



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 12:02 PM UTC

PDB ID : 7MXA / pdb_00007mxa
Title : PRMT5:MEP50 complexed with inhibitor PF-06855800
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Deposited on : 2021-05-18
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 : 4-5-2 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

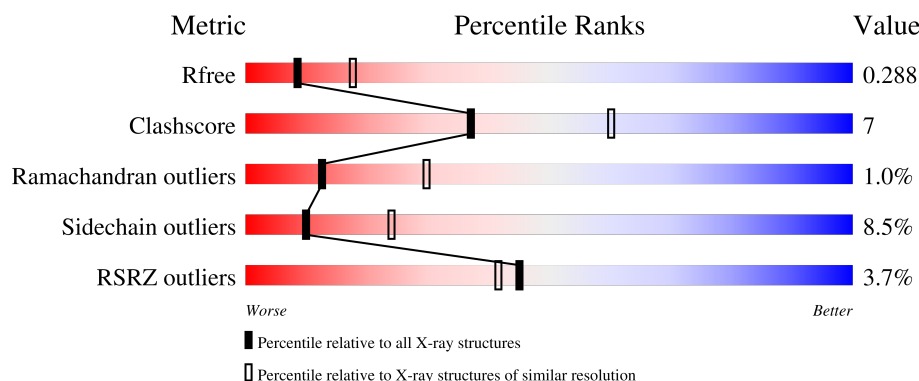
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.71 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}	180053	4348 (2.74-2.70)
Clashscore	190562	4665 (2.74-2.70)
Ramachandran outliers	187476	4584 (2.74-2.70)
Sidechain outliers	187428	4585 (2.74-2.70)
RSRZ outliers	180081	4348 (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	637	2% 76% 20% ..
2	B	366	6% 59% 22% • 16%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7537 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 Protein arginine N-methyltransferase 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	621	Total	C	N	O	S	0	1	0
			5031	3217	865	924	25			

- Molecule 2 is a protein called Methylosome protein 50.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	307	Total	C	N	O	S	0	0	0
			2317	1454	396	453	14			

There are 25 discrepancies between the modelled and reference sequences:

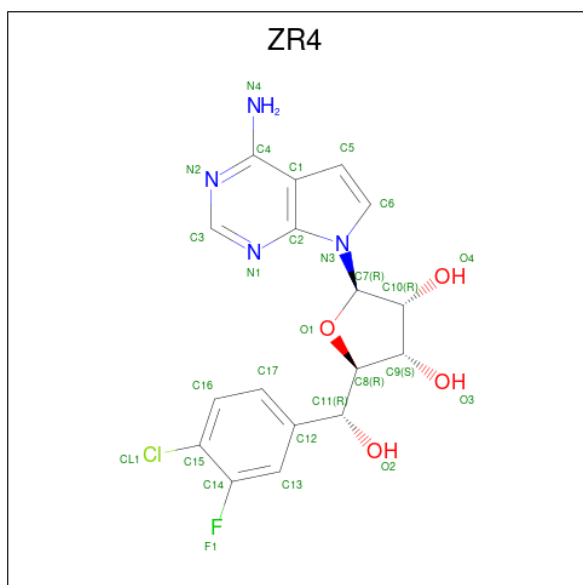
Chain	Residue	Modelled	Actual	Comment	Reference
B	-23	MET	-	expression tag	UNP Q9BQA1
B	-22	ALA	-	expression tag	UNP Q9BQA1
B	-21	SER	-	expression tag	UNP Q9BQA1
B	-20	HIS	-	expression tag	UNP Q9BQA1
B	-19	HIS	-	expression tag	UNP Q9BQA1
B	-18	HIS	-	expression tag	UNP Q9BQA1
B	-17	HIS	-	expression tag	UNP Q9BQA1
B	-16	HIS	-	expression tag	UNP Q9BQA1
B	-15	HIS	-	expression tag	UNP Q9BQA1
B	-14	ASP	-	expression tag	UNP Q9BQA1
B	-13	TYR	-	expression tag	UNP Q9BQA1
B	-12	ASP	-	expression tag	UNP Q9BQA1
B	-11	GLY	-	expression tag	UNP Q9BQA1
B	-10	ALA	-	expression tag	UNP Q9BQA1
B	-9	THR	-	expression tag	UNP Q9BQA1
B	-8	THR	-	expression tag	UNP Q9BQA1
B	-7	GLU	-	expression tag	UNP Q9BQA1
B	-6	ASN	-	expression tag	UNP Q9BQA1
B	-5	LEU	-	expression tag	UNP Q9BQA1
B	-4	TYR	-	expression tag	UNP Q9BQA1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	PHE	-	expression tag	UNP Q9BQA1
B	-2	GLN	-	expression tag	UNP Q9BQA1
B	-1	GLY	-	expression tag	UNP Q9BQA1
B	0	SER	-	expression tag	UNP Q9BQA1
B	1	LEU	-	expression tag	UNP Q9BQA1

