
2:B:309:GLU:HG2	2:B:2580:ILE:HG12	1.77	0.67
2:B:763:CYS:HB2	2:B:784:CYS:HB2	1.75	0.67
2:B:270:LYS:NZ	5:B:8101:HOH:O	2.10	0.67
2:B:590:TRP:CD1	2:B:623:ARG:HH21	2.12	0.66
1:A:25:LYS:HD3	1:A:25:LYS:H	1.60	0.66
2:B:643:GLU:H	2:B:643:GLU:CD	2.03	0.66
1:A:319:HIS:HB2	1:A:510:LEU:HB3	1.77	0.65
2:B:394:THR:HG22	2:B:396:SER:H	1.63	0.63
1:A:34:SER:HB2	1:A:37:LEU:HD12	1.79	0.63
2:B:515:ASP:OD2	2:B:2589:HIS:HD2	1.82	0.63
2:B:252:ILE:HD12	2:B:287:GLN:HB3	1.81	0.62
2:B:831:ILE:HD11	2:B:856:LEU:HD21	1.82	0.62
2:B:419:ASN:HB3	2:B:472:ILE:HG12	1.82	0.61
2:B:297:ARG:NH2	5:B:8105:HOH:O	2.31	0.61
2:B:248:LYS:HG3	2:B:249:SER:N	2.16	0.60
1:A:60:THR:HG23	5:A:607:HOH:O	1.99	0.60
2:B:517:GLU:OE2	2:B:2589:HIS:HE1	1.83	0.60
2:B:932:ARG:NH2	5:B:8103:HOH:O	2.34	0.60
2:B:567:HIS:O	2:B:576:ARG:NH2	2.35	0.59
2:B:860:LEU:HD12	2:B:865:ILE:HD12	1.83	0.59
2:B:451:GLN:NE2	2:B:456:ARG:HD2	2.17	0.58
1:A:248:VAL:HG23	1:A:257:SER:HB3	1.84	0.58
2:B:567:HIS:HB3	2:B:568:PRO:HD2	1.86	0.58
2:B:643:GLU:OE1	2:B:643:GLU:N	2.23	0.58
1:A:408:LYS:NZ	1:A:412:LEU:O	2.30	0.57
1:A:186:HIS:CG	1:A:190:LEU:HD21	2.40	0.57
2:B:598:LEU:HD22	2:B:628:VAL:HG23	1.87	0.57
1:A:294:GLN:NE2	5:A:603:HOH:O	2.38	0.56
2:B:421:LEU:HD13	2:B:425:SER:HA	1.87	0.56
1:A:15:ARG:HH22	2:B:271:GLN:HE21	1.54	0.56
2:B:412:MET:HG2	2:B:473:PHE:HE2	1.70	0.55
2:B:412:MET:HG2	2:B:473:PHE:CE2	2.42	0.55
2:B:881:HIS:HD2	2:B:918:TYR:N	1.91	0.55
2:B:418:SER:N	5:B:8107:HOH:O	2.39	0.55
1:A:60:THR:HG21	1:A:98:SER:HB3	1.87	0.54
1:A:93:GLU:HG3	1:A:117:GLU:H	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:ASP:C	1:A:320:THR:HG22	2.32	0.54
2:B:198:THR:O	2:B:202:ILE:HG13	2.07	0.54
2:B:248:LYS:NZ	2:B:249:SER:H	2.06	0.54
1:A:8:GLU:HG3	1:A:9:TRP:CD1	2.44	0.53
1:A:292:THR:HG22	2:B:320:GLN:NE2	2.24	0.53
1:A:181:LEU:HD13	1:A:214:TRP:CG	2.44	0.52
2:B:754:GLU:OE1	2:B:790:GLN:HG3	2.09	0.52
1:A:75:ASP:HB3	1:A:78:ALA:HB2	1.90	0.52
2:B:415:GLN:HA	2:B:418:SER:HB3	1.91	0.52
2:B:657:ASP:OD2	2:B:660:LYS:HG3	2.09	0.52
1:A:386:GLN:HG2	1:A:407:MET:HB3	1.92	0.52
1:A:515:ARG:HD3	1:A:517:LEU:HD21	1.92	0.51
2:B:412:MET:HE2	2:B:417:LYS:CD	2.41	0.50
2:B:569:PRO:N	2:B:576:ARG:HH21	2.10	0.50
2:B:650:GLN:OE1	2:B:690:PRO:HB3	2.11	0.50
2:B:430:SER:O	2:B:434:VAL:HG23	2.13	0.49
2:B:601:MET:HE2	2:B:616:PHE:CE2	2.47	0.49
1:A:20:PHE:HB3	1:A:544:ASN:HB3	1.95	0.49
2:B:197:TRP:CE3	2:B:202:ILE:HG12	2.46	0.49
2:B:672:ILE:HG23	2:B:705:HIS:HB2	1.94	0.49
2:B:412:MET:C	2:B:417:LYS:HZ3	2.20	0.49
2:B:580:THR:HA	2:B:630:ARG:HG3	1.95	0.49
2:B:412:MET:HE2	2:B:417:LYS:HD3	1.94	0.48
2:B:551:GLU:OE1	2:B:551:GLU:N	2.46	0.48
1:A:380:ARG:HG2	1:A:380:ARG:HH11	1.77	0.48
2:B:574:CYS:HA	2:B:625:CYS:HB3	1.95	0.48
2:B:377:LEU:HD12	2:B:457:VAL:HG11	1.95	0.48
2:B:849:GLU:HG3	2:B:851:ASN:H	1.79	0.48
1:A:320:THR:CG2	1:A:320:THR:O	2.62	0.47
2:B:265:MET:HG2	2:B:290:VAL:HG21	1.96	0.47
2:B:840:GLU:OE1	2:B:926:THR:HG23	2.15	0.47
2:B:619:ALA:O	2:B:2679:ARG:NH2	2.47	0.46
2:B:643:GLU:CD	2:B:643:GLU:N	2.71	0.46
1:A:217:PRO:HD3	1:A:230:ILE:HD11	1.97	0.46
2:B:926:THR:O	2:B:930:VAL:HG13	2.16	0.46
2:B:248:LYS:HG3	2:B:249:SER:H	1.80	0.46
