



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:17 AM UTC

PDB ID : 3M1S / pdb_00003m1s
Title : Structure of Ruthenium Half-Sandwich Complex Bound to Glycogen Synthase Kinase 3
Authors : Atilla-Gokcumen, G.E.; Di Costanzo, L.; Zimmermann, G.; Meggers, E.
Deposited on : 2010-03-05
Resolution : 3.13 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

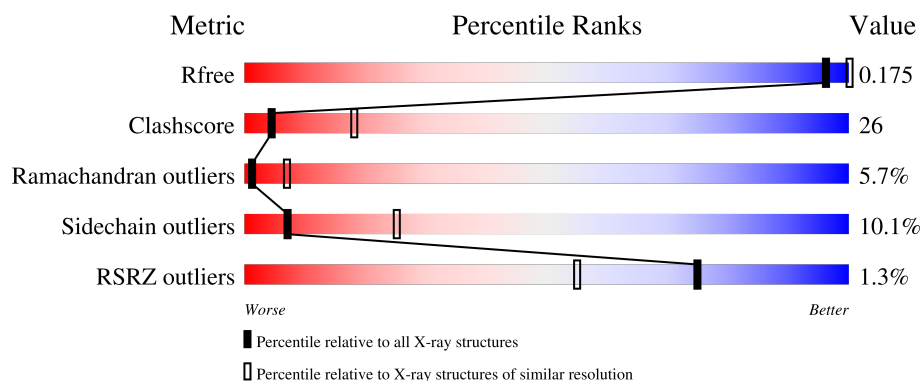
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.13 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	2351 (3.18-3.10)
Clashscore	190562	2452 (3.18-3.10)
Ramachandran outliers	187476	2324 (3.18-3.10)
Sidechain outliers	187428	2324 (3.18-3.10)
RSRZ outliers	180081	2351 (3.18-3.10)

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	420	43%33%6%17%
1	B	420	41%33%7%17%

2 Entry composition [i](#)

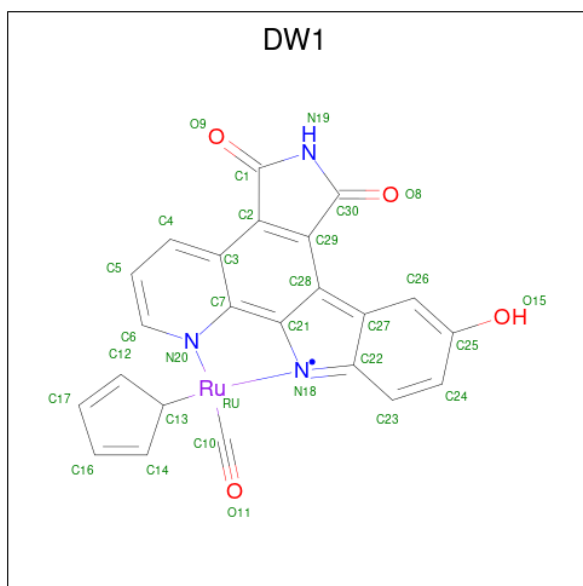
There are 3 unique types of molecules in this entry. The entry contains 5579 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glycogen synthase kinase-3 beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	348	Total	C	N	O	S	6	1	0
			2710	1749	455	495	11			
1	B	349	Total	C	N	O	S	0	2	0
			2716	1754	455	496	11			

- Molecule 2 is Ruthenium pyridocarbazole (CCD ID: DW1) (formula: $C_{23}H_{13}N_3O_4Ru$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	Ru	0	0
			31	23	3	4	1		
2	B	1	Total	C	N	O	Ru	0	0
			31	23	3	4	1		

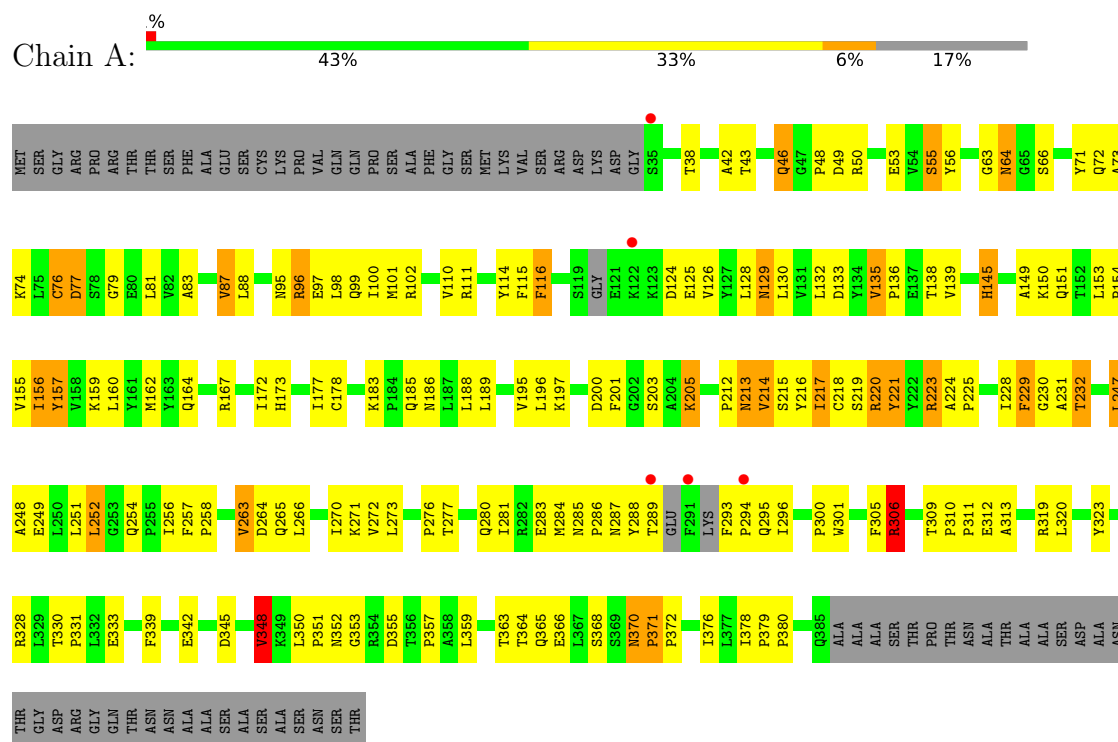
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	45	Total 45	O 45	0	0
3	B	46	Total 46	O 46	0	0

