



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:46 PM UTC

PDB ID : 3SHR / pdb_00003shr
Title : Crystal Structure of cGMP-dependent Protein Kinase Reveals Novel Site of Interchain Communication
Authors : Osborne, B.W.; Wu, J.; Taylor, S.S.; Dostmann, W.R.
Deposited on : 2011-06-16
Resolution : 2.50 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

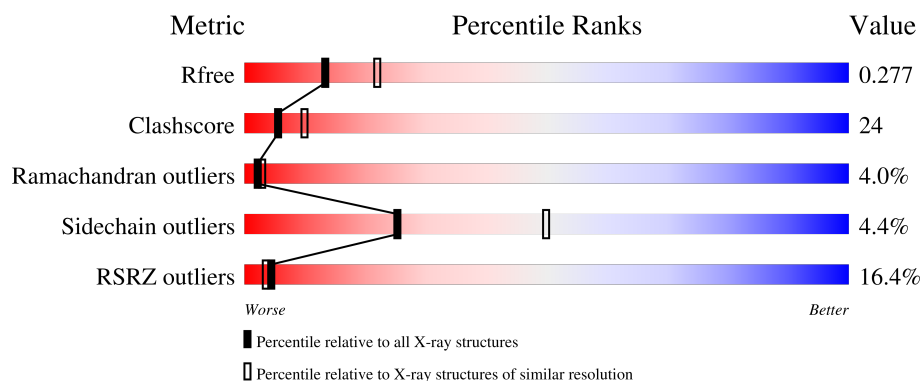
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	299	
1	B	299	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4277 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 cGMP-dependent protein kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	278	Total	C	N	O	S	0	0	0
			2138	1361	354	410	13			
1	B	278	Total	C	N	O	S	0	0	0
			2085	1323	348	401	13			

There are 42 discrepancies between the modelled and reference sequences:

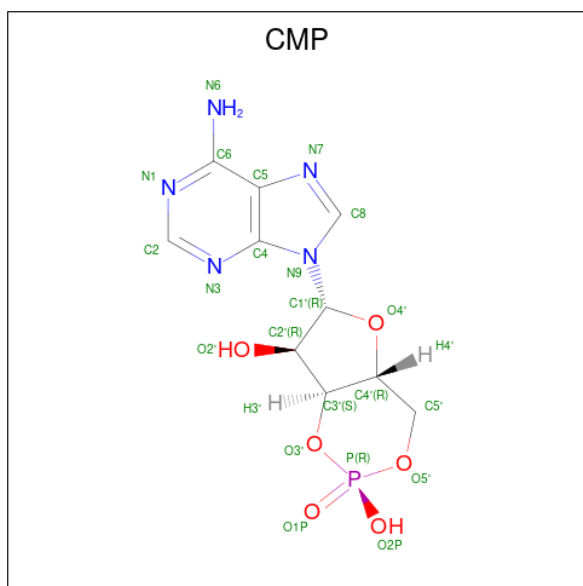
Chain	Residue	Modelled	Actual	Comment	Reference
B	57	MET	-	expression tag	UNP P00516
B	58	ARG	-	expression tag	UNP P00516
B	59	GLY	-	expression tag	UNP P00516
B	60	SER	-	expression tag	UNP P00516
B	61	HIS	-	expression tag	UNP P00516
B	62	HIS	-	expression tag	UNP P00516
B	63	HIS	-	expression tag	UNP P00516
B	64	HIS	-	expression tag	UNP P00516
B	65	HIS	-	expression tag	UNP P00516
B	66	HIS	-	expression tag	UNP P00516
B	67	GLY	-	expression tag	UNP P00516
B	68	MET	-	expression tag	UNP P00516
B	69	ALA	-	expression tag	UNP P00516
B	70	SER	-	expression tag	UNP P00516
B	71	ILE	-	expression tag	UNP P00516
B	72	GLU	-	expression tag	UNP P00516
B	73	GLY	-	expression tag	UNP P00516
B	74	ARG	-	expression tag	UNP P00516
B	75	GLY	-	expression tag	UNP P00516
B	76	SER	-	expression tag	UNP P00516
B	77	MET	-	expression tag	UNP P00516
A	57	MET	-	expression tag	UNP P00516
A	58	ARG	-	expression tag	UNP P00516
A	59	GLY	-	expression tag	UNP P00516
A	60	SER	-	expression tag	UNP P00516

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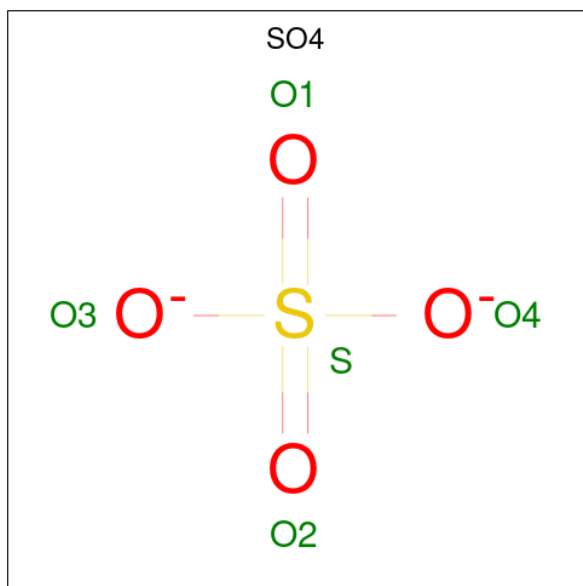
Chain	Residue	Modelled	Actual	Comment	Reference
A	61	HIS	-	expression tag	UNP P00516
A	62	HIS	-	expression tag	UNP P00516
A	63	HIS	-	expression tag	UNP P00516
A	64	HIS	-	expression tag	UNP P00516
A	65	HIS	-	expression tag	UNP P00516
A	66	HIS	-	expression tag	UNP P00516
A	67	GLY	-	expression tag	UNP P00516
A	68	MET	-	expression tag	UNP P00516
A	69	ALA	-	expression tag	UNP P00516
A	70	SER	-	expression tag	UNP P00516
A	71	ILE	-	expression tag	UNP P00516
A	72	GLU	-	expression tag	UNP P00516
A	73	GLY	-	expression tag	UNP P00516
A	74	ARG	-	expression tag	UNP P00516
A	75	GLY	-	expression tag	UNP P00516
A	76	SER	-	expression tag	UNP P00516
A	77	MET	-	expression tag	UNP P00516

- Molecule 2 is ADENOSINE-3',5'-CYCLIC-MONOPHOSPHATE (CCD ID: CMP) (formula: $C_{10}H_{12}N_5O_6P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	B	1	Total	C	N	O	P	0	0
			22	10	5	6	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).

