



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 10:11 PM GMT

PDB ID : 5CH2
Title : Crystal structure of an active polycomb repressive complex 2 in the basal state
Authors : Jiao, L.; Liu, X.
Deposited on : 2015-07-10
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

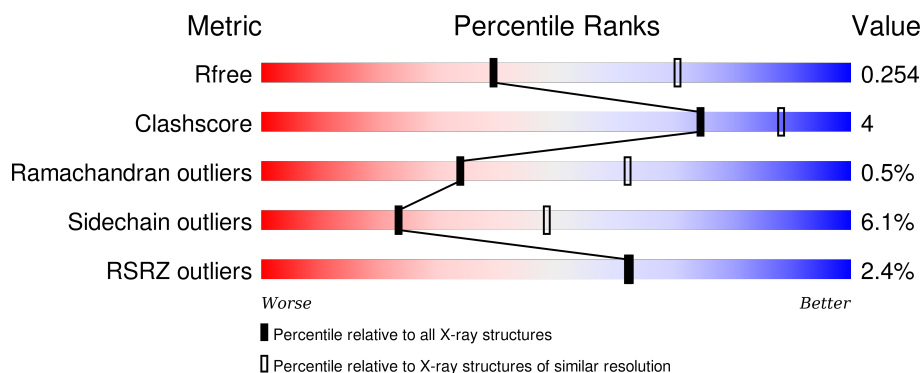
1 Overall quality at a glance

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}	91344	2439 (2.74-2.70)
Clashscore	102246	2771 (2.74-2.70)
Ramachandran outliers	100387	2726 (2.74-2.70)
Sidechain outliers	100360	2727 (2.74-2.70)
RSRZ outliers	91569	2443 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	<div> <div>100%</div> <div> <div>69%</div> <div>10%</div> <div>21%</div> </div> </div>
2	B	937	<div> <div>2%</div> <div> <div>68%</div> <div>11%</div> <div>20%</div> </div> </div>
3	E	20	<div> <div>10%</div> <div> <div>25%</div> <div>5%</div> <div>5%</div> <div>65%</div> </div> </div>

2 Entry composition

There are 6 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
1	A	479	Total	C	N	O	S	0	0	0
			3762	2403	645	694	20			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-39	MET	-	initiating methionine	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 polycomb protein Ezh2, putative polycomb protein Suz12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	754	Total	C	N	O	S	0	0	0
			6072	3827	1097	1107	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

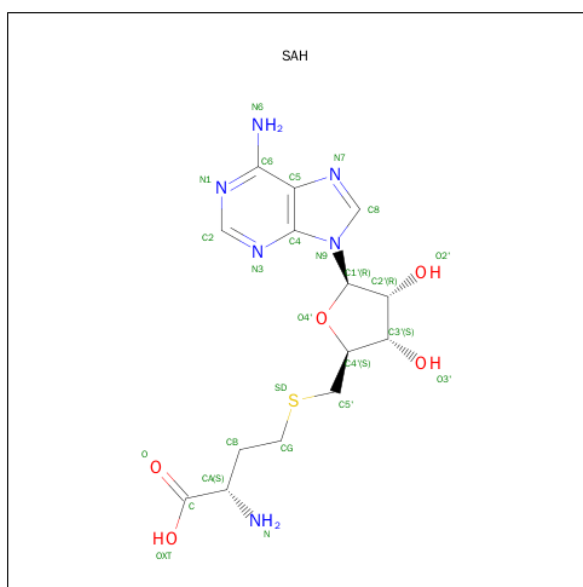
- Molecule 3 is a protein called 20-Mer peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	7	Total	C	N	O	S	0	0	0
			49	29	10	9	1			

- 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		

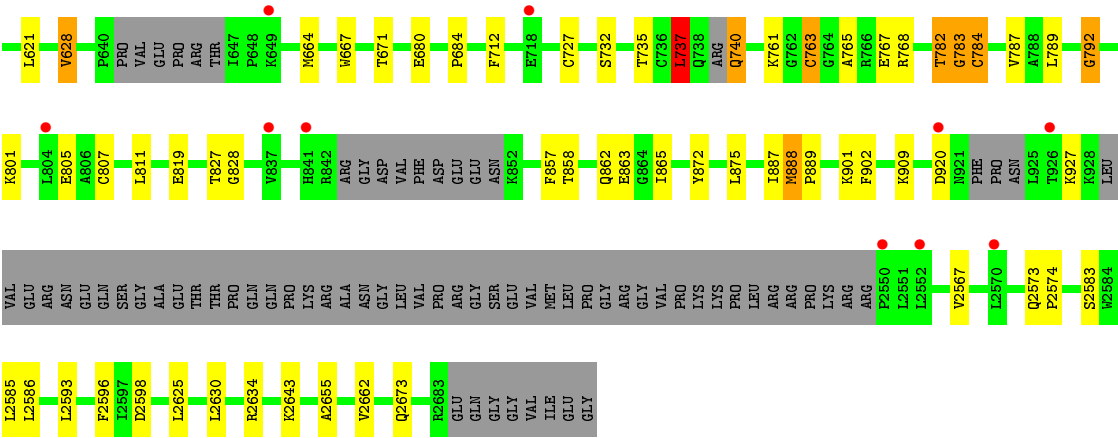
- Molecule 5 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: C₁₄H₂₀N₆O₅S).