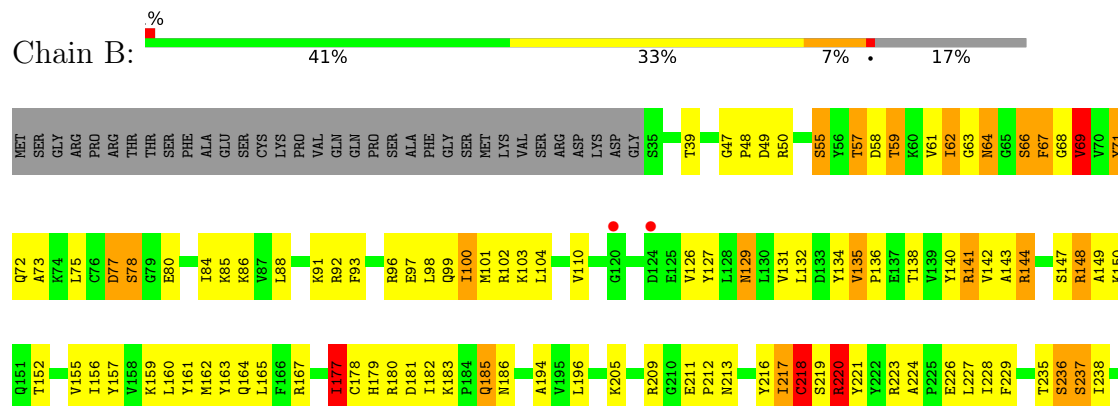
3 Residue-property plots [i](#)

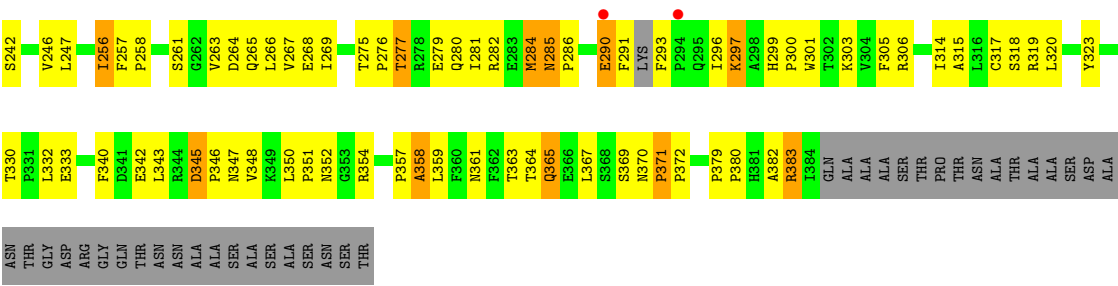
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Glycogen synthase kinase-3 beta



• Molecule 1: Glycogen synthase kinase-3 beta





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.04Å 86.11Å 177.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.22 – 3.13 38.22 – 3.13	Depositor EDS
% Data completeness (in resolution range)	92.6 (38.22-3.13) 92.5 (38.22-3.13)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.91 (at 3.12Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.169 , 0.228 0.168 , 0.175	Depositor DCC
R_{free} test set	1100 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å ²)	56.4	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 54.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.023 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5579	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 3.01% 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: DW1

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	0.80	0/2784	1.13	10/3800 (0.3%)
1	B	0.79	0/2797	1.13	16/3823 (0.4%)
All	All	0.79	0/5581	1.13	26/7623 (0.3%)

There are no bond length outliers.

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	285	ASN	CA-C-N	9.73	129.36	119.24
1	A	285	ASN	C-N-CA	9.73	129.36	119.24
1	B	285	ASN	CA-C-N	9.41	129.03	119.24
1	B	285	ASN	C-N-CA	9.41	129.03	119.24
1	B	379	PRO	CA-C-N	7.77	129.55	119.84
1	B	379	PRO	C-N-CA	7.77	129.55	119.84
1	B	126	VAL	N-CA-C	7.33	118.43	107.80
1	B	135	VAL	CA-C-N	6.69	126.28	119.19
1	B	135	VAL	C-N-CA	6.69	126.28	119.19
1	A	371	PRO	N-CA-C	6.09	118.13	110.70
1	A	126	VAL	N-CA-C	6.06	117.32	108.53
1	A	135	VAL	CA-C-N	6.02	127.36	119.84
1	A	135	VAL	C-N-CA	6.02	127.36	119.84
1	B	69	VAL	CB-CA-C	-5.63	103.86	111.63
1	A	254	GLN	N-CA-C	5.58	113.24	108.22
1	B	345	ASP	CA-C-N	5.45	125.14	119.64
1	B	345	ASP	C-N-CA	5.45	125.14	119.64
1	B	104	LEU	N-CA-C	5.39	117.20	108.41
1	B	177	ILE	CB-CA-C	-5.36	103.88	111.28
1	A	376	ILE	CB-CA-C	-5.29	105.16	112.24
1	A	100	ILE	CB-CA-C	-5.24	102.69	111.29
1	B	320	LEU	N-CA-C	-5.24	106.95	113.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	371	PRO	N-CA-C	5.18	117.02	110.70
1	A	295	GLN	N-CA-C	5.13	117.67	108.17
1	B	50	ARG	CA-C-N	5.08	126.19	119.84
1	B	50	ARG	C-N-CA	5.08	126.19	119.84

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	2710	0	2646	133	0
1	B	2716	0	2653	154	0
2	A	31	0	11	0	0
2	B	31	0	12	1	0
3	A	45	0	0	3	0
3	B	46	0	0	3	0
All	All	5579	0	5322	284	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 26.