- Molecule 3 is 7-[(5R)-5-C-(4-chloro-3-fluorophenyl)-beta-D-ribofuranosyl]-7H-pyrrolo[2,3-d]pyrimidin-4-amine (CCD ID: ZR4) (formula: C₁₇H₁₆ClFN₄O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Cl	F	N	O	
			27	17	1	1	4	4	

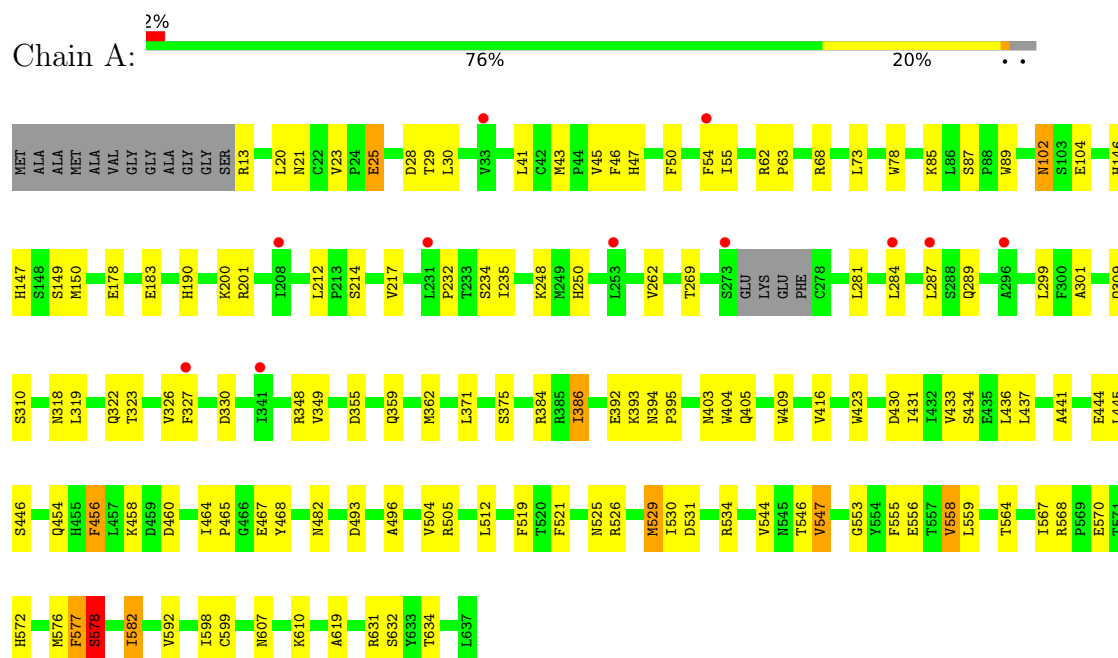
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	130	Total	O		
			130	130	0	0
4	B	32	Total	O		
			32	32	0	0