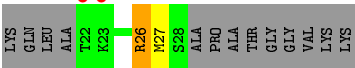
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	48	Total	O	0	0
			48	48		
6	B	63	Total	O	0	0
			63	63		



• Molecule 3: 20-Mer peptide



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)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.180 , 0.249 0.180 , 0.254	Depositor DCC
R_{free} test set	1826 reflections (5.19%)	DCC
Wilson B-factor (Å ²)	43.0	Xtriage
Anisotropy	0.093	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 64.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 37064 reflections	Xtriage
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

Xtriage'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, 0.375 respectively for untwinned datasets, and 0.333, 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, SAH

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	0/6202	0.72	3/8366 (0.0%)
3	E	0.55	0/48	0.98	0/62
All	All	0.52	0/10123	0.71	3/13704 (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	6.17	137.13	121.70
2	B	737	LEU	C-N-CA	5.77	136.14	121.70
2	B	792	GLY	C-N-CA	5.24	134.80	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	25	1
2	B	6072	0	5977	56	1
3	E	49	0	49	1	0
4	B	8	0	0	0	0
5	B	26	0	19	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	48	0	0	0	0
6	B	63	0	0	0	0
All	All	10028	0	9664	78	1

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 4.

All (78) 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:460:ARG:O	2:B:464:MET:HG2	1.81	0.80
1:A:160:ASP:O	1:A:161:THR:HB	1.86	0.75
2:B:454:LEU:HD23	2:B:456:ARG:HH21	1.53	0.72
2:B:763:CYS:HB3	2:B:765:ALA:H	1.57	0.69
2:B:2630:LEU:O	2:B:2634:ARG:HG3	1.96	0.66
1:A:326:GLN:HB2	1:A:329:MET:HE1	1.80	0.64
2:B:452:SER:HB3	2:B:454:LEU:HD13	1.81	0.62
2:B:454:LEU:N	2:B:455:ARG:HA	2.16	0.61
1:A:67:ILE:HB	1:A:85:GLN:HB3	1.84	0.59
1:A:316:ALA:HB1	1:A:511:ILE:HD11	1.84	0.59
2:B:887:ILE:HD12	2:B:902:PHE:CD1	2.38	0.58
2:B:768:ARG:HH21	2:B:782:THR:HB	1.69	0.57
2:B:2583:SER:HA	2:B:2586:LEU:HD12	1.85	0.57
2:B:2625:LEU:HD23	2:B:2662:VAL:HG12	1.87	0.56
1:A:326:GLN:HB2	1:A:329:MET:CE	2.35	0.56
1:A:186:HIS:CG	1:A:190:LEU:HD21	2.41	0.56
2:B:2625:LEU:HD23	2:B:2662:VAL:CG1	2.36	0.55
2:B:789:LEU:HD21	2:B:901:LYS:HB3	1.89	0.55
2:B:612:ARG:HE	2:B:613:PRO:HD2	1.71	0.54
2:B:735:THR:H	2:B:783:GLY:HA2	1.72	0.54
2:B:2573:GLN:HG2	2:B:2574:PRO:HD2	1.88	0.54
2:B:452:SER:N	2:B:454:LEU:HD22	2.17	0.54
2:B:768:ARG:HD3	2:B:784:CYS:O	2.08	0.53
1:A:66:VAL:HG22	1:A:86:LEU:HD13	1.91	0.53
2:B:614:GLU:HA	2:B:628:VAL:CG2	2.39	0.52
2:B:314:ILE:HG21	2:B:2585:LEU:HD21	1.91	0.51