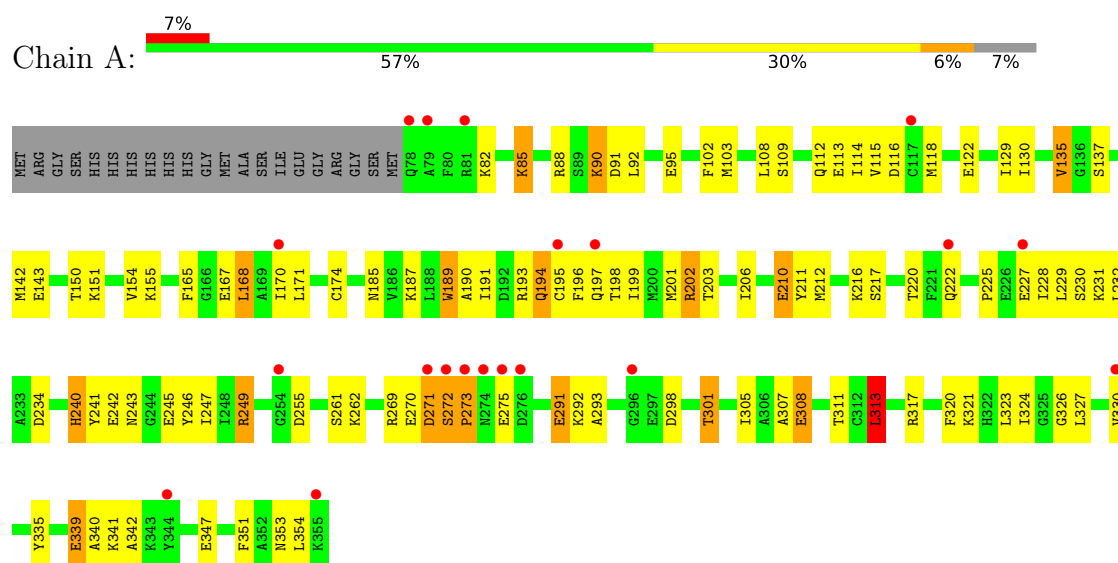


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		

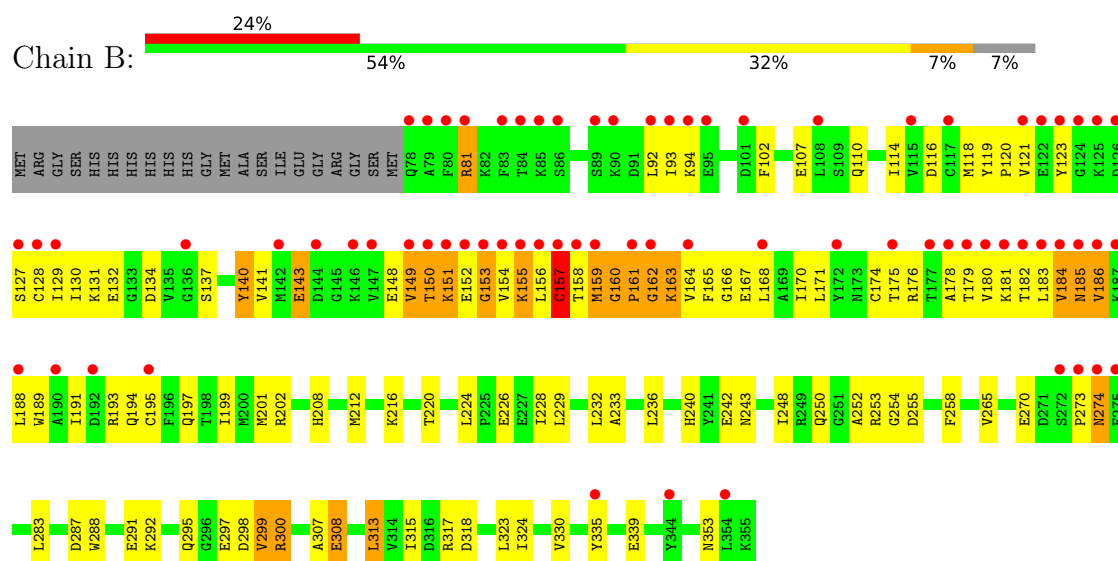
3 Residue-property plots [i](#)

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: cGMP-dependent protein kinase 1



• Molecule 1: cGMP-dependent protein kinase 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	180.16Å 66.04Å 81.55Å 90.00° 113.84° 90.00°	Depositor
Resolution (Å)	50.00 – 2.50 50.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.50) 92.9 (50.00-2.50)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 2.45Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.221 , 0.277 0.247 , 0.277	Depositor DCC
R_{free} test set	1492 reflections (4.64%)	wwPDB-VP
Wilson B-factor (Å ²)	40.1	Xtriage
Anisotropy	0.446	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 37.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4277	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.77% 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: CMP, SO4

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	0/2172	0.95	9/2932 (0.3%)
1	B	0.44	0/2119	0.95	9/2873 (0.3%)
All	All	0.45	0/4291	0.95	18/5805 (0.3%)