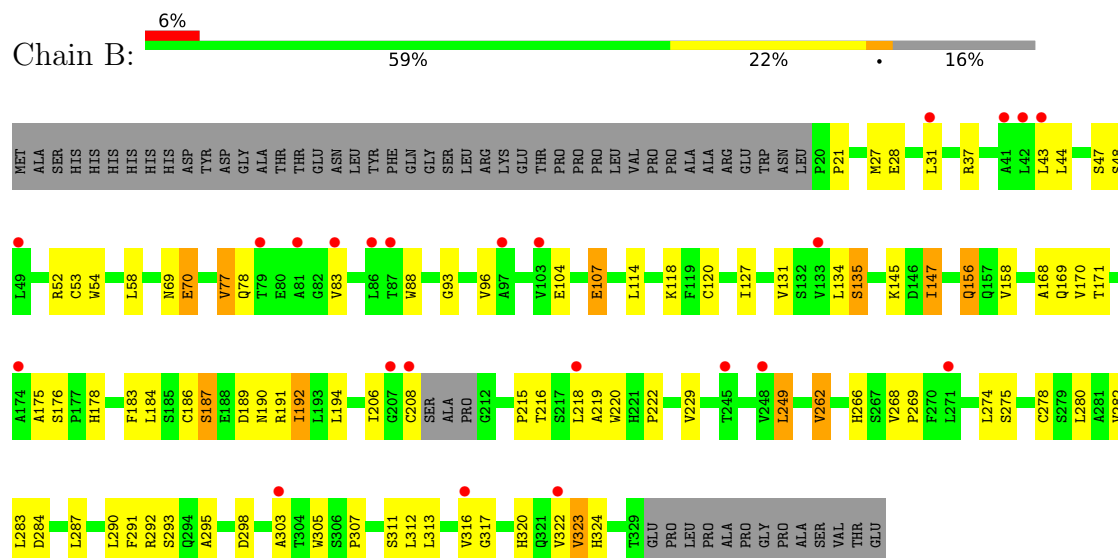
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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: Protein arginine N-methyltransferase 5



• Molecule 2: Methylosome protein 50



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	102.17Å 138.02Å 178.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	82.12 – 2.71 82.12 – 2.71	Depositor EDS
% Data completeness (in resolution range)	99.8 (82.12-2.71) 99.8 (82.12-2.71)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.66 (at 2.73Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.232 , 0.307 (Not available) , 0.288	Depositor DCC
R_{free} test set	1668 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	64.6	Xtriage
Anisotropy	1.023	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 68.4	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	7537	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZR4

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	0.77	0/5171	1.13	14/7034 (0.2%)
2	B	0.76	0/2372	1.12	2/3239 (0.1%)
All	All	0.77	0/7543	1.13	16/10273 (0.2%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	529	MET	CA-C-N	7.09	134.72	121.97
1	A	529	MET	C-N-CA	7.09	134.72	121.97
1	A	577	PHE	CA-CB-CG	6.98	120.78	113.80
1	A	456	PHE	CA-CB-CG	6.28	120.08	113.80
1	A	104	GLU	N-CA-C	-5.99	104.38	111.03
1	A	607	ASN	CA-CB-CG	5.92	118.52	112.60
1	A	394	ASN	CA-CB-CG	5.83	118.43	112.60
1	A	525	ASN	CA-C-N	5.40	127.78	120.38
1	A	525	ASN	C-N-CA	5.40	127.78	120.38
1	A	404	TRP	CA-C-N	5.28	127.36	120.28
1	A	404	TRP	C-N-CA	5.28	127.36	120.28
2	B	96	VAL	N-CA-C	5.15	115.27	107.75
1	A	409	TRP	N-CA-C	5.15	116.89	111.28
1	A	547	VAL	CA-C-N	5.07	128.05	120.95
1	A	547	VAL	C-N-CA	5.07	128.05	120.95
2	B	275	SER	N-CA-C	5.01	116.42	108.96