2:B:828:GLY:HA2	2:B:872:TYR:O	2.10	0.51
2:B:457:VAL:HG12	2:B:461:ASP:HB2	1.93	0.51
1:A:258:ARG:NH2	1:A:329:MET:HE3	2.26	0.50
1:A:293:LYS:HE3	1:A:308:ARG:HE	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:372:GLU:O	2:B:376:THR:HG23	2.13	0.49
2:B:236:ARG:HH11	2:B:236:ARG:HG3	1.76	0.49
2:B:604:THR:HG21	2:B:2655:ALA:HB1	1.95	0.49
2:B:763:CYS:HB3	2:B:765:ALA:N	2.27	0.48
2:B:535:ILE:HD11	2:B:684:PRO:HG2	1.96	0.47
2:B:612:ARG:NE	2:B:613:PRO:HD2	2.30	0.47
2:B:737:LEU:H	2:B:740:GLN:HG3	1.78	0.47
2:B:594:GLU:HG2	2:B:621:LEU:HD22	1.97	0.47
1:A:83:ILE:HB	2:B:288:TYR:CE2	2.50	0.47
2:B:888:MET:HG2	2:B:889:PRO:HD2	1.98	0.46
2:B:317:LEU:HD22	2:B:525:ASN:HB3	1.97	0.46
2:B:198:THR:HG23	2:B:201:LYS:H	1.80	0.46
2:B:313:ASN:OD1	2:B:827:THR:HA	2.16	0.45
2:B:509:LEU:HB3	2:B:712:PHE:CE1	2.51	0.45
1:A:163:ILE:HB	1:A:181:LEU:HB2	1.98	0.45
1:A:217:PRO:HG3	1:A:228:ILE:HG21	1.98	0.45
2:B:499:ALA:HB1	2:B:600:TRP:CE3	2.53	0.44
2:B:591:SER:O	2:B:595:VAL:HG13	2.18	0.44
1:A:300:THR:HA	1:A:301:PRO:HD3	1.90	0.44
2:B:680:GLU:HG3	2:B:862:GLN:HG3	2.00	0.43
2:B:314:ILE:CG2	2:B:2585:LEU:HD21	2.48	0.43
2:B:667:TRP:O	2:B:671:THR:HG22	2.18	0.43
2:B:535:ILE:HD13	2:B:535:ILE:HA	1.73	0.43
2:B:403:ALA:HB2	2:B:420:LEU:HD23	2.00	0.43
1:A:120:VAL:HB	1:A:134:LEU:HB2	2.00	0.43
1:A:175:GLN:HG2	2:B:2567:VAL:HG21	2.00	0.43
2:B:452:SER:CB	2:B:454:LEU:HD13	2.48	0.43
1:A:523:PHE:HE1	1:A:545:ARG:HB2	1.84	0.43
1:A:196:HIS:HB2	1:A:201:TYR:HB2	2.00	0.43
2:B:863:GLU:HG3	2:B:865:ILE:HD12	1.99	0.42
1:A:300:THR:HB	1:A:311:MET:HG2	2.01	0.42
1:A:46:TYR:CE1	1:A:109:PRO:HB3	2.54	0.42
1:A:106:THR:HG23	1:A:108:GLN:HB2	2.01	0.42
2:B:927:LYS:HG3	5:B:8009:SAH:H2	2.01	0.42
2:B:450:ASP:O	2:B:454:LEU:HD21	2.20	0.41
2:B:268:LYS:HB2	2:B:285:ARG:HG3	2.02	0.41
1:A:319:HIS:HB2	1:A:510:LEU:HB3	2.02	0.41
2:B:531:SER:O	2:B:534:GLU:HB3	2.20	0.41
2:B:454:LEU:N	2:B:455:ARG:CA	2.83	0.41
1:A:350:SER:HB3	1:A:519:ILE:HB	2.02	0.41
1:A:90:ASP:HB3	2:B:294:LYS:HG3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:ALA:HB1	1:A:141:ILE:HB	2.03	0.40
1:A:70:LEU:HD21	1:A:548:ILE:HD13	2.02	0.40
2:B:539:MET:HB3	2:B:543:ARG:NH1	2.36	0.40
2:B:2593:LEU:HA	2:B:2596:PHE:HD2	1.87	0.40
2:B:857:PHE:HA	3:E:26:ARG:HB3	2.02	0.40
2:B:811:LEU:HD13	2:B:875:LEU:HB3	2.03	0.40

All (1) 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]	2.16	0.04

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%)	452 (96%)	19 (4%)	0	100	100
2	B	724/937 (77%)	687 (95%)	32 (4%)	5 (1%)	26	54
3	E	5/20 (25%)	2 (40%)	2 (40%)	1 (20%)	0	0
All	All	1200/1562 (77%)	1141 (95%)	53 (4%)	6 (0%)	34	62