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	313	LEU	N-CA-C	-7.02	97.80	109.46
1	A	135	VAL	N-CA-C	-6.92	97.12	107.37
1	A	189	TRP	N-CA-C	-6.49	98.32	108.90
1	B	313	LEU	N-CA-C	-6.46	98.71	109.24
1	B	153	GLY	N-CA-C	-6.40	106.60	114.92
1	B	299	VAL	N-CA-C	6.17	116.81	108.17
1	B	116	ASP	N-CA-C	6.09	117.72	111.14
1	A	217	SER	N-CA-C	-5.84	106.13	113.72
1	B	160	GLY	CA-C-N	5.82	127.11	119.84
1	B	160	GLY	C-N-CA	5.82	127.11	119.84
1	A	240	HIS	N-CA-C	5.49	118.52	109.85
1	A	154	VAL	N-CA-C	5.47	116.26	107.73
1	B	240	HIS	N-CA-C	5.44	118.32	109.24
1	B	119	TYR	CA-C-N	5.35	125.52	119.90
1	B	119	TYR	C-N-CA	5.35	125.52	119.90
1	A	143	GLU	N-CA-C	-5.23	106.84	113.43
1	A	185	ASN	N-CA-C	-5.21	102.58	110.28
1	A	339	GLU	N-CA-C	-5.06	105.89	111.71

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	2138	0	2102	88	0
1	B	2085	0	1974	114	0
2	A	22	0	11	1	0
2	B	22	0	11	5	0
3	A	10	0	0	1	0
All	All	4277	0	4098	198	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 24.