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	5031	0	4925	65	0
2	B	2317	0	2233	39	0
3	A	27	0	0	3	0
4	A	130	0	0	0	0
4	B	32	0	0	0	0
All	All	7537	0	7158	103	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 (103) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:567:ILE:HA	1:A:572:HIS:HD2	1.28	0.97
1:A:147:HIS:CD2	1:A:201:ARG:HH12	1.84	0.96
1:A:147:HIS:HD2	1:A:201:ARG:HH12	1.08	0.92
1:A:567:ILE:HA	1:A:572:HIS:CD2	2.05	0.90
1:A:190:HIS:CE1	1:A:547:VAL:HG21	2.12	0.84
1:A:212:LEU:HG	1:A:250:HIS:CE1	2.15	0.82
1:A:21:ASN:HD21	1:A:85:LYS:HZ1	1.35	0.74
1:A:434:SER:HB2	1:A:436:LEU:HG	1.70	0.72
2:B:145:LYS:HA	2:B:169:GLN:HB2	1.74	0.70
1:A:441:ALA:HB2	1:A:555:PHE:HB2	1.73	0.69
1:A:190:HIS:HE1	1:A:547:VAL:HG21	1.57	0.69
1:A:25:GLU:HB3	1:A:28:ASP:HB2	1.75	0.68
1:A:147:HIS:HD2	1:A:201:ARG:NH1	1.88	0.67
1:A:599:CYS:HB3	1:A:619:ALA:HB3	1.78	0.65
1:A:21:ASN:HD21	1:A:85:LYS:NZ	1.94	0.65
1:A:319:LEU:HD22	1:A:323:THR:HG21	1.80	0.63
2:B:262:VAL:HG12	2:B:305:TRP:HE1	1.62	0.63
1:A:330:ASP:OD2	1:A:578:SER:HB2	2.00	0.62
1:A:568:ARG:HG2	1:A:570:GLU:HG2	1.82	0.61
2:B:176:SER:HA	2:B:220:TRP:NE1	2.17	0.60
1:A:436:LEU:O	1:A:446:SER:HB2	2.03	0.59
1:A:21:ASN:ND2	1:A:85:LYS:NZ	2.51	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:PHE:H	1:A:102:ASN:HD21	1.51	0.58
2:B:58:LEU:HB2	2:B:77:VAL:HG12	1.87	0.57
1:A:45:VAL:HG23	1:A:46:PHE:HD1	1.69	0.56
1:A:416:VAL:HG11	1:A:423:TRP:CD1	2.41	0.56
1:A:465:PRO:HB3	1:A:559:LEU:HD23	1.87	0.56
2:B:104:GLU:HG2	2:B:120:CYS:HA	1.87	0.56
2:B:175:ALA:HA	2:B:183:PHE:HB3	1.88	0.56
2:B:312:LEU:HD21	2:B:324:HIS:HB3	1.86	0.56
1:A:468:TYR:CE1	1:A:521:PHE:HB2	2.42	0.55
1:A:519:PHE:CE1	1:A:534:ARG:HB3	2.42	0.55
1:A:553:GLY:HA3	1:A:582:ILE:HG22	1.88	0.55
2:B:27:MET:H	2:B:70:GLU:HG2	1.72	0.55
2:B:134:LEU:HD23	2:B:175:ALA:HB1	1.87	0.55
1:A:23:VAL:HG22	1:A:29:THR:HG21	1.89	0.54
1:A:493:ASP:HB3	1:A:496:ALA:HB2	1.88	0.54
1:A:327:PHE:CB	3:A:701:ZR4:CL1	2.94	0.53
1:A:437:LEU:HD21	1:A:468:TYR:CD2	2.44	0.53
2:B:303:ALA:HB1	2:B:313:LEU:HD11	1.91	0.53
2:B:262:VAL:HG12	2:B:305:TRP:NE1	2.24	0.53
2:B:170:VAL:HA	2:B:187:SER:HB2	1.91	0.52
1:A:348:ARG:NH1	1:A:460:ASP:OD1	2.42	0.52
1:A:68:ARG:NH1	2:B:54:TRP:CD2	2.79	0.51
1:A:50:PHE:CE1	1:A:62:ARG:NH1	2.78	0.51
2:B:37:ARG:O	2:B:307:PRO:HG3	2.10	0.51
2:B:282:VAL:HB	2:B:291:PHE:HB3	1.92	0.51
2:B:93:GLY:HA2	2:B:107:GLU:HA	1.94	0.50