All (284) 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:B:220:ARG:HG2	1:B:220:ARG:HH11	0.97	1.08
1:B:220:ARG:HH11	1:B:220:ARG:CG	1.76	0.98
1:A:156:ILE:HG23	1:A:157:TYR:H	1.31	0.94
1:B:220:ARG:HG2	1:B:220:ARG:NH1	1.77	0.94
1:A:223:ARG:HG3	1:A:223:ARG:HH11	1.29	0.93
1:B:86:LYS:HE2	1:B:127:TYR:CD2	2.05	0.91
1:A:96:ARG:HH21	1:A:96:ARG:HG3	1.36	0.89
1:B:141:ARG:HH21	1:B:141:ARG:HG3	1.36	0.89
1:A:167:ARG:HD3	3:A:427:HOH:O	1.73	0.86
1:A:196:LEU:HD23	1:A:197:LYS:N	1.94	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:141:ARG:HG3	1:B:141:ARG:NH2	1.92	0.81
1:A:156:ILE:HG23	1:A:157:TYR:N	1.97	0.80
1:B:217:ILE:O	1:B:218:CYS:HB2	1.81	0.80
1:B:167:ARG:HD3	3:B:428:HOH:O	1.81	0.79
1:B:183:LYS:HE2	1:B:186:ASN:ND2	2.00	0.77
1:B:96:ARG:O	1:B:100:ILE:HG13	1.85	0.76
1:B:162:MET:HG3	1:B:247:LEU:HD13	1.68	0.74
1:B:284:MET:HE1	1:B:323:TYR:CD1	2.23	0.73
1:A:342:GLU:O	1:A:348:VAL:HG21	1.90	0.72
1:A:196:LEU:HD23	1:A:196:LEU:C	2.14	0.71
1:A:156:ILE:CG2	1:A:157:TYR:H	2.04	0.70
1:A:215:SER:HB3	1:A:231:ALA:O	1.92	0.69
1:B:162:MET:HE2	1:B:247:LEU:HB2	1.74	0.69
1:B:305:PHE:CD2	1:B:314:ILE:HG12	2.27	0.68
1:A:370:ASN:HD22	1:A:372:PRO:HD2	1.58	0.68
1:A:63:GLY:O	1:A:64:ASN:HB3	1.94	0.67
1:A:115:PHE:O	1:A:116:PHE:HB3	1.95	0.67
1:A:149:ALA:O	1:A:151:GLN:N	2.28	0.67
1:A:159:LYS:HE2	1:A:339:PHE:O	1.95	0.66
1:A:74:LYS:HE2	1:A:79:GLY:O	1.95	0.66
1:A:370:ASN:ND2	1:A:372:PRO:HD2	2.11	0.65
1:A:71:TYR:O	1:A:83:ALA:HA	1.95	0.65
1:B:358:ALA:HB1	1:B:361:ASN:ND2	2.12	0.65
1:B:315:ALA:O	1:B:319:ARG:HG2	1.97	0.64
1:B:96:ARG:CZ	1:B:205:LYS:HG3	2.27	0.64
1:A:312:GLU:H	1:A:312:GLU:CD	2.05	0.64
1:B:370:ASN:OD1	1:B:372:PRO:HD2	1.98	0.64
1:B:220:ARG:HG3	1:B:221[B]:TYR:H	1.62	0.63
1:A:98:LEU:O	1:A:102:ARG:HG3	1.98	0.63
1:B:277:THR:O	1:B:281:ILE:HD12	1.97	0.63
1:B:160:LEU:HD23	1:B:343:LEU:HD22	1.79	0.62
1:A:185:GLN:HB2	3:A:435:HOH:O	1.98	0.62
1:B:276:PRO:HB2	1:B:281:ILE:CD1	2.29	0.62
1:B:220:ARG:HG3	1:B:221[A]:TYR:H	1.63	0.61
1:A:223:ARG:HH11	1:A:223:ARG:CG	2.08	0.61
1:A:320:LEU:O	1:A:328:ARG:HD3	2.02	0.59
1:B:71:TYR:N	1:B:71:TYR:CD2	2.65	0.59
1:B:345:ASP:O	1:B:348:VAL:HG12	2.02	0.59
1:A:153:LEU:O	1:A:154:PRO:C	2.45	0.59
1:B:141:ARG:HH21	1:B:141:ARG:CG	2.11	0.59
1:B:220:ARG:HG3	1:B:221[A]:TYR:N	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:PHE:C	1:A:203:SER:H	2.10	0.58
1:B:98:LEU:O	1:B:102:ARG:HG3	2.03	0.58
1:B:180:ARG:HG2	1:B:238:ILE:HD11	1.86	0.58
1:B:88:LEU:HD12	1:B:127:TYR:CE1	2.37	0.58
1:A:149:ALA:C	1:A:151:GLN:H	2.12	0.58
1:A:256:ILE:C	1:A:258:PRO:HD3	2.28	0.58
1:A:145:HIS:ND1	1:A:145:HIS:C	2.62	0.58
1:B:265:GLN:O	1:B:269:ILE:HG13	2.03	0.58
1:A:160:LEU:O	1:A:164:GLN:HG3	2.04	0.57
1:B:220:ARG:HG3	1:B:221[B]:TYR:N	2.18	0.57
1:A:363:THR:OG1	1:A:366:GLU:HG3	2.05	0.57
1:A:357:PRO:O	1:A:359:LEU:HG	2.05	0.57
1:B:132:LEU:HD13	2:B:421:DW1:O9	2.03	0.57
1:A:351:PRO:C	1:A:353:GLY:H	2.13	0.57
1:A:249:GLU:HB2	3:A:442:HOH:O	2.03	0.57
1:B:142:VAL:HG12	1:B:143:ALA:N	2.19	0.57
1:B:177:ILE:HG22	1:B:178:CYS:N	2.19	0.57
1:A:72:GLN:NE2	1:A:81:LEU:HD22	2.20	0.57
1:A:220:ARG:HG3	1:A:265:GLN:HE22	1.69	0.57
1:B:97:GLU:O	1:B:101:MET:HG2	2.05	0.57
1:B:61:VAL:HG12	1:B:61:VAL:O	2.04	0.56
1:A:205:LYS:NZ	1:A:213:ASN:HB3	2.20	0.56
1:A:270:ILE:C	1:A:272:VAL:H	2.14	0.56
1:B:100:ILE:HG23	1:B:177:ILE:HD12	1.87	0.56
1:B:129:ASN:N	1:B:129:ASN:HD22	2.04	0.56
1:B:345:ASP:OD1	1:B:346:PRO:HD2	2.06	0.56
1:A:370:ASN:HD22	1:A:370:ASN:C	2.14	0.55
1:B:357:PRO:O	1:B:359:LEU:HG	2.07	0.55
1:A:97:GLU:HG3	1:A:201:PHE:C	2.31	0.55
1:A:214:VAL:HB	1:A:216:TYR:CE2	2.41	0.55
1:A:270:ILE:O	1:A:272:VAL:N	2.39	0.55
1:A:330:THR:HG23	1:A:333:GLU:OE1	2.06	0.55
1:B:242:SER:O	1:B:246:VAL:HG23	2.06	0.55
1:B:63:GLY:O	1:B:64:ASN:HB3	2.05	0.55
1:A:248:ALA:O	1:A:252:LEU:HB2	2.07	0.55
1:B:235:THR:O	1:B:237:SER:N	2.40	0.55
1:A:277:THR:H	1:A:280:GLN:HB2	1.71	0.54
1:A:72:GLN:CD	1:A:81:LEU:HD22	2.32	0.54
1:A:96:ARG:HG3	1:A:96:ARG:NH2	2.13	0.54
1:B:185:GLN:HB2	3:B:461:HOH:O	2.06	0.54
1:A:95:ASN:ND2	1:A:128:LEU:HD23	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:ARG:HG3	1:A:223:ARG:NH1	2.10	0.54