All (198) 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:401:CMP:H2	2:B:401:CMP:C2	0.97	1.49
2:A:401:CMP:H2	2:A:401:CMP:C2	0.97	1.49
1:B:212:MET:HE3	1:B:212:MET:HA	1.48	0.95
1:B:151:LYS:HD2	1:B:152:GLU:HG2	1.49	0.92
1:B:250:GLN:HE22	1:B:270:GLU:H	0.94	0.90
1:B:129:ILE:HG22	1:B:130:ILE:HG13	1.55	0.87
1:B:156:LEU:O	1:B:157:CYS:HB3	1.74	0.87
1:B:250:GLN:NE2	1:B:270:GLU:H	1.73	0.84
1:B:248:ILE:HG23	1:B:300:ARG:HD3	1.61	0.82
1:B:250:GLN:HE22	1:B:270:GLU:N	1.76	0.82
1:B:167:GLU:HG2	1:B:168:LEU:HD12	1.64	0.78
1:B:220:THR:HG21	1:B:288:TRP:CZ3	2.21	0.75
1:A:255:ASP:HA	1:A:293:ALA:HB1	1.68	0.74
1:B:131:LYS:HA	1:B:179:THR:HG23	1.69	0.74
1:B:107:GLU:HG2	1:B:110:GLN:HE21	1.53	0.73
1:B:141:VAL:HG22	1:B:164:VAL:HG22	1.70	0.73
1:A:242:GLU:O	1:A:245:GLU:HG3	1.90	0.72
1:B:178:ALA:HB3	2:B:401:CMP:H5'1	1.71	0.71
1:B:201:MET:HA	1:B:201:MET:HE2	1.72	0.70
1:B:150:THR:HG22	1:B:155:LYS:HD3	1.74	0.68
1:A:195:CYS:O	1:A:199:ILE:HG12	1.93	0.68
1:A:225:PRO:HG2	1:A:228:ILE:HG12	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:LYS:HG3	1:A:116:ASP:HB3	1.76	0.66
1:A:137:SER:HB2	1:A:193:ARG:HB2	1.77	0.65
1:A:342:ALA:HB1	1:B:330:VAL:HG13	1.78	0.64
1:A:122:GLU:OE1	1:A:187:LYS:HE2	1.97	0.64
1:B:193:ARG:O	1:B:197:GLN:HB2	1.97	0.63
1:B:175:THR:O	1:B:176:ARG:C	2.41	0.63
1:B:164:VAL:HG12	1:B:167:GLU:OE2	1.99	0.62
1:A:249:ARG:HH11	1:A:249:ARG:HG3	1.64	0.62
1:A:92:LEU:C	1:A:92:LEU:HD23	2.25	0.61
1:A:202:ARG:O	1:A:206:ILE:HG13	1.99	0.61
1:A:102:PHE:CZ	1:A:171:LEU:HD22	2.35	0.61
1:B:212:MET:HE1	1:B:229:LEU:C	2.27	0.59
1:B:107:GLU:HB2	1:B:110:GLN:HG3	1.83	0.59
1:B:143:GLU:O	1:B:161:PRO:HB3	2.03	0.58
1:B:212:MET:CE	1:B:229:LEU:HB3	2.33	0.58
1:A:91:ASP:O	1:A:95:GLU:HG3	2.04	0.58
1:A:240:HIS:CD2	1:A:311:THR:HG23	2.39	0.58
1:B:188:LEU:HD23	1:B:188:LEU:H	1.69	0.58
1:A:170:ILE:HD12	1:A:170:ILE:N	2.19	0.57
1:B:156:LEU:O	1:B:157:CYS:CB	2.51	0.56
1:B:228:ILE:O	1:B:232:LEU:HB2	2.05	0.56
1:B:158:THR:O	1:B:159:MET:HB2	2.06	0.56
1:B:167:GLU:HG2	1:B:168:LEU:N	2.20	0.56
1:A:241:TYR:CZ	1:A:247:ILE:HG23	2.41	0.55
1:A:225:PRO:HD2	1:A:228:ILE:HD11	1.88	0.55
1:B:224:LEU:HD12	1:B:229:LEU:HD21	1.88	0.55
1:B:120:PRO:HD3	1:B:189:TRP:HZ3	1.71	0.55
1:A:307:ALA:O	1:A:308:GLU:HB3	2.07	0.55
1:B:107:GLU:H	1:B:110:GLN:NE2	2.04	0.55
1:A:103:MET:HE3	1:A:196:PHE:HE2	1.71	0.54
1:A:129:ILE:HG22	1:A:130:ILE:HG13	1.89	0.54
1:B:170:ILE:HD12	1:B:170:ILE:N	2.23	0.54
1:B:118:MET:HG2	1:B:191:ILE:HB	1.89	0.54
1:B:212:MET:HE1	1:B:229:LEU:HB3	1.88	0.54
1:B:134:ASP:HB2	1:B:176:ARG:HG3	1.90	0.54
1:A:114:ILE:HG13	1:A:199:ILE:HG21	1.91	0.53
1:B:166:GLY:H	2:B:401:CMP:HO2'	1.55	0.53
1:B:212:MET:HE1	1:B:229:LEU:O	2.09	0.53
1:A:210:GLU:HG3	1:A:211:TYR:N	2.22	0.53
1:B:159:MET:HE1	2:B:401:CMP:H8	1.89	0.53
1:B:212:MET:HA	1:B:212:MET:CE	2.29	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:GLU:OE1	1:A:168:LEU:HD13	2.09	0.53
1:B:291:GLU:CD	1:B:291:GLU:H	2.17	0.52
1:A:114:ILE:O	1:A:118:MET:HG3	2.09	0.52
1:A:85:LYS:HG2	1:A:90:LYS:HD3	1.89	0.52
1:A:118:MET:HA	1:A:190:ALA:O	2.09	0.52
1:B:194:GLN:NE2	1:B:194:GLN:HA	2.25	0.52
1:A:170:ILE:HD12	1:A:170:ILE:H	1.73	0.52
1:B:208:HIS:CE1	1:B:233:ALA:HB3	2.44	0.52
1:B:236:LEU:HD23	1:B:315:ILE:HB	1.92	0.52
1:A:228:ILE:HG13	1:A:229:LEU:N	2.25	0.51
1:A:142:MET:HG2	1:A:165:PHE:HE2	1.75	0.51
1:A:170:ILE:H	1:A:170:ILE:CD1	2.24	0.51
1:A:353:ASN:O	1:A:353:ASN:ND2	2.43	0.51
1:A:216:LYS:HA	1:A:222:GLN:HG2	1.94	0.50
1:A:113:GLU:HB3	1:A:199:ILE:HD12	1.93	0.50
1:A:249:ARG:N	1:A:249:ARG:HD2	2.27	0.50
1:A:269:ARG:HD2	1:A:301:THR:O	2.11	0.50
1:A:220:THR:O	1:B:353:ASN:ND2	2.45	0.50
1:A:90:LYS:HG3	1:A:115:VAL:CG1	2.41	0.50
1:B:242:GLU:O	1:B:243:ASN:C	2.55	0.50
1:B:140:TYR:CD2	1:B:140:TYR:N	2.80	0.50
1:B:155:LYS:NZ	1:B:183:LEU:HD21	2.26	0.49
1:B:92:LEU:HD13	1:B:143:GLU:OE1	2.12	0.49
1:A:102:PHE:CE1	1:A:171:LEU:HD13	2.47	0.49
1:B:162:GLY:O	1:B:163:LYS:C	2.54	0.49
1:B:188:LEU:H	1:B:188:LEU:CD2	2.25	0.49
1:B:283:LEU:HD22	1:B:287:ASP:HB3	1.94	0.49
1:A:170:ILE:HG12	1:A:196:PHE:CD1	2.48	0.49
1:B:180:VAL:HG12	1:B:181:LYS:N	2.27	0.49
1:B:252:ALA:O	1:B:299:VAL:HA	2.13	0.49
1:B:141:VAL:CG2	1:B:164:VAL:HG22	2.39	0.49
1:A:150:THR:HG22	1:A:155:LYS:HA	1.95	0.49
1:B:292:LYS:HB3	1:B:297:GLU:CB	2.42	0.49
1:B:253:ARG:HA	1:B:298:ASP:O	2.13	0.48
1:A:347:GLU:HG3	1:B:324:ILE:HG21	1.95	0.48
1:B:255:ASP:OD1	1:B:317:ARG:NH2	2.47	0.48
1:B:114:ILE:HG13	1:B:199:ILE:HG21	1.96	0.48