2:B:175:ALA:HA	2:B:183:PHE:CB	2.41	0.50
2:B:249:LEU:HD13	2:B:287:LEU:HD12	1.94	0.50
1:A:327:PHE:HB3	3:A:701:ZR4:CL1	2.49	0.49
1:A:327:PHE:HB2	3:A:701:ZR4:CL1	2.50	0.49
1:A:362:MET:SD	1:A:456:PHE:CE1	3.05	0.49
2:B:47:SER:HB3	2:B:83:VAL:H	1.78	0.49
2:B:31:LEU:HB2	2:B:317:GLY:O	2.12	0.48
1:A:301:ALA:HB1	1:A:505:ARG:HG2	1.95	0.48
1:A:437:LEU:HD21	1:A:468:TYR:CE2	2.48	0.48
1:A:349:VAL:HG12	1:A:384:ARG:HH11	1.78	0.48
1:A:433:VAL:HG22	1:A:464:ILE:HB	1.94	0.48
2:B:219:ALA:HB3	2:B:229:VAL:HG23	1.96	0.48
2:B:44:LEU:HD21	2:B:316:VAL:HG11	1.96	0.47
2:B:147:ILE:HG23	2:B:168:ALA:O	2.13	0.47
1:A:41:LEU:HG	1:A:43:MET:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:156:GLN:HB3	2:B:158:VAL:HG22	1.97	0.47
1:A:232:PRO:O	1:A:235:ILE:HG12	2.15	0.47
2:B:107:GLU:HB2	2:B:118:LYS:HD3	1.96	0.47
1:A:371:LEU:HD13	1:A:433:VAL:HG12	1.95	0.47
1:A:45:VAL:HG23	1:A:46:PHE:CD1	2.50	0.46
1:A:362:MET:SD	1:A:456:PHE:CD1	3.09	0.46
1:A:150:MET:SD	1:A:201:ARG:HA	2.56	0.45
1:A:214:SER:HB2	1:A:217:VAL:HG23	1.98	0.45
1:A:512:LEU:HD22	1:A:546:THR:HG21	1.98	0.45
1:A:610:LYS:HD2	1:A:634:THR:CB	2.47	0.45
2:B:43:LEU:HB2	2:B:88:TRP:CZ2	2.52	0.45
1:A:21:ASN:ND2	1:A:85:LYS:HZ3	2.15	0.44
2:B:186:CYS:HB3	2:B:192:ILE:HG23	1.99	0.44
2:B:284:ASP:HB3	2:B:290:LEU:HD11	1.99	0.44
1:A:47:HIS:HB3	1:A:50:PHE:HB2	2.00	0.44
1:A:610:LYS:HD2	1:A:634:THR:HB	2.00	0.44
1:A:87:SER:HB3	1:A:89:TRP:CD1	2.53	0.44
2:B:295:ALA:HB1	2:B:323:VAL:HG21	2.00	0.44
1:A:318:ASN:HD21	1:A:395:PRO:HD2	1.82	0.44
2:B:186:CYS:HB2	2:B:215:PRO:HB2	2.00	0.44
1:A:430:ASP:HA	1:A:458:LYS:HD2	1.99	0.44
1:A:465:PRO:HA	1:A:559:LEU:HA	2.00	0.44
1:A:359:GLN:HB2	1:A:386:ILE:HG22	2.00	0.43
2:B:322:VAL:HG12	2:B:322:VAL:O	2.18	0.43
1:A:592:VAL:HG21	1:A:598:ILE:HD11	2.00	0.43
1:A:610:LYS:HD2	1:A:634:THR:OG1	2.18	0.43
1:A:55:ILE:HD12	1:A:102:ASN:HD22	1.84	0.42
1:A:576:MET:HE2	1:A:576:MET:HB3	1.95	0.42
2:B:278:CYS:SG	2:B:298:ASP:O	2.77	0.42
2:B:135:SER:OG	2:B:178:HIS:HA	2.19	0.42
2:B:184:LEU:HB3	2:B:218:LEU:HD13	2.02	0.42
1:A:284:LEU:HA	1:A:287:LEU:HD12	2.02	0.42
1:A:73:LEU:HB2	1:A:78:TRP:CE2	2.54	0.42
1:A:558:VAL:HG22	1:A:564:THR:HG22	2.02	0.42
2:B:28:GLU:HB3	2:B:48:SER:HB3	2.01	0.42
2:B:171:THR:HG21	2:B:216:THR:HA	2.03	0.41
1:A:62:ARG:HA	1:A:63:PRO:HD3	1.92	0.41
2:B:189:ASP:OD1	2:B:191:ARG:HB2	2.21	0.41
2:B:280:LEU:HB3	2:B:293:SER:HB3	2.03	0.41
2:B:222:PRO:HG2	2:B:269:PRO:HG2	2.02	0.40