1:B:220:ARG:CG	1:B:220:ARG:NH1	2.47	0.54
1:A:276:PRO:HB2	1:A:281:ILE:HG13	1.89	0.54
1:B:268:GLU:OE1	1:B:268:GLU:HA	2.06	0.54
1:A:129:ASN:N	1:A:129:ASN:HD22	2.06	0.54
1:A:183:LYS:HE2	1:A:186:ASN:ND2	2.23	0.54
1:B:279:GLU:O	1:B:280:GLN:C	2.51	0.54
1:A:130:LEU:N	1:A:130:LEU:HD23	2.22	0.54
1:A:281:ILE:HA	1:A:284:MET:HE3	1.90	0.54
1:A:101:MET:HE3	1:A:132:LEU:HD21	1.89	0.53
1:A:138:THR:O	1:A:139:VAL:C	2.50	0.53
1:B:88:LEU:HA	1:B:127:TYR:HD1	1.73	0.53
1:A:370:ASN:ND2	1:A:370:ASN:C	2.64	0.53
1:A:46:GLN:HE22	1:A:111:ARG:HD2	1.74	0.53
1:A:263:VAL:HG23	1:B:216:TYR:CD1	2.44	0.52
1:B:228:ILE:HG21	1:B:266:LEU:HG	1.92	0.52
1:B:147:SER:O	1:B:148:ARG:C	2.53	0.52
1:B:64:ASN:HA	1:B:67:PHE:CE1	2.45	0.52
1:B:135:VAL:HG13	1:B:136:PRO:HD2	1.91	0.52
1:B:361:ASN:N	1:B:361:ASN:OD1	2.43	0.52
1:A:196:LEU:C	1:A:196:LEU:CD2	2.83	0.52
1:B:301:TRP:CD1	1:B:318:SER:HB3	2.46	0.51
1:A:201:PHE:C	1:A:203:SER:N	2.68	0.51
1:A:286:PRO:C	1:A:288:TYR:H	2.19	0.51
1:B:276:PRO:HB2	1:B:281:ILE:HG13	1.91	0.51
1:B:365:GLN:HE21	1:B:365:GLN:HA	1.75	0.51
1:B:103:LYS:NZ	3:B:427:HOH:O	2.43	0.51
1:B:220:ARG:CG	1:B:221[B]:TYR:H	2.24	0.51
1:B:284:MET:HE1	1:B:323:TYR:HD1	1.74	0.51
1:A:228:ILE:C	1:A:230:GLY:H	2.17	0.51
1:B:160:LEU:HD11	1:B:350:LEU:HD21	1.92	0.51
1:B:194:ALA:CB	1:B:350:LEU:HD11	2.41	0.51
1:B:224:ALA:O	1:B:227:LEU:HB2	2.11	0.51
1:A:162:MET:HE2	1:A:247:LEU:HB2	1.93	0.51
1:A:172:ILE:HG13	1:A:173:HIS:N	2.24	0.51
1:B:220:ARG:CG	1:B:221[A]:TYR:H	2.24	0.51
1:A:160:LEU:HD11	1:A:350:LEU:HD21	1.93	0.51
1:A:342:GLU:O	1:A:348:VAL:CG2	2.57	0.51
1:B:71:TYR:N	1:B:71:TYR:HD2	2.08	0.51
1:B:155:VAL:O	1:B:156:ILE:C	2.54	0.50
1:A:76:CYS:O	1:A:77:ASP:C	2.54	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:280:GLN:O	1:A:284:MET:HE3	2.12	0.50
1:B:364:THR:O	1:B:367:LEU:N	2.41	0.50
1:A:263:VAL:HG23	1:B:216:TYR:CE1	2.46	0.50
1:B:62:ILE:HD11	1:B:72:GLN:HB2	1.93	0.50
1:B:71:TYR:HD2	1:B:71:TYR:H	1.60	0.50
1:B:226:GLU:HB3	1:B:284:MET:HB3	1.94	0.50
1:A:38:THR:O	1:A:55:SER:HA	2.12	0.50
1:B:129:ASN:N	1:B:129:ASN:ND2	2.59	0.50
1:A:365:GLN:O	1:A:368:SER:HB3	2.12	0.50
1:B:352:ASN:HD21	1:B:354:ARG:HD3	1.77	0.50
1:A:280:GLN:O	1:A:283:GLU:HB2	2.12	0.49
1:B:363:THR:O	1:B:364:THR:C	2.54	0.49
1:A:220:ARG:O	1:A:221[A]:TYR:CB	2.60	0.49
1:B:78:SER:C	1:B:80:GLU:H	2.18	0.49
1:B:91:LYS:C	1:B:93:PHE:H	2.20	0.49
1:A:160:LEU:HD11	1:A:350:LEU:CD2	2.42	0.49
1:B:305:PHE:O	1:B:306:ARG:C	2.56	0.49
1:A:56:TYR:C	1:A:56:TYR:CD2	2.90	0.49
1:A:155:VAL:O	1:A:156:ILE:C	2.55	0.49
1:B:275:THR:HG23	1:B:276:PRO:HD2	1.94	0.49
1:B:267:VAL:HG12	1:B:268:GLU:N	2.28	0.48
1:B:84:ILE:HG12	1:B:131:VAL:HG22	1.95	0.48
1:B:220:ARG:O	1:B:223:ARG:HG3	2.13	0.48
1:B:235:THR:O	1:B:236:SER:C	2.57	0.48
1:B:179:HIS:O	1:B:180:ARG:HB2	2.14	0.48
1:B:358:ALA:HB1	1:B:361:ASN:HD21	1.78	0.48
1:A:177:ILE:CG2	1:A:178:CYS:N	2.77	0.48
1:A:263:VAL:HG12	1:A:264:ASP:N	2.28	0.48
1:B:194:ALA:HB2	1:B:350:LEU:HD11	1.96	0.48
1:A:72:GLN:HG2	1:A:73:ALA:H	1.80	0.47
1:B:157:TYR:CZ	1:B:351:PRO:HG2	2.50	0.47
1:A:177:ILE:HG22	1:A:178:CYS:N	2.29	0.47
1:A:305:PHE:O	1:A:306:ARG:C	2.57	0.47
1:A:305:PHE:O	1:A:306:ARG:O	2.32	0.47
1:A:348:VAL:O	1:A:348:VAL:HG12	2.14	0.47
1:B:220:ARG:CG	1:B:221[B]:TYR:N	2.78	0.47
1:B:220:ARG:CG	1:B:221[A]:TYR:N	2.78	0.47
1:B:332:LEU:HD12	1:B:332:LEU:HA	1.73	0.47
1:A:128:LEU:HD12	1:A:129:ASN:N	2.30	0.47
1:A:219:SER:O	1:A:220:ARG:C	2.57	0.47
1:A:43:THR:O	1:A:114:TYR:HA	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:276:PRO:HB2	1:B:281:ILE:HD11	1.97	0.46
1:A:251:LEU:HD11	1:A:313:ALA:HB1	1.97	0.46
1:A:330:THR:O	1:A:331:PRO:C	2.55	0.46
1:A:257:PHE:N	1:A:258:PRO:HD3	2.30	0.46
1:A:220:ARG:HG3	1:A:265:GLN:NE2	2.29	0.46
1:B:266:LEU:HA	1:B:266:LEU:HD23	1.60	0.46
1:A:124:ASP:O	1:A:125:GLU:HG3	2.16	0.46
1:A:379:PRO:O	1:A:380:PRO:C	2.58	0.46
1:B:229:PHE:CE1	1:B:266:LEU:HD11	2.51	0.46
1:B:72:GLN:HG2	1:B:73:ALA:N	2.31	0.45
1:B:86:LYS:HE2	1:B:127:TYR:HD2	1.74	0.45
1:A:129:ASN:C	1:A:130:LEU:HD23	2.42	0.45
1:A:319:ARG:HA	1:A:319:ARG:HH11	1.81	0.45
1:B:183:LYS:HE2	1:B:186:ASN:HD21	1.79	0.45
1:B:59:THR:HA	1:B:72:GLN:O	2.17	0.45
1:B:91:LYS:C	1:B:93:PHE:N	2.75	0.45