1:A:270:GLU:O	1:A:271:ASP:C	2.56	0.48
1:A:109:SER:O	1:A:113:GLU:HG3	2.14	0.47
1:B:248:ILE:HD12	1:B:300:ARG:HD3	1.96	0.47
1:A:118:MET:HE2	1:A:189:TRP:C	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:VAL:HG13	1:B:339:GLU:HG2	1.96	0.47
1:B:160:GLY:O	1:B:162:GLY:N	2.47	0.47
1:A:88:ARG:HG3	1:A:88:ARG:HH11	1.79	0.47
1:A:212:MET:CE	1:A:216:LYS:HE3	2.45	0.47
1:A:272:SER:CB	1:A:273:PRO:CD	2.93	0.47
1:B:121:VAL:HG13	1:B:121:VAL:O	2.15	0.47
1:B:216:LYS:HZ1	1:B:226:GLU:CD	2.23	0.47
1:A:324:ILE:C	1:A:326:GLY:H	2.23	0.47
1:A:335:TYR:O	1:A:339:GLU:HB2	2.14	0.47
1:A:242:GLU:N	1:A:245:GLU:OE1	2.43	0.47
1:A:135:VAL:HA	1:A:174:CYS:O	2.14	0.47
1:A:232:LEU:HA	1:A:323:LEU:HD11	1.97	0.47
1:B:273:PRO:O	1:B:274:ASN:C	2.58	0.46
1:B:335:TYR:O	1:B:339:GLU:HG3	2.15	0.46
1:A:231:LYS:HG2	1:A:323:LEU:HG	1.96	0.46
1:A:273:PRO:C	1:A:275:GLU:H	2.22	0.46
1:B:179:THR:HG22	1:B:179:THR:O	2.14	0.46
1:A:249:ARG:HH11	1:A:249:ARG:CG	2.26	0.46
1:B:188:LEU:HD23	1:B:188:LEU:N	2.31	0.46
1:A:137:SER:CB	1:A:193:ARG:HB2	2.44	0.46
1:B:248:ILE:HD11	1:B:258:PHE:CE1	2.51	0.46
1:B:317:ARG:NH1	1:B:318:ASP:OD1	2.48	0.46
1:A:228:ILE:HG13	1:A:229:LEU:H	1.80	0.46
1:B:216:LYS:NZ	1:B:226:GLU:OE1	2.48	0.46
1:B:149:VAL:HG12	1:B:149:VAL:O	2.16	0.46
1:B:307:ALA:O	1:B:308:GLU:HB3	2.16	0.46
1:A:191:ILE:CG1	1:A:195:CYS:HB3	2.46	0.45
1:A:291:GLU:H	1:A:291:GLU:CD	2.22	0.45
1:B:107:GLU:H	1:B:110:GLN:HE21	1.62	0.45
1:A:201:MET:C	1:A:203:THR:H	2.25	0.45
1:B:114:ILE:O	1:B:118:MET:HG3	2.16	0.45
1:B:168:LEU:CD1	1:B:168:LEU:H	2.29	0.45
1:B:154:VAL:O	1:B:154:VAL:HG13	2.17	0.45
1:A:197:GLN:O	1:A:201:MET:HG2	2.17	0.44
1:A:340:ALA:O	1:A:341:LYS:C	2.60	0.44
1:A:351:PHE:CE1	1:B:295:GLN:HG2	2.52	0.44
1:B:121:VAL:O	1:B:121:VAL:HG22	2.16	0.44
1:B:127:SER:N	1:B:182:THR:OG1	2.50	0.44
1:B:154:VAL:O	1:B:154:VAL:HG22	2.17	0.44
1:B:107:GLU:HG2	1:B:110:GLN:NE2	2.28	0.44
1:B:151:LYS:C	1:B:153:GLY:H	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:307:ALA:O	1:A:308:GLU:CB	2.66	0.44
1:B:265:VAL:HG22	1:B:283:LEU:HB2	2.00	0.44
1:A:320:PHE:O	1:A:321:LYS:C	2.61	0.43
1:B:154:VAL:O	1:B:155:LYS:C	2.61	0.43
1:A:198:THR:O	1:A:201:MET:HB2	2.17	0.43
1:B:184:VAL:HG22	1:B:185:ASN:N	2.33	0.43
1:B:248:ILE:HD11	1:B:258:PHE:HE1	1.84	0.43
1:B:317:ARG:NH1	1:B:318:ASP:CG	2.76	0.43
1:B:226:GLU:OE1	1:B:226:GLU:HA	2.19	0.43
1:B:323:LEU:HD23	1:B:323:LEU:C	2.43	0.43
1:B:102:PHE:CD2	1:B:171:LEU:HD13	2.54	0.43
1:B:165:PHE:HB2	2:B:401:CMP:H1'	2.01	0.43
1:A:291:GLU:OE2	1:A:292:LYS:HD2	2.18	0.43
1:B:140:TYR:HB3	1:B:189:TRP:O	2.19	0.43
1:A:194:GLN:OE1	1:A:194:GLN:HA	2.19	0.42
1:B:186:VAL:HG21	1:B:188:LEU:HD22	2.01	0.42
1:A:330:VAL:CG1	1:B:339:GLU:HG2	2.50	0.42
1:B:193:ARG:HB3	1:B:193:ARG:HH11	1.85	0.42
1:B:195:CYS:O	1:B:199:ILE:HG13	2.19	0.42
1:B:202:ARG:HH21	1:B:202:ARG:HG2	1.84	0.42
1:A:151:LYS:HB2	1:A:151:LYS:HE3	1.84	0.42
1:A:261:SER:HB3	1:A:313:LEU:HD13	2.00	0.42
1:B:151:LYS:HB3	1:B:152:GLU:H	1.65	0.42
1:A:88:ARG:HG3	1:A:88:ARG:NH1	2.35	0.42
1:A:227:GLU:OE2	1:A:327:LEU:HA	2.20	0.42
1:A:255:ASP:HB3	1:A:317:ARG:NH1	2.34	0.41
1:B:156:LEU:HD23	1:B:156:LEU:HA	1.91	0.41
1:A:262:LYS:HG3	3:A:403:SO4:O4	2.20	0.41
1:A:212:MET:SD	1:A:230:SER:HA	2.60	0.41
1:B:212:MET:HE2	1:B:229:LEU:HB3	2.01	0.41
1:B:81:ARG:HG3	1:B:81:ARG:NH1	2.35	0.41
1:A:170:ILE:N	1:A:170:ILE:CD1	2.81	0.41
1:A:198:THR:O	1:A:199:ILE:C	2.63	0.41
1:B:93:ILE:O	1:B:94:LYS:C	2.63	0.41
1:A:118:MET:HG2	1:A:191:ILE:HB	2.03	0.41
1:A:168:LEU:HD12	1:A:168:LEU:HA	1.85	0.41
1:A:232:LEU:HA	1:A:323:LEU:CD1	2.51	0.41
1:A:269:ARG:HG2	1:A:269:ARG:NH1	2.36	0.41
1:B:134:ASP:HB2	1:B:176:ARG:CG	2.50	0.41
1:B:170:ILE:N	1:B:170:ILE:CD1	2.84	0.41
1:B:121:VAL:HG13	1:B:188:LEU:HG	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:LEU:H	1:A:108:LEU:HD12	1.87	0.40
1:A:242:GLU:O	1:A:243:ASN:C	2.63	0.40
1:B:254:GLY:HA3	1:B:300:ARG:NH1	2.36	0.40
1:B:128:CYS:SG	1:B:129:ILE:N	2.94	0.40
1:A:242:GLU:HB2	1:A:245:GLU:OE1	2.22	0.40
1:A:249:ARG:N	1:A:249:ARG:CD	2.84	0.40
1:B:148:GLU:CB	1:B:155:LYS:NZ	2.84	0.40
1:B:180:VAL:CG1	1:B:181:LYS:N	2.84	0.40
1:B:194:GLN:HA	1:B:194:GLN:HE21	1.86	0.40
1:A:246:TYR:CD2	1:A:305:ILE:HG12	2.55	0.40
1:B:127:SER:H	1:B:182:THR:HG1	1.70	0.40
1:B:132:GLU:HB3	1:B:179:THR:OG1	2.22	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	276/299 (92%)	249 (90%)	21 (8%)	6 (2%)	5	9
1	B	276/299 (92%)	230 (83%)	30 (11%)	16 (6%)	1	1
All	All	552/598 (92%)	479 (87%)	51 (9%)	22 (4%)	2	3