There are no symmetry-related clashes.

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	618/637 (97%)	580 (94%)	35 (6%)	3 (0%)	24	46
2	B	303/366 (83%)	279 (92%)	18 (6%)	6 (2%)	6	14
All	All	921/1003 (92%)	859 (93%)	53 (6%)	9 (1%)	12	30

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	531	ASP
1	A	578	SER
2	B	135	SER
2	B	147	ILE
2	B	323	VAL
2	B	127	ILE
2	B	266	HIS
2	B	21	PRO
1	A	445	LEU

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	555/562 (99%)	510 (92%)	45 (8%)	11	26
2	B	260/310 (84%)	236 (91%)	24 (9%)	8	20
All	All	815/872 (94%)	746 (92%)	69 (8%)	10	24

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ARG
1	A	20	LEU
1	A	25	GLU
1	A	30	LEU
1	A	102	ASN
1	A	146	HIS
1	A	149	SER
1	A	178	GLU
1	A	183	GLU
1	A	200	LYS
1	A	234	SER
1	A	248	LYS
1	A	262	VAL
1	A	269	THR
1	A	281	LEU
1	A	289	GLN
1	A	299	LEU
1	A	309	GLN
1	A	310	SER
1	A	322	GLN
1	A	326	VAL
1	A	355	ASP
1	A	375	SER
1	A	386	ILE
1	A	392	GLU
1	A	393	LYS
1	A	403	ASN
1	A	405	GLN
1	A	431	ILE
1	A	444	GLU
1	A	454	GLN
1	A	467	GLU
1	A	482	ASN
1	A	504	VAL
1	A	526	ARG
1	A	529	MET
1	A	530	ILE
1	A	544	VAL
1	A	556	GLU
1	A	558	VAL
1	A	577	PHE
1	A	578	SER

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Mol	Chain	Res	Type
1	A	582	ILE
1	A	631	ARG
1	A	632	SER
2	B	52	ARG
2	B	53	CYS
2	B	69	ASN
2	B	70	GLU
2	B	77	VAL
2	B	78	GLN
2	B	107	GLU
2	B	114	LEU
2	B	131	VAL
2	B	156	GLN
2	B	187	SER
2	B	190	ASN
2	B	192	ILE
2	B	194	LEU
2	B	206	ILE
2	B	208	CYS
2	B	249	LEU
2	B	262	VAL
2	B	268	VAL
2	B	274	LEU
2	B	283	LEU
2	B	292	ARG
2	B	311	SER
2	B	320	HIS

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	21	ASN
1	A	102	ASN
1	A	147	HIS
1	A	175	HIS
1	A	251	GLN
1	A	295	ASN
1	A	309	GLN
1	A	339	GLN
1	A	396	ASN
1	A	405	GLN
1	A	482	ASN

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Mol	Chain	Res	Type
1	A	572	HIS
2	B	139	GLN
2	B	178	HIS
2	B	190	ASN
2	B	294	GLN
2	B	310	HIS

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](#)

1 ligand 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	ZR4	A	701	-	30,30,30	0.20	0	41,45,45	0.54	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	ZR4	A	701	-	-	0/12/28/28	0/4/4/4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