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	391	GLU
2	B	783	GLY
2	B	792	GLY
2	B	425	SER
3	E	26	ARG
2	B	434	VAL

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	404/495 (82%)	383 (95%)	21 (5%)	29	56
2	B	659/816 (81%)	616 (94%)	43 (6%)	21	45
3	E	4/13 (31%)	3 (75%)	1 (25%)	1	2
All	All	1067/1324 (81%)	1002 (94%)	65 (6%)	23	48

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	THR
1	A	72	GLN
1	A	76	LYS
1	A	82	GLU
1	A	90	ASP
1	A	171	GLU
1	A	173	GLU
1	A	175	GLN
1	A	188	TYR
1	A	226	ILE
1	A	258	ARG
1	A	298	TYR
1	A	332	ARG
1	A	336	VAL
1	A	349	LYS
1	A	351	LYS
1	A	384	VAL
1	A	385	ASP
1	A	390	ILE
1	A	492	ARG
1	A	520	ASP
2	B	201	LYS
2	B	234	GLN
2	B	265	MET
2	B	282	SER
2	B	285	ARG

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Mol	Chain	Res	Type
2	B	297	ARG
2	B	362	SER
2	B	363	GLN
2	B	376	THR
2	B	396	SER
2	B	397	ASN
2	B	435	ARG
2	B	442	GLU
2	B	455	ARG
2	B	457	VAL
2	B	473	PHE
2	B	490	GLU
2	B	517	GLU
2	B	535	ILE
2	B	586	GLN
2	B	612	ARG
2	B	628	VAL
2	B	664	MET
2	B	727	CYS
2	B	732	SER
2	B	737	LEU
2	B	740	GLN
2	B	761	LYS
2	B	763	CYS
2	B	767	GLU
2	B	782	THR
2	B	787	VAL
2	B	801	LYS
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	920	ASP
2	B	2598	ASP
2	B	2643	LYS
2	B	2673	GLN
3	E	27	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
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 carbohydrates 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	SAH	B	8009	-	22,28,28	0.52	0	18,40,40	0.66	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
5	SAH	B	8009	-	-	0/7/31/31	0/3/3/3

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	8009	SAH	1	0

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%) 84 85	16, 38, 72, 97	0
2	B	754/937 (80%)	0.05	23 (3%) 52 53	18, 50, 87, 117	0
3	E	7/20 (35%)	0.73	2 (28%) 1 0	64, 74, 84, 90	0
All	All	1240/1562 (79%)	-0.01	30 (2%) 62 62	16, 46, 81, 117	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	276	TYR	4.2
2	B	391	GLU	4.0
2	B	363	GLN	3.9
2	B	472	ILE	3.7
2	B	577	ILE	3.7
1	A	492	ARG	3.0
2	B	362	SER	3.0
2	B	523	ARG	2.9
2	B	926	THR	2.8
2	B	401	PHE	2.8
3	E	22	THR	2.7
2	B	920	ASP	2.7
2	B	452	SER	2.6
1	A	390	ILE	2.6
2	B	718	GLU	2.6
2	B	414	PRO	2.5
2	B	2570	LEU	2.5
2	B	252	ILE	2.4
2	B	2550	PRO	2.3
1	A	303	VAL	2.3
2	B	649	LYS	2.2
2	B	837	VAL	2.2
2	B	468	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	556	ARG	2.2
2	B	804	LEU	2.1
2	B	841	HIS	2.1
1	A	304	SER	2.1
3	E	23	LYS	2.1
2	B	435	ARG	2.1
2	B	2552	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
4	ZN	B	8007	1/1	1.00	0.17	1.28	31,31,31,31	0
4	ZN	B	8006	1/1	1.00	0.17	1.01	40,40,40,40	0
4	ZN	B	8001	1/1	1.00	0.15	0.11	41,41,41,41	0
5	SAH	B	8009	26/26	0.94	0.20	0.07	46,56,66,67	0
4	ZN	B	8005	1/1	0.99	0.14	-0.05	46,46,46,46	0
4	ZN	B	8002	1/1	0.99	0.14	-0.62	44,44,44,44	0
4	ZN	B	8003	1/1	0.99	0.14	-0.69	51,51,51,51	0
4	ZN	B	8004	1/1	0.99	0.11	-1.24	50,50,50,50	0
4	ZN	B	8008	1/1	0.99	0.07	-1.59	52,52,52,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.