1:B:96:ARG:O	1:B:96:ARG:HG3	2.16	0.45
1:B:299:HIS:CE1	1:B:303:LYS:CB	2.99	0.45
1:B:296:ILE:HG22	1:B:297:LYS:O	2.16	0.45
1:B:364:THR:HG22	1:B:365:GLN:N	2.31	0.45
1:A:330:THR:HG23	1:A:333:GLU:CD	2.42	0.45
1:A:48:PRO:O	1:A:50:ARG:N	2.50	0.45
1:A:95:ASN:O	1:A:99:GLN:HG3	2.17	0.45
1:A:252:LEU:HA	1:A:252:LEU:HD23	1.62	0.45
1:B:66:SER:C	1:B:68:GLY:H	2.25	0.45
1:B:330:THR:OG1	1:B:333:GLU:HB2	2.17	0.45
1:A:345:ASP:O	1:A:348:VAL:HB	2.16	0.44
1:B:86:LYS:CE	1:B:127:TYR:CD2	2.91	0.44
1:A:305:PHE:C	1:A:306:ARG:O	2.60	0.44
1:B:332:LEU:HD21	1:B:367:LEU:HA	1.98	0.44
1:B:357:PRO:O	1:B:359:LEU:N	2.50	0.44
1:A:135:VAL:HB	1:A:188:LEU:HB3	2.00	0.44
1:B:345:ASP:HA	1:B:346:PRO:HD3	1.74	0.44
1:B:276:PRO:HB2	1:B:281:ILE:CG1	2.48	0.44
1:B:365:GLN:HA	1:B:365:GLN:NE2	2.33	0.44
1:A:371:PRO:N	1:A:372:PRO:CD	2.80	0.44
1:A:159:LYS:O	1:A:160:LEU:C	2.61	0.44
1:B:284:MET:HB2	1:B:285:ASN:H	1.53	0.44
1:A:129:ASN:N	1:A:129:ASN:ND2	2.64	0.44
1:A:342:GLU:O	1:A:342:GLU:HG2	2.17	0.44
1:B:227:LEU:HD23	1:B:227:LEU:HA	1.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:264:ASP:O	1:B:268:GLU:HG2	2.18	0.44
1:B:182:ILE:HB	1:B:242:SER:HB2	1.99	0.43
1:B:194:ALA:HB2	1:B:350:LEU:CD1	2.48	0.43
1:B:177:ILE:CG2	1:B:178:CYS:N	2.80	0.43
1:B:258:PRO:HD2	1:B:268:GLU:HG3	2.00	0.43
1:A:220:ARG:O	1:A:221[A]:TYR:HB2	2.18	0.43
1:B:134:TYR:C	1:B:134:TYR:CD2	2.96	0.43
1:B:357:PRO:O	1:B:358:ALA:C	2.61	0.43
1:B:78:SER:C	1:B:80:GLU:N	2.76	0.43
1:B:256:ILE:HD13	1:B:257:PHE:CE1	2.54	0.43
1:A:293:PHE:HA	1:A:294:PRO:HD3	1.73	0.43
1:B:209:ARG:C	1:B:211:GLU:H	2.27	0.43
1:A:286:PRO:O	1:A:288:TYR:N	2.44	0.43
1:B:162:MET:O	1:B:165:LEU:HB3	2.19	0.43
1:A:371:PRO:N	1:A:372:PRO:HD2	2.34	0.43
1:B:75:LEU:HD12	1:B:80:GLU:HB3	2.00	0.43
1:B:290:GLU:O	1:B:291:PHE:C	2.62	0.43
1:A:224:ALA:O	1:A:225:PRO:C	2.61	0.43
1:A:217:ILE:O	1:A:218:CYS:CB	2.66	0.42
1:B:382:ALA:O	1:B:383:ARG:HB2	2.19	0.42
1:A:172:ILE:HG13	1:A:173:HIS:HD2	1.83	0.42
1:A:213:ASN:O	1:A:232:THR:HG22	2.19	0.42
1:A:284:MET:HE2	1:A:323:TYR:HB3	2.01	0.42
1:A:229:PHE:CZ	1:A:293:PHE:HZ	2.38	0.42
1:B:371:PRO:N	1:B:372:PRO:CD	2.82	0.42
1:B:69:VAL:CG1	1:B:71:TYR:CE2	3.02	0.42
1:A:359:LEU:HA	1:A:359:LEU:HD23	1.64	0.42
1:B:135:VAL:HG13	1:B:136:PRO:CD	2.49	0.42
1:A:132:LEU:O	1:A:133:ASP:C	2.63	0.42
1:A:189:LEU:HD23	1:A:189:LEU:HA	1.87	0.42
1:A:205:LYS:NZ	1:A:213:ASN:OD1	2.40	0.42
1:B:98:LEU:HA	1:B:98:LEU:HD12	1.75	0.42
1:B:161:TYR:O	1:B:196:LEU:HD13	2.19	0.42
1:A:266:LEU:O	1:A:270:ILE:HG13	2.19	0.42
1:B:211:GLU:HA	1:B:212:PRO:HD3	1.79	0.42
1:A:55:SER:HB2	1:A:76:CYS:SG	2.60	0.42
1:B:365:GLN:HE21	1:B:365:GLN:CA	2.33	0.42
1:A:42:ALA:HB1	1:A:114:TYR:HB3	2.02	0.41
1:B:148:ARG:O	1:B:150:LYS:N	2.52	0.41
1:B:156:ILE:HD13	1:B:342:GLU:OE1	2.20	0.41
1:B:261:SER:O	1:B:265:GLN:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:163:TYR:HB2	1:B:340:PHE:CD1	2.55	0.41
1:B:299:HIS:ND1	1:B:300:PRO:HD2	2.35	0.41
1:B:59:THR:HG23	1:B:73:ALA:HB2	2.02	0.41
1:B:62:ILE:CG1	1:B:72:GLN:HB2	2.50	0.41
1:A:223:ARG:CG	1:A:223:ARG:NH1	2.76	0.41
1:B:57:THR:O	1:B:58:ASP:HB2	2.19	0.41
1:B:291:PHE:O	1:B:293:PHE:N	2.53	0.41
1:A:310:PRO:HA	1:A:311:PRO:HD3	1.97	0.41
1:B:219:SER:O	1:B:220:ARG:C	2.64	0.41
1:B:160:LEU:CD2	1:B:343:LEU:HD22	2.48	0.41
1:A:160:LEU:HA	1:A:160:LEU:HD23	1.80	0.41
1:B:69:VAL:HG11	1:B:71:TYR:CE2	2.56	0.41
1:A:135:VAL:HA	1:A:136:PRO:HD3	1.74	0.41
1:A:273:LEU:HB3	1:A:323:TYR:CE2	2.56	0.41
1:B:96:ARG:NH2	1:B:205:LYS:HG3	2.35	0.41
1:A:216:TYR:HB3	1:B:228:ILE:O	2.21	0.40
1:A:288:TYR:O	1:A:289:THR:C	2.63	0.40
1:A:280:GLN:O	1:A:284:MET:CE	2.70	0.40
1:B:39:THR:OG1	1:B:55:SER:OG	2.38	0.40
1:B:85:LYS:NZ	1:B:97:GLU:OE2	2.44	0.40
1:B:140:TYR:CE2	1:B:144:ARG:NH1	2.89	0.40
1:A:87:VAL:HG23	1:A:88:LEU:O	2.21	0.40
1:B:140:TYR:HE2	1:B:144:ARG:NH1	2.19	0.40
1:A:196:LEU:HD23	1:A:197:LYS:CA	2.51	0.40
1:B:155:VAL:O	1:B:159:LYS:HG3	2.21	0.40
1:B:282:ARG:HA	1:B:286:PRO:HA	2.03	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	342/420 (81%)	283 (83%)	37 (11%)	22 (6%)	1	5
1	B	347/420 (83%)	290 (84%)	39 (11%)	18 (5%)	1	8
All	All	689/840 (82%)	573 (83%)	76 (11%)	40 (6%)	1	7