2:B:211:GLU:O	2:B:214:PRO:HD2	2.16	0.46
2:B:2630:LEU:HD11	2:B:2667:VAL:HG12	1.98	0.45
1:A:151:PRO:HD3	2:B:237:HIS:CD2	2.52	0.45
1:A:411:TRP:CZ3	1:A:412:LEU:HD13	2.52	0.45
2:B:859:LEU:HD12	2:B:891:ILE:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:THR:OG1	2:B:271:GLN:NE2	2.49	0.45
1:A:161:THR:O	1:A:161:THR:HG22	2.17	0.45
2:B:394:THR:HG22	2:B:396:SER:N	2.29	0.45
2:B:607:TYR:CE1	2:B:639:LEU:HD13	2.51	0.45
2:B:195:THR:HG23	2:B:196:GLU:H	1.81	0.45
2:B:795:LYS:HD2	2:B:795:LYS:HA	1.80	0.45
1:A:25:LYS:HB2	1:A:34:SER:O	2.17	0.44
1:A:22:ASP:OD1	1:A:22:ASP:C	2.61	0.43
2:B:588:PRO:O	2:B:623:ARG:NH2	2.51	0.43
2:B:665:SER:OG	2:B:666:ASP:N	2.49	0.43
2:B:875:LEU:HA	2:B:875:LEU:HD23	1.82	0.43
2:B:893:TYR:CE2	2:B:896:HIS:HA	2.53	0.43
2:B:451:GLN:HE22	2:B:456:ARG:NH1	2.17	0.43
1:A:42:ASP:OD1	1:A:527:GLN:HG2	2.18	0.43
2:B:858:THR:HA	2:B:866:TRP:CD1	2.54	0.43
1:A:300:THR:HA	1:A:301:PRO:HD3	1.87	0.43
1:A:124:ASN:ND2	1:A:127:GLU:OE1	2.49	0.43
2:B:264:THR:HG21	2:B:287:GLN:OE1	2.19	0.43
2:B:517:GLU:OE2	2:B:2589:HIS:CE1	2.68	0.43
2:B:2664:PRO:O	2:B:2667:VAL:HG22	2.19	0.43
2:B:413:THR:O	2:B:416:GLN:HB2	2.19	0.42
1:A:75:ASP:HB3	1:A:78:ALA:CB	2.49	0.42
2:B:476:LYS:HD2	2:B:476:LYS:HA	1.83	0.42
1:A:25:LYS:HD3	1:A:25:LYS:N	2.32	0.42
2:B:879:ILE:HD13	2:B:887:ILE:HD11	2.00	0.42
2:B:417:LYS:O	2:B:421:LEU:HD23	2.20	0.42
2:B:617:VAL:HG13	2:B:621:LEU:HD12	2.01	0.42
2:B:659:ARG:HA	2:B:659:ARG:HD2	1.91	0.42
2:B:889:PRO:HA	2:B:901:LYS:O	2.19	0.42
2:B:624:PRO:O	2:B:627:ASP:HB3	2.20	0.42
1:A:135:VAL:HG21	2:B:297:ARG:HB3	2.01	0.42
1:A:163:ILE:HD12	1:A:190:LEU:HD13	2.01	0.42
1:A:398:VAL:O	1:A:398:VAL:HG12	2.19	0.42
1:A:43:VAL:HA	1:A:58:ALA:O	2.20	0.41
1:A:386:GLN:HG3	1:A:408:LYS:C	2.45	0.41
2:B:444:TRP:CD1	2:B:444:TRP:C	2.97	0.41
2:B:889:PRO:HB3	2:B:902:PHE:CE1	2.55	0.41
1:A:15:ARG:NH2	2:B:271:GLN:HE21	2.16	0.41
1:A:535:GLU:HG2	1:A:536:TRP:CD1	2.55	0.41
2:B:377:LEU:HD12	2:B:457:VAL:CG1	2.50	0.41
2:B:901:LYS:O	2:B:901:LYS:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:685:CYS:HB2	2:B:713:CYS:HB3	2.01	0.41
2:B:221:VAL:O	2:B:225:LEU:HG	2.21	0.41
1:A:64:HIS:CD2	1:A:88:ARG:HB2	2.55	0.41
1:A:386:GLN:HG3	1:A:408:LYS:O	2.21	0.41
2:B:597:THR:HA	2:B:600:TRP:CE2	2.56	0.41
2:B:2643:LYS:HB3	2:B:2646:ARG:HD2	2.03	0.41
1:A:209:GLN:HG2	1:A:243:ASN:C	2.46	0.41
2:B:2626:PRO:HG3	2:B:2664:PRO:HD3	2.02	0.41
1:A:46:TYR:CE1	1:A:109:PRO:HB3	2.55	0.41
1:A:262:GLU:O	1:A:264:THR:HG23	2.20	0.41
1:A:394:GLN:O	1:A:398:VAL:HG23	2.21	0.41
1:A:492:ARG:HG2	1:A:492:ARG:NH1	2.36	0.41
2:B:380:TYR:C	2:B:383:PRO:HD2	2.46	0.41
2:B:455:ARG:NH1	5:B:8121:HOH:O	2.54	0.41
1:A:56:VAL:HG22	1:A:69:ARG:HB2	2.02	0.41
1:A:320:THR:O	1:A:320:THR:HG23	2.21	0.41
1:A:391:SER:O	1:A:393:ALA:N	2.53	0.41
2:B:800:GLY:HA3	2:B:2560:LEU:HD23	2.03	0.41
1:A:291:MET:HE3	2:B:319:SER:HA	2.04	0.40
2:B:877:ARG:O	4:B:8009:SAM:HE2	2.21	0.40
1:A:316:ALA:HB1	1:A:511:ILE:HD11	2.03	0.40
1:A:334:TYR:O	1:A:341:PRO:HA	2.21	0.40
2:B:654:PRO:O	2:B:664:MET:HG3	2.21	0.40
2:B:601:MET:HE2	2:B:616:PHE:CD2	2.56	0.40
1:A:95:ASN:HA	1:A:115:GLY:HA3	2.04	0.40