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	272	SER
1	B	157	CYS
1	B	174	CYS
1	A	271	ASP
1	A	273	PRO
1	A	308	GLU

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Mol	Chain	Res	Type
1	A	354	LEU
1	B	150	THR
1	B	274	ASN
1	A	202	ARG
1	B	137	SER
1	B	159	MET
1	B	161	PRO
1	B	163	LYS
1	B	185	ASN
1	B	308	GLU
1	B	151	LYS
1	B	155	LYS
1	B	184	VAL
1	B	149	VAL
1	B	186	VAL
1	B	162	GLY

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	224/255 (88%)	212 (95%)	12 (5%)	20	41
1	B	208/255 (82%)	201 (97%)	7 (3%)	32	60
All	All	432/510 (85%)	413 (96%)	19 (4%)	25	50

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	LYS
1	A	90	LYS
1	A	112	GLN
1	A	168	LEU
1	A	194	GLN
1	A	210	GLU
1	A	234	ASP

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Mol	Chain	Res	Type
1	A	249	ARG
1	A	291	GLU
1	A	298	ASP
1	A	301	THR
1	A	313	LEU
1	B	81	ARG
1	B	123	TYR
1	B	140	TYR
1	B	143	GLU
1	B	157	CYS
1	B	300	ARG
1	B	313	LEU

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	240	HIS
1	A	243	ASN
1	A	295	GLN
1	A	353	ASN
1	B	110	GLN
1	B	173	ASN
1	B	194	GLN
1	B	208	HIS
1	B	222	GLN
1	B	243	ASN
1	B	250	GLN
1	B	332	ASN
1	B	353	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

4 ligands are 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	$\# Z > 2$
2	CMP	B	401	-	25,25,25	1.02	2 (8%)	37,39,39	1.71	2 (5%)
3	SO4	A	403	-	4,4,4	0.37	0	6,6,6	0.06	0
3	SO4	A	402	-	4,4,4	0.38	0	6,6,6	0.09	0
2	CMP	A	401	-	25,25,25	0.91	1 (4%)	37,39,39	1.61	2 (5%)

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
2	CMP	B	401	-	-	0/4/31/31	0/4/4/4
2	CMP	A	401	-	-	0/4/31/31	0/4/4/4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	CMP	P-O5'	2.85	1.60	1.57
2	B	401	CMP	P-O3'	2.75	1.62	1.57
2	A	401	CMP	P-O5'	2.56	1.60	1.57

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	CMP	O3'-C3'-C4'	-8.72	104.12	110.71
2	A	401	CMP	O3'-C3'-C4'	-7.90	104.75	110.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	CMP	O2P-P-O1P	3.69	119.90	108.56
2	B	401	CMP	O2P-P-O1P	3.49	119.28	108.56

There are no chirality outliers.

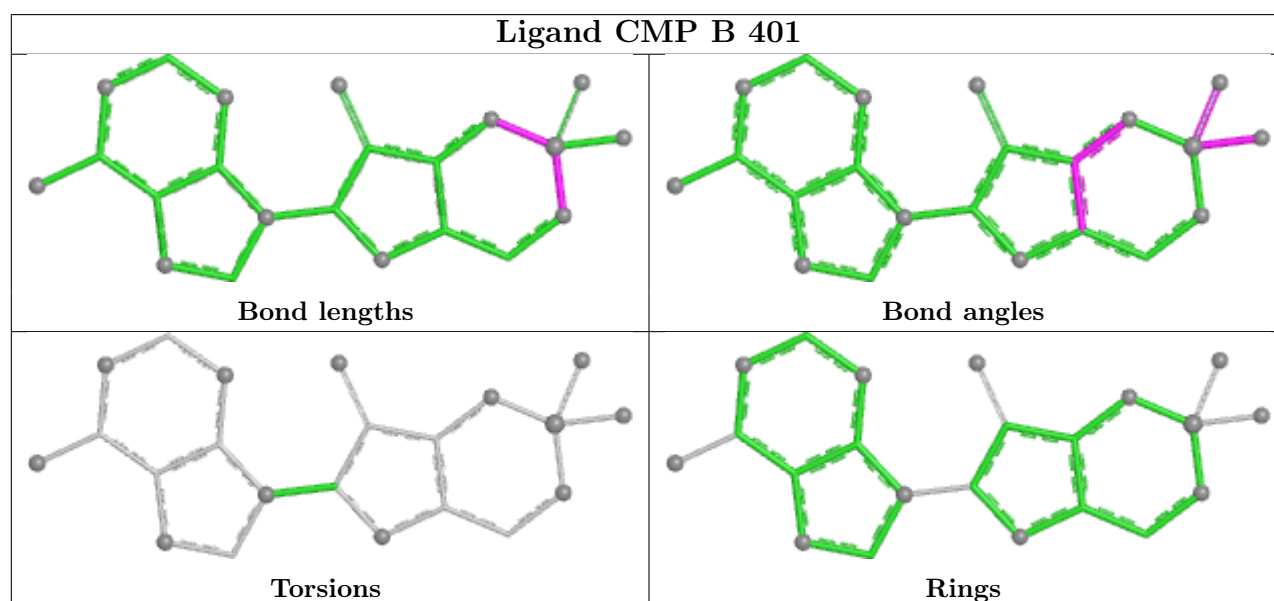
There are no torsion outliers.