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	77	ASP
1	A	150	LYS
1	A	220	ARG
1	A	221[A]	TYR
1	A	221[B]	TYR
1	A	271	LYS
1	A	301	TRP
1	B	77	ASP
1	B	236	SER
1	B	290	GLU
1	A	49	ASP
1	A	287	ASN
1	A	352	ASN
1	B	62	ILE
1	B	149	ALA
1	B	181	ASP
1	B	358	ALA
1	A	64	ASN
1	A	76	CYS
1	A	116	PHE
1	A	156	ILE
1	B	48	PRO
1	B	64	ASN
1	B	67	PHE
1	B	92	ARG
1	B	365	GLN
1	A	348	VAL
1	B	47	GLY
1	B	218	CYS
1	B	220	ARG
1	B	277	THR
1	A	157	TYR
1	A	229	PHE
1	A	306	ARG
1	A	370	ASN

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Mol	Chain	Res	Type
1	A	200	ASP
1	B	148	ARG
1	B	383	ARG
1	A	300	PRO
1	A	212	PRO

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	289/364 (79%)	263 (91%)	26 (9%)	9	29
1	B	291/364 (80%)	259 (89%)	32 (11%)	6	21
All	All	580/728 (80%)	522 (90%)	58 (10%)	7	25

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	GLN
1	A	53	GLU
1	A	55	SER
1	A	66	SER
1	A	87	VAL
1	A	96	ARG
1	A	110	VAL
1	A	129	ASN
1	A	145	HIS
1	A	195	VAL
1	A	205	LYS
1	A	213	ASN
1	A	214	VAL
1	A	217	ILE
1	A	223	ARG
1	A	232	THR
1	A	247	LEU
1	A	252	LEU

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Mol	Chain	Res	Type
1	A	263	VAL
1	A	296	ILE
1	A	306	ARG
1	A	309	THR
1	A	348	VAL
1	A	355	ASP
1	A	364	THR
1	A	378	ILE
1	B	49	ASP
1	B	55	SER
1	B	57	THR
1	B	59	THR
1	B	66	SER
1	B	69	VAL
1	B	71	TYR
1	B	77	ASP
1	B	78	SER
1	B	100	ILE
1	B	110	VAL
1	B	129	ASN
1	B	138	THR
1	B	141	ARG
1	B	144	ARG
1	B	152	THR
1	B	164	GLN
1	B	177	ILE
1	B	185	GLN
1	B	213	ASN
1	B	217	ILE
1	B	218	CYS
1	B	220	ARG
1	B	237	SER
1	B	256	ILE
1	B	263	VAL
1	B	284	MET
1	B	297	LYS
1	B	317	CYS
1	B	347	ASN
1	B	369	SER
1	B	380	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	129	ASN
1	A	186	ASN
1	A	352	ASN
1	A	370	ASN
1	B	129	ASN
1	B	186	ASN
1	B	365	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	DW1	B	421	-	26,37,37	1.81	7 (26%)	24,60,60	2.78	9 (37%)
2	DW1	A	421	-	26,37,37	1.80	7 (26%)	24,60,60	2.91	9 (37%)

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	DW1	B	421	-	-	-	0/7/7/7
2	DW1	A	421	-	-	-	0/7/7/7

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	421	DW1	C23-C22	-3.67	1.36	1.40
2	B	421	DW1	C2-C1	-3.49	1.38	1.49
2	B	421	DW1	C7-C3	-3.46	1.37	1.45
2	B	421	DW1	C23-C22	-3.27	1.36	1.40
2	A	421	DW1	C29-C28	-3.25	1.39	1.44
2	A	421	DW1	C2-C1	-3.23	1.39	1.49
2	A	421	DW1	C7-C3	-3.22	1.37	1.45
2	B	421	DW1	C29-C28	-2.78	1.40	1.44
2	A	421	DW1	C2-C3	-2.77	1.40	1.44
2	B	421	DW1	C29-C30	-2.66	1.40	1.49
2	B	421	DW1	C2-C3	-2.61	1.40	1.44
2	A	421	DW1	C29-C30	-2.56	1.41	1.49
2	A	421	DW1	C6-C5	2.34	1.40	1.35
2	B	421	DW1	C6-C5	2.16	1.39	1.35

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	421	DW1	C1-N19-C30	-11.04	103.00	112.59
2	B	421	DW1	C1-N19-C30	-10.74	103.25	112.59
2	A	421	DW1	C24-C23-C22	-3.80	116.25	120.80
2	A	421	DW1	C25-C26-C27	-3.47	117.56	120.89
2	A	421	DW1	C23-C24-C25	3.41	123.49	119.88
2	B	421	DW1	C7-C3-C2	-3.07	114.66	118.43
2	B	421	DW1	C7-C21-C28	2.87	126.97	124.32
2	B	421	DW1	C25-C26-C27	-2.67	118.33	120.89
2	A	421	DW1	C7-C3-C2	-2.62	115.22	118.43
2	A	421	DW1	C2-C1-N19	2.48	114.39	105.32
2	B	421	DW1	O9-C1-C2	-2.45	124.91	128.47
2	B	421	DW1	C2-C1-N19	2.40	114.09	105.32
2	B	421	DW1	C24-C23-C22	-2.27	118.09	120.80
2	A	421	DW1	O8-C30-C29	-2.20	125.28	128.47
2	A	421	DW1	C21-C7-N20	2.12	117.14	110.07
2	A	421	DW1	O9-C1-C2	-2.10	125.42	128.47
2	B	421	DW1	C21-C7-N20	2.07	116.97	110.07
2	B	421	DW1	C23-C24-C25	2.06	122.06	119.88

There are no chirality outliers.