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	464/605 (77%)	442 (95%)	18 (4%)	4 (1%)	14 29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	793/937 (85%)	759 (96%)	32 (4%)	2 (0%)	36	56
All	All	1257/1542 (82%)	1201 (96%)	50 (4%)	6 (0%)	24	44

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	310	ALA
1	A	393	ALA
2	B	666	ASP
2	B	2683	ARG
1	A	309	PRO
1	A	392	LEU

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	396/495 (80%)	395 (100%)	1 (0%)	86	94
2	B	709/816 (87%)	705 (99%)	4 (1%)	78	89
All	All	1105/1311 (84%)	1100 (100%)	5 (0%)	81	91

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	320	THR
2	B	620	ILE
2	B	628	VAL
2	B	856	LEU
2	B	2662	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	GLN
1	A	119	ASN
1	A	209	GLN
1	A	212	ASN
1	A	326	GLN
2	B	222	ASN
2	B	237	HIS
2	B	271	GLN
2	B	449	ASN
2	B	451	GLN
2	B	526	GLN
2	B	662	GLN
2	B	695	ASN
2	B	881	HIS
2	B	2558	GLN
2	B	2589	HIS
2	B	2592	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	SAM	B	8009	-	27,29,29	1.15	4 (14%)	34,42,42	1.83	8 (23%)