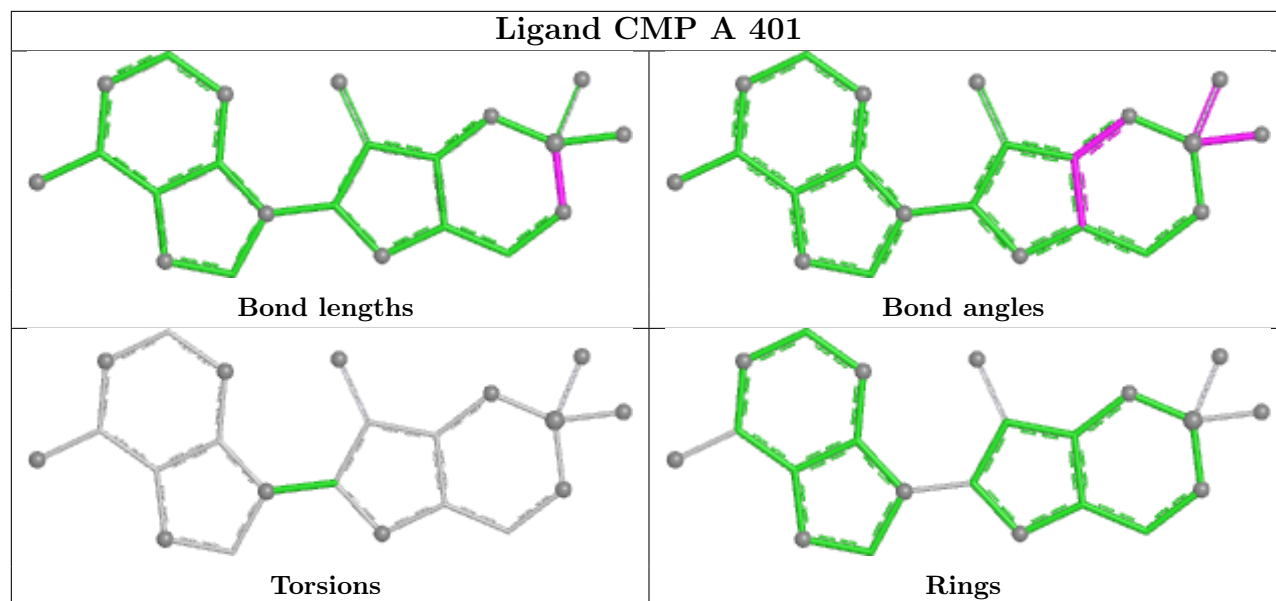
There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	CMP	5	0
3	A	403	SO4	1	0
2	A	401	CMP	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	278/299 (92%)	0.49	20 (7%) 21 19	19, 43, 69, 93	0
1	B	278/299 (92%)	0.98	71 (25%) 1 1	16, 51, 89, 94	0
All	All	556/598 (92%)	0.74	91 (16%) 4 3	16, 47, 84, 94	0

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	183	LEU	5.3
1	B	153	GLY	5.1
1	B	79	ALA	4.6
1	A	273	PRO	4.6
1	A	274	ASN	4.4
1	A	78	GLN	4.3
1	B	156	LEU	4.3
1	A	272	SER	4.3
1	B	84	THR	4.3
1	B	117	CYS	4.0
1	B	155	LYS	4.0
1	B	123	TYR	3.9
1	B	149	VAL	3.9
1	B	80	PHE	3.8
1	B	124	GLY	3.8
1	A	271	ASP	3.7
1	B	126	ASP	3.7
1	B	154	VAL	3.6
1	B	122	GLU	3.6
1	B	78	GLN	3.6
1	B	180	VAL	3.6
1	B	83	PHE	3.5
1	A	330	VAL	3.5
1	A	254	GLY	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	142	MET	3.4
1	B	186	VAL	3.2
1	B	188	LEU	3.2
1	B	164	VAL	3.2
1	B	150	THR	3.2
1	B	92	LEU	3.1
1	B	90	LYS	3.1
1	B	187	LYS	3.0
1	B	128	CYS	3.0
1	B	127	SER	3.0
1	B	121	VAL	3.0
1	B	159	MET	2.9
1	A	276	ASP	2.9
1	A	275	GLU	2.9
1	B	184	VAL	2.8
1	B	144	ASP	2.8
1	A	81	ARG	2.8
1	B	275	GLU	2.8
1	B	177	THR	2.8
1	B	85	LYS	2.8
1	B	181	LYS	2.8
1	B	274	ASN	2.8
1	B	273	PRO	2.8
1	B	158	THR	2.7
1	B	195	CYS	2.7
1	B	182	THR	2.7
1	B	175	THR	2.6
1	B	335	TYR	2.6
1	B	162	GLY	2.6
1	B	152	GLU	2.5
1	B	147	VAL	2.5
1	B	108	LEU	2.5
1	B	179	THR	2.5
1	B	161	PRO	2.5
1	B	185	ASN	2.5
1	B	89	SER	2.5
1	B	93	ILE	2.5
1	B	157	CYS	2.4
1	A	296	GLY	2.4
1	B	272	SER	2.4
1	B	151	LYS	2.4
1	A	170	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	81	ARG	2.4
1	B	168	LEU	2.4
1	B	115	VAL	2.4
1	B	146	LYS	2.4
1	A	344	TYR	2.3
1	A	79	ALA	2.3
1	B	172	TYR	2.3
1	B	344	TYR	2.3
1	B	86	SER	2.3
1	A	355	LYS	2.3
1	B	94	LYS	2.2
1	B	125	LYS	2.2
1	A	117	CYS	2.2
1	B	101	ASP	2.2
1	A	227	GLU	2.2
1	A	195	CYS	2.2
1	B	129	ILE	2.2
1	B	354	LEU	2.1
1	B	190	ALA	2.1
1	B	178	ALA	2.1
1	A	197	GLN	2.1
1	B	136	GLY	2.1
1	B	95	GLU	2.1
1	A	222	GLN	2.0
1	B	192	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