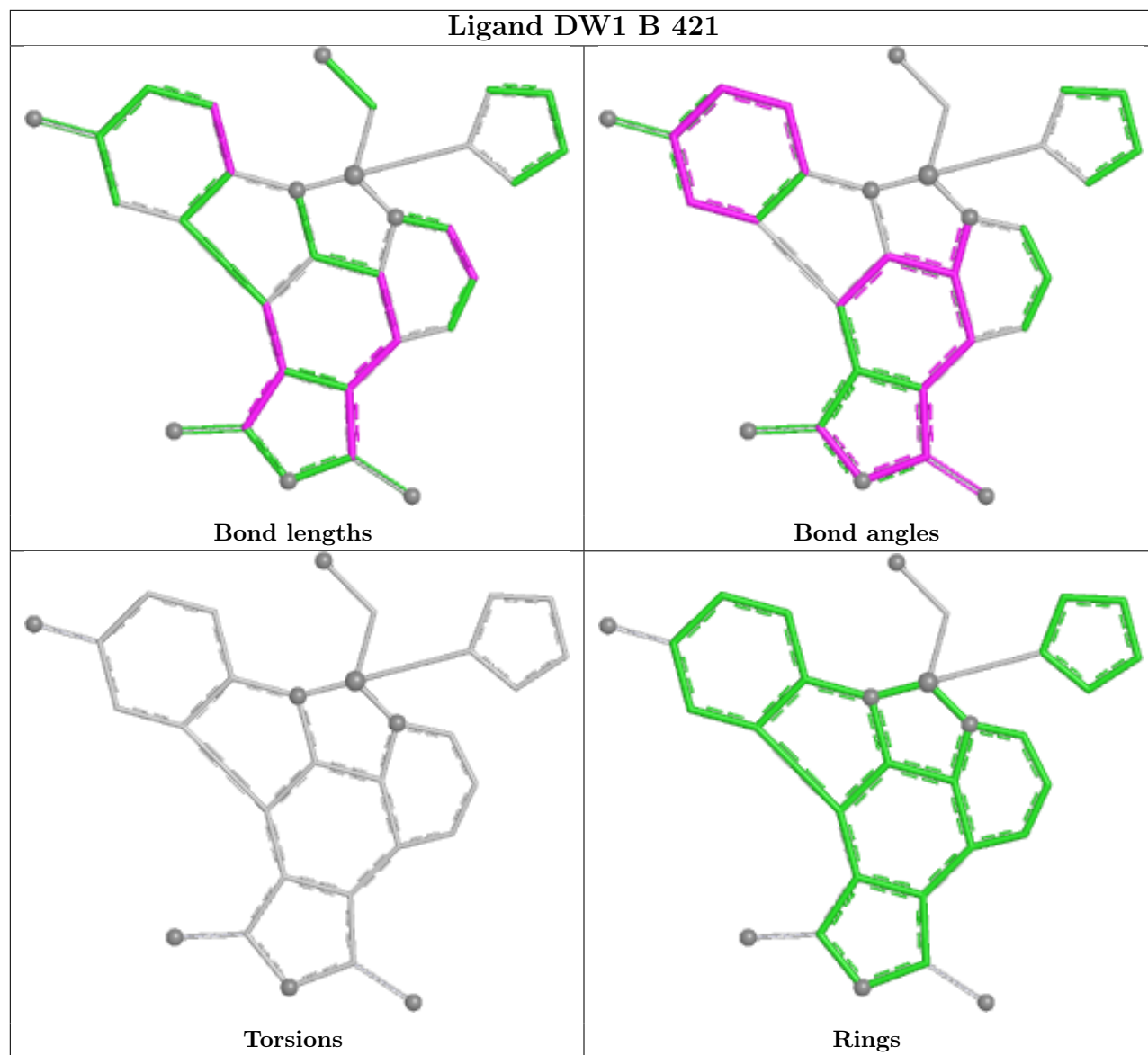
There are no torsion outliers.

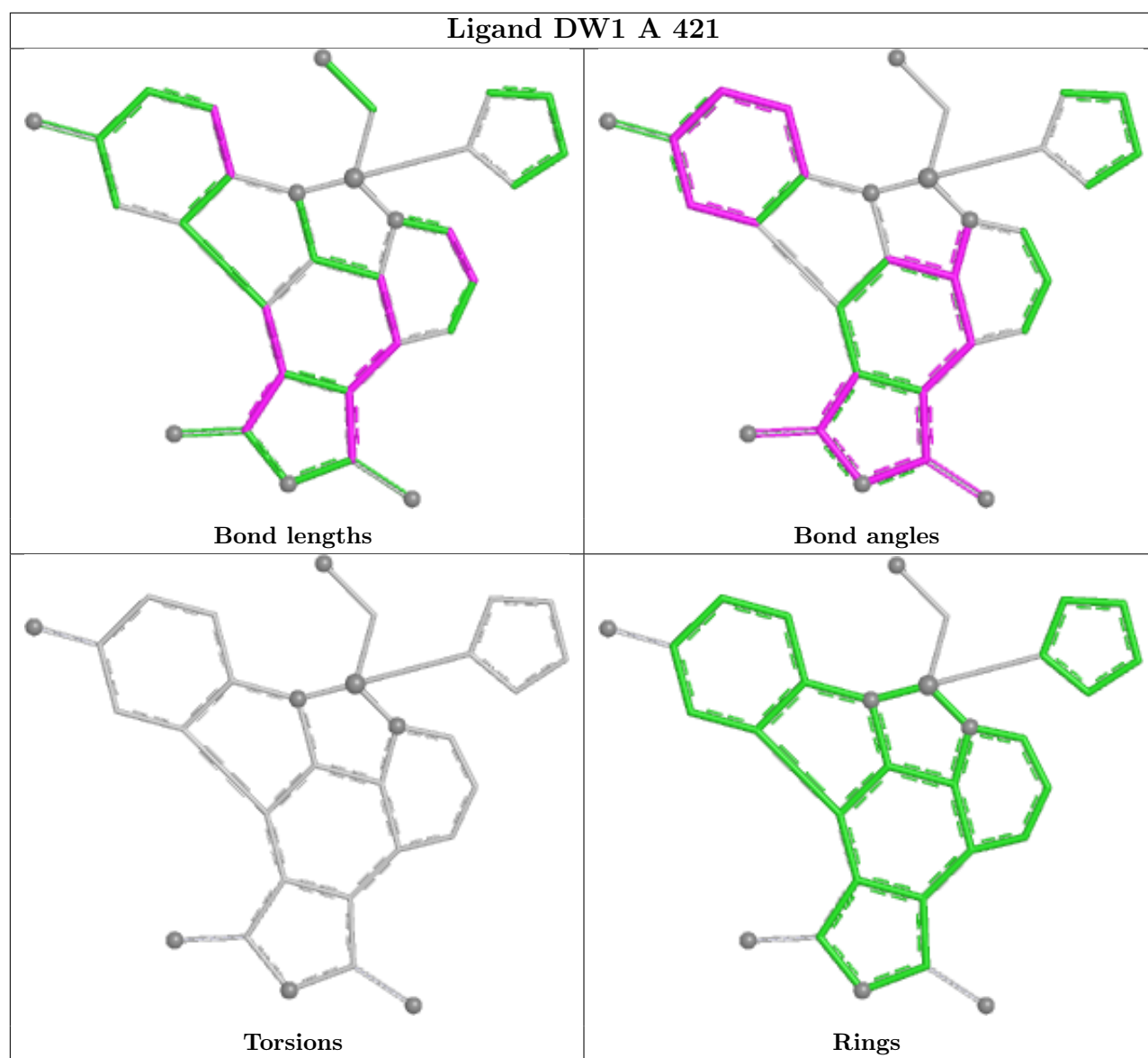
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	421	DW1	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	348/420 (82%)	-0.44	5 (1%)	73 53	23, 44, 84, 112	2 (0%)
1	B	349/420 (83%)	-0.47	4 (1%)	78 59	20, 43, 85, 111	2 (0%)
All	All	697/840 (82%)	-0.46	9 (1%)	75 55	20, 43, 86, 112	4 (0%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	291	PHE	4.1
1	B	124	ASP	3.2
1	A	35	SER	3.0
1	A	294	PRO	2.8
1	A	289	THR	2.8
1	B	120	GLY	2.5
1	B	290	GLU	2.2
1	A	122	LYS	2.2
1	B	294	PRO	2.1