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	SAM	B	8009	-	-	4/17/33/33	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	8009	SAM	C2-N3	2.70	1.38	1.33
4	B	8009	SAM	C2-N1	2.67	1.38	1.33
4	B	8009	SAM	C8-N7	2.47	1.36	1.31
4	B	8009	SAM	C5-N7	-2.02	1.35	1.39

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	8009	SAM	N3-C2-N1	-5.19	120.73	128.58
4	B	8009	SAM	C5-C4-N3	-4.55	120.45	126.72
4	B	8009	SAM	C2-N3-C4	3.29	119.86	111.83
4	B	8009	SAM	N9-C8-N7	-3.17	109.44	113.94
4	B	8009	SAM	C5-N7-C8	2.93	108.06	103.45
4	B	8009	SAM	N3-C4-N9	2.76	131.86	127.17
4	B	8009	SAM	OXT-C-O	-2.20	119.08	124.08
4	B	8009	SAM	C4-C5-N7	-2.18	108.08	110.58

There are no chirality outliers.

All (4) torsion outliers are listed below:

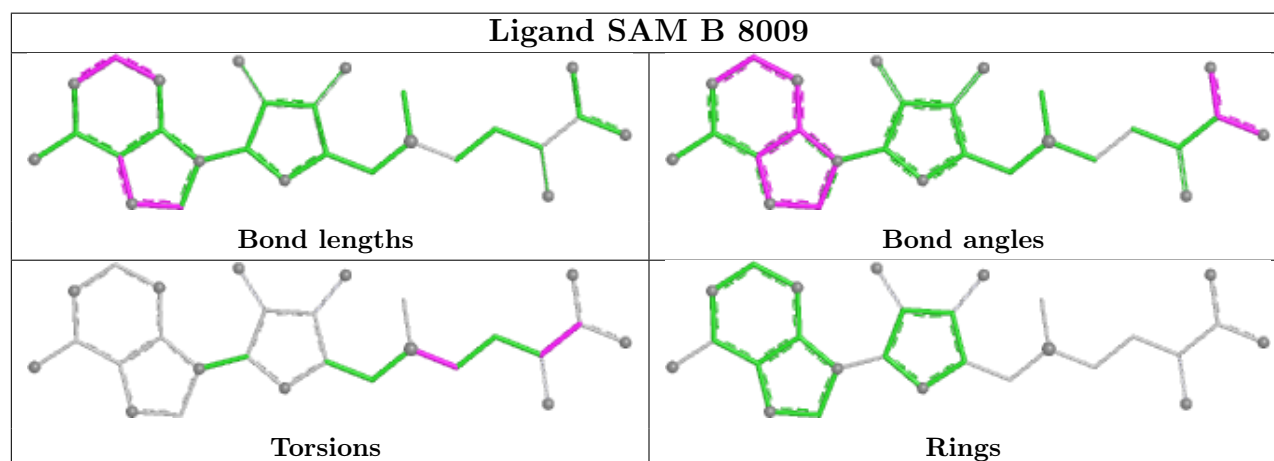
Mol	Chain	Res	Type	Atoms
4	B	8009	SAM	CB-CG-SD-CE
4	B	8009	SAM	CB-CG-SD-C5'
4	B	8009	SAM	O-C-CA-CB
4	B	8009	SAM	OXT-C-CA-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	8009	SAM	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	470/605 (77%)	-0.11	18 (3%) 44 39	18, 39, 94, 129	2 (0%)
2	B	809/937 (86%)	0.21	47 (5%) 29 24	24, 51, 98, 132	0
All	All	1279/1542 (82%)	0.09	65 (5%) 33 29	18, 47, 98, 132	2 (0%)