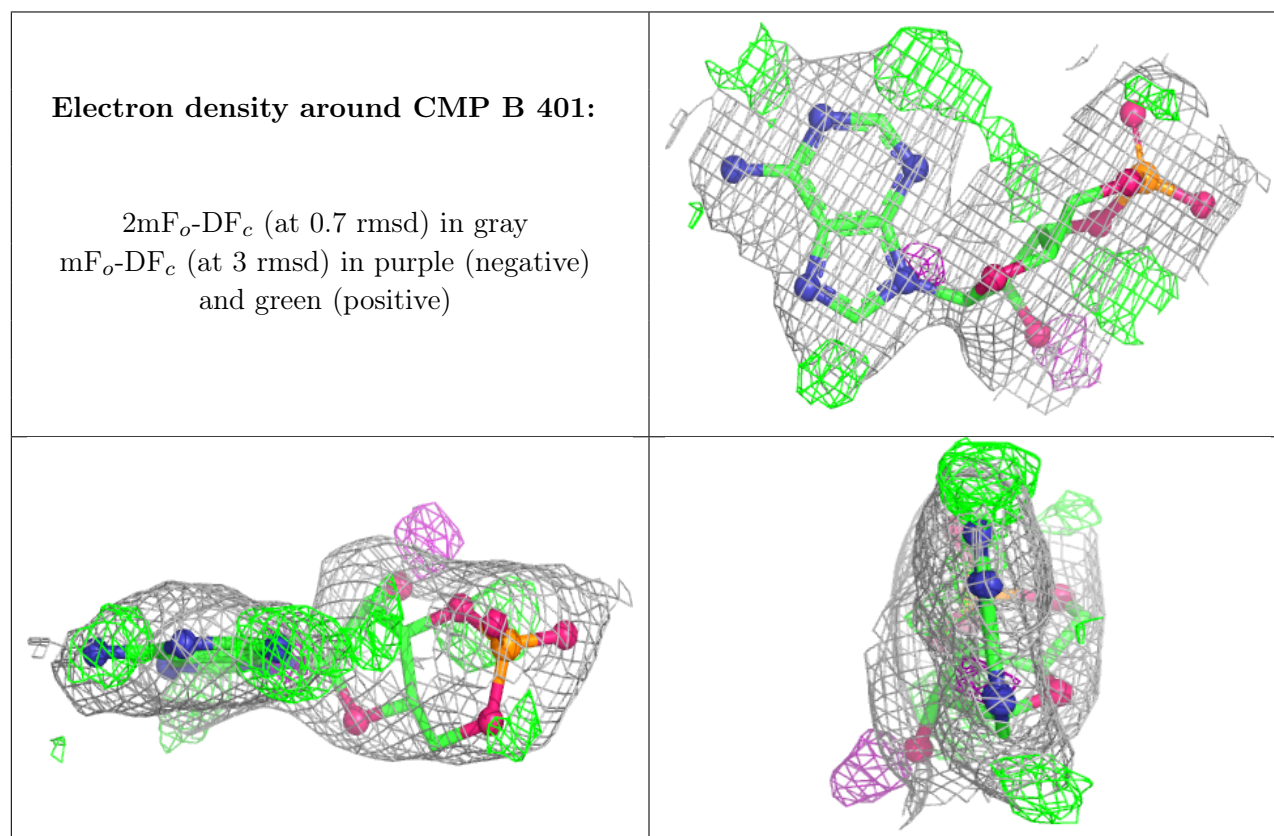
There are no oligosaccharides in this entry.

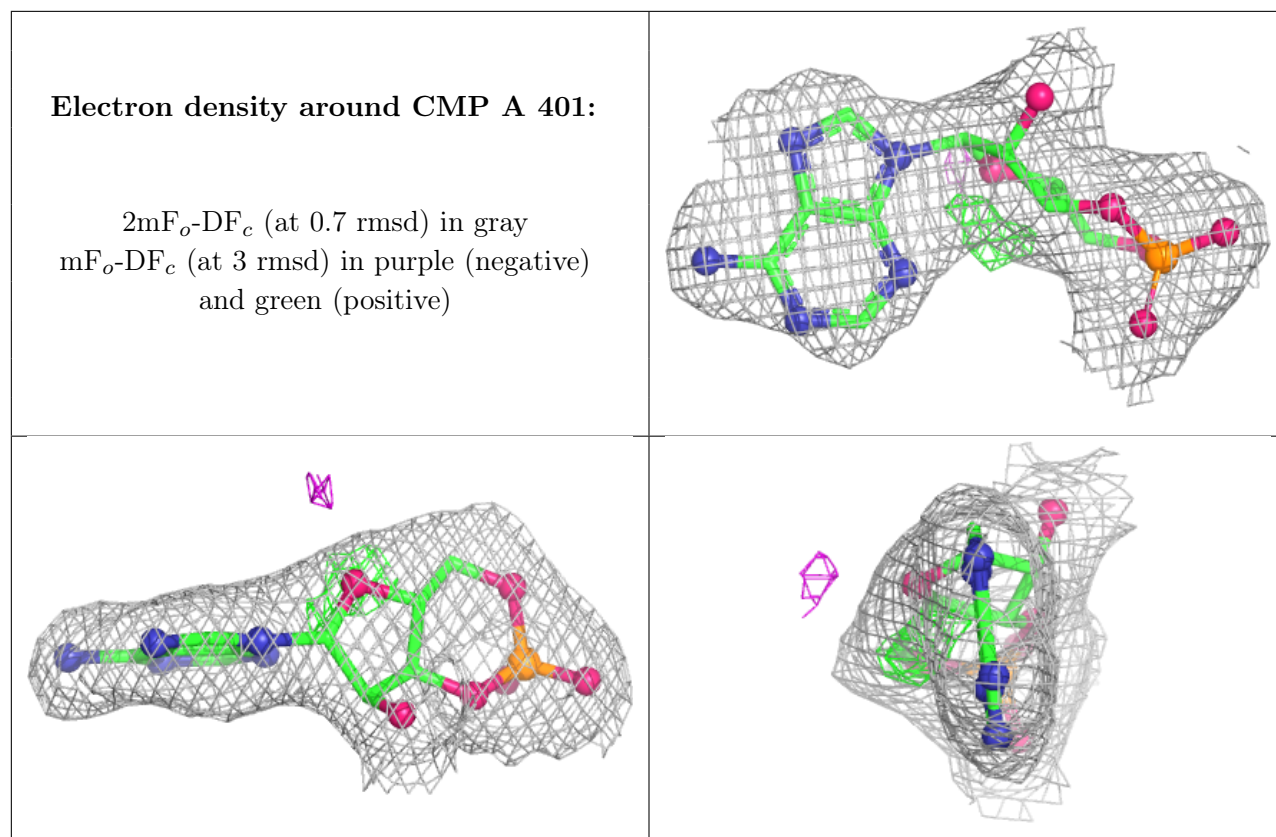
6.4 Ligands ⓘ

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
2	CMP	B	401	22/22	0.79	0.18	56,64,65,66	0
3	SO4	A	403	5/5	0.84	0.14	83,83,83,83	0
3	SO4	A	402	5/5	0.94	0.10	68,68,69,69	0
2	CMP	A	401	22/22	0.96	0.09	23,37,47,50	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers [i](#)

There are no such residues in this entry.