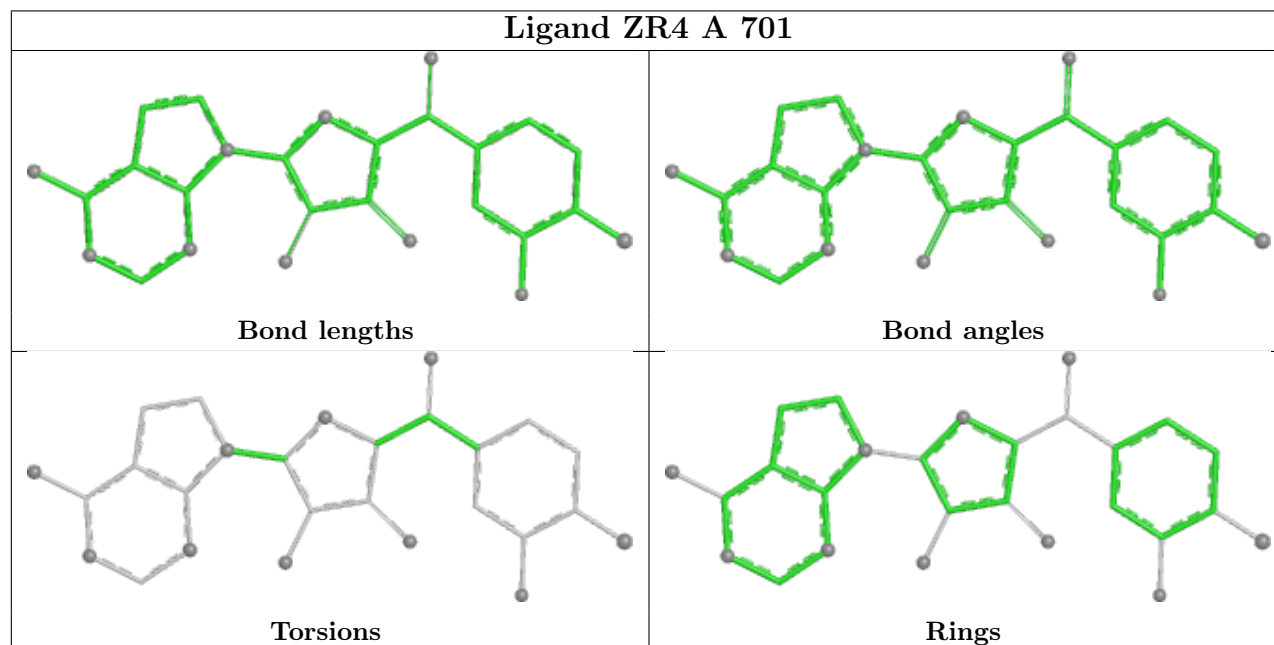
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	701	ZR4	3	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	621/637 (97%)	0.33	11 (1%) 67 65	29, 77, 112, 133	1 (0%)
2	B	307/366 (83%)	0.85	23 (7%) 20 18	71, 99, 126, 144	0
All	All	928/1003 (92%)	0.50	34 (3%) 45 41	29, 87, 121, 144	1 (0%)

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	231	LEU	4.0
1	A	208	ILE	3.4
1	A	284	LEU	3.3
2	B	207	GLY	3.2
2	B	41	ALA	3.1
2	B	248	VAL	3.1
2	B	208	CYS	3.1
2	B	86	LEU	3.0
2	B	245	THR	3.0
1	A	273	SER	3.0
2	B	303	ALA	3.0
2	B	316	VAL	2.9
2	B	218	LEU	2.7
1	A	33	VAL	2.6
2	B	87	THR	2.6
2	B	81	ALA	2.6
2	B	174	ALA	2.5
1	A	287	LEU	2.4
2	B	322	VAL	2.4
1	A	54	PHE	2.4
2	B	43	LEU	2.3
2	B	42	LEU	2.3
2	B	103	VAL	2.3
2	B	31	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	79	THR	2.2
2	B	49	LEU	2.2
1	A	327	PHE	2.2
1	A	253	LEU	2.2
2	B	271	LEU	2.2
1	A	341	ILE	2.1
1	A	296	ALA	2.1
2	B	133	VAL	2.1
2	B	97	ALA	2.1
2	B	83	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

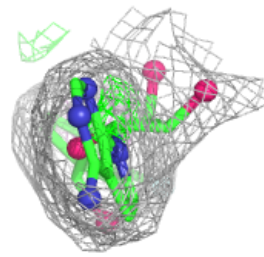
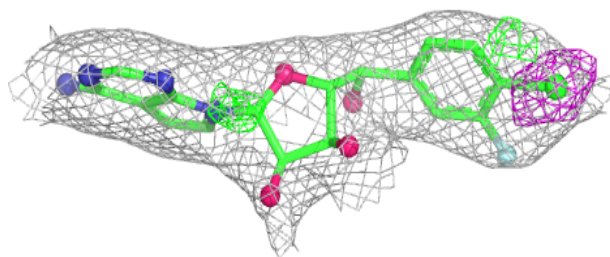
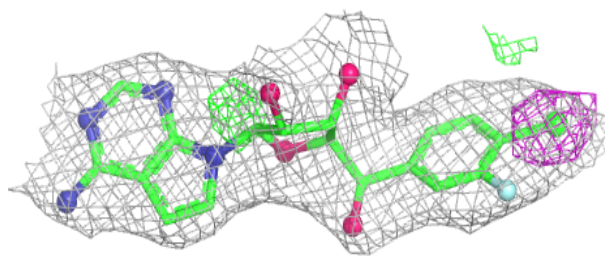
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	ZR4	A	701	27/27	0.90	0.10	53,60,67,71	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 ZR4 A 701:

$2mF_o-DF_c$ (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.