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	558	LEU	4.5
2	B	628	VAL	4.2
2	B	259	PRO	4.2
2	B	323	PHE	4.1
2	B	580	THR	4.1
2	B	254	ALA	4.0
2	B	195	THR	4.0
2	B	326	HIS	3.8
2	B	647	ILE	3.8
2	B	358	ILE	3.6
2	B	196	GLU	3.5
2	B	642	VAL	3.5
1	A	560	SER	3.3
1	A	401	PRO	3.3
2	B	588	PRO	3.2
2	B	622	GLY	3.2
1	A	403	VAL	3.0
2	B	567	HIS	3.0
2	B	579	GLY	3.0
2	B	408	SER	3.0
1	A	34	SER	2.9
2	B	632	LEU	2.9
2	B	359	GLN	2.8
1	A	301	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
2	B	598	LEU	2.7
2	B	491	ALA	2.7
1	A	489	GLY	2.7
2	B	644	PRO	2.7
1	A	6	SER	2.7
2	B	2684	GLU	2.7
2	B	577	ILE	2.6
1	A	36	ASP	2.6
2	B	645	ARG	2.5
2	B	666	ASP	2.5
2	B	554	GLN	2.5
2	B	2549	ARG	2.5
2	B	646	THR	2.5
2	B	643	GLU	2.4
2	B	553	ARG	2.4
2	B	589	PRO	2.4
2	B	850	GLU	2.4
2	B	932	ARG	2.4
2	B	610	THR	2.3
1	A	559	GLY	2.3
2	B	2598	ASP	2.3
2	B	276	TYR	2.3
2	B	742	GLU	2.3
1	A	35	GLN	2.3
2	B	682	PHE	2.3
1	A	393	ALA	2.3
1	A	25	LYS	2.2
2	B	412	MET	2.2
2	B	454	LEU	2.2
2	B	411	SER	2.2
1	A	309	PRO	2.2
2	B	382	GLU	2.2
2	B	494	GLN	2.1
1	A	557	GLY	2.1
1	A	402	GLY	2.1
2	B	741	ARG	2.1
2	B	357	LYS	2.1
2	B	551	GLU	2.1
1	A	397	GLN	2.0
1	A	372	GLU	2.0
2	B	637	LEU	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

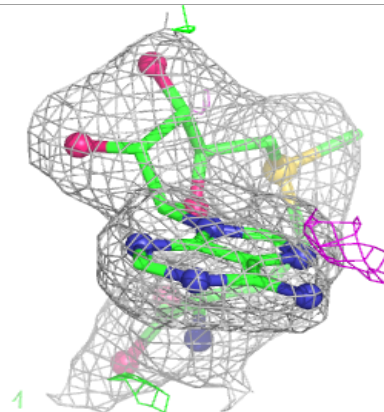
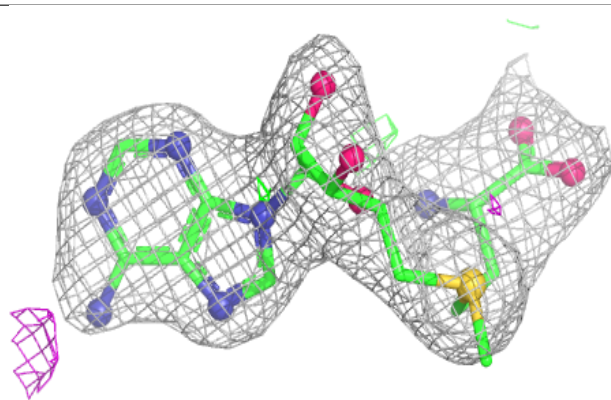
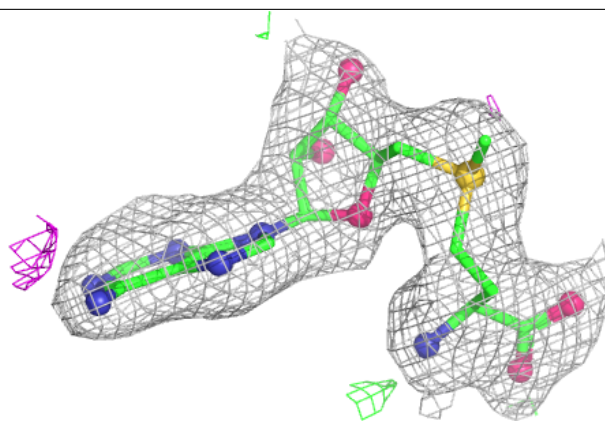
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	SAM	B	8009	27/27	0.96	0.08	31,42,54,56	0
3	ZN	B	8003	1/1	0.99	0.03	40,40,40,40	0
3	ZN	B	8005	1/1	0.99	0.03	48,48,48,48	0
3	ZN	B	8008	1/1	0.99	0.02	73,73,73,73	0
3	ZN	B	8002	1/1	0.99	0.02	33,33,33,33	0
3	ZN	B	8006	1/1	1.00	0.03	49,49,49,49	0
3	ZN	B	8007	1/1	1.00	0.03	32,32,32,32	0
3	ZN	B	8004	1/1	1.00	0.02	52,52,52,52	0
3	ZN	B	8001	1/1	1.00	0.03	36,36,36,36	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.