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,

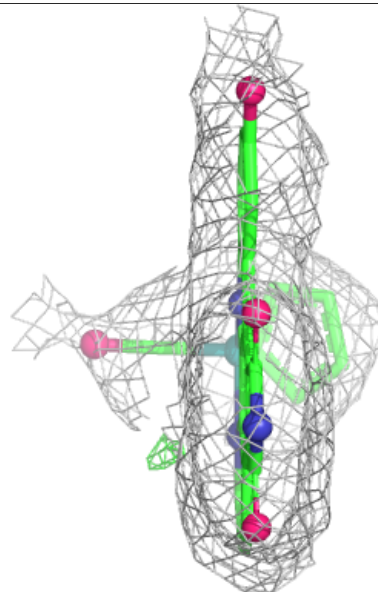
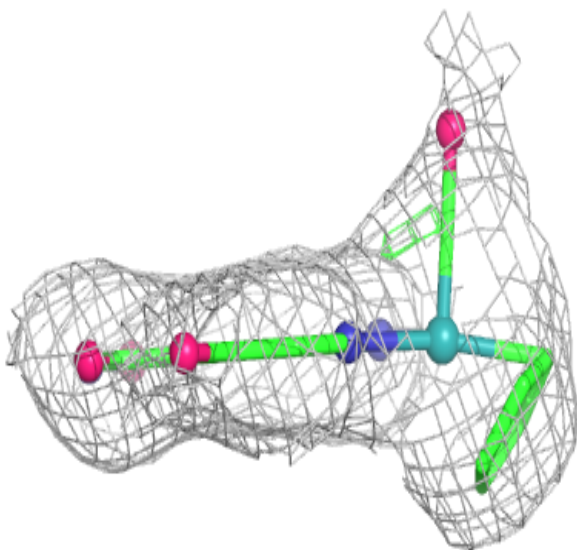
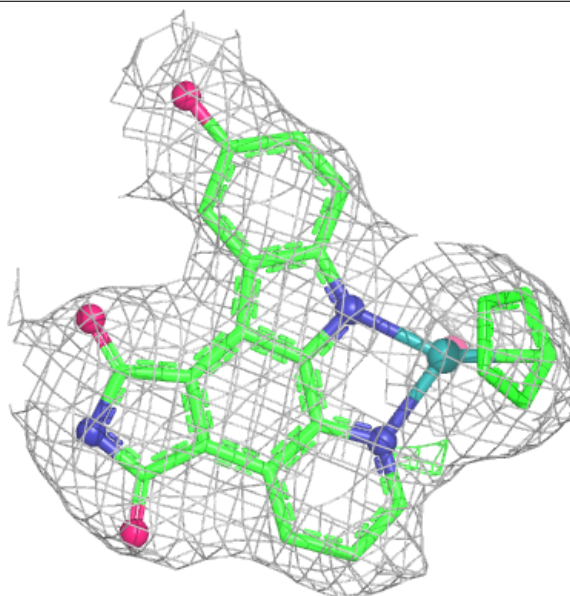
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	DW1	A	421	31/31	0.99	0.06	32,39,44,46	0
2	DW1	B	421	31/31	0.99	0.05	37,43,49,53	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.

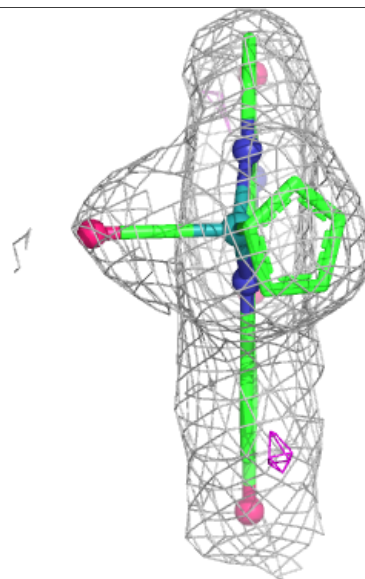
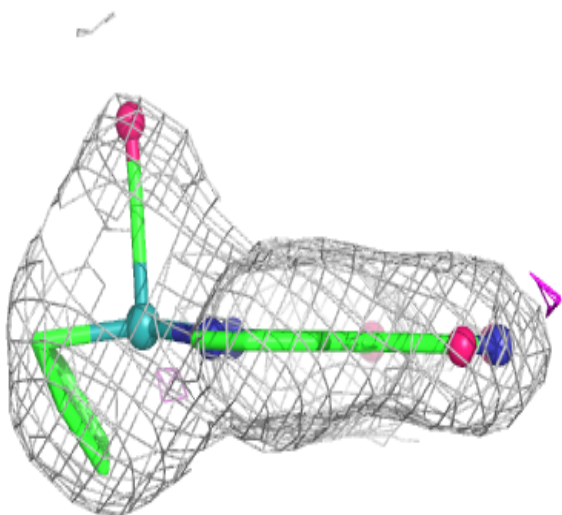
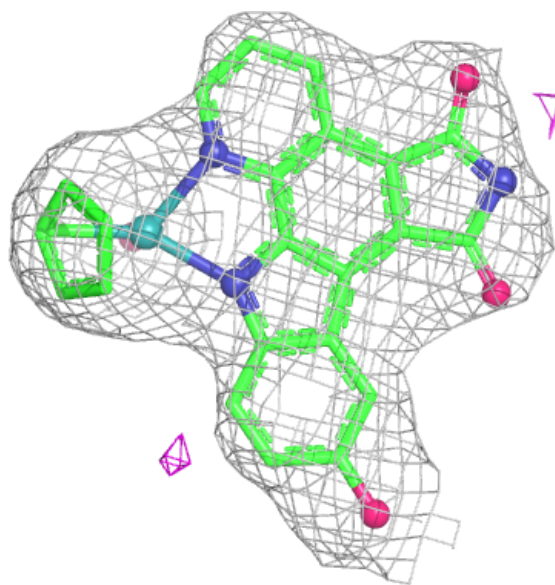
Electron density around DW1 A 421:

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



Electron density around DW1 B 421:

$2mF_o-DF_c$ (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.