



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 06:16 PM UTC

PDB ID : 4KIQ / pdb_00004kiq
Title : Crystal structure of mitogen-activated protein kinase 14 (P38-H5) complex with ETHYL 6-((5-(CYCLOPROPYLCARBAMOYL)-2-METHYLPHENYL)CARBAMOYL)-1H-INDOLE-1-CARBOXYLATE
Authors : Sack, J.S.; Tokarski, J.S.
Deposited on : 2013-05-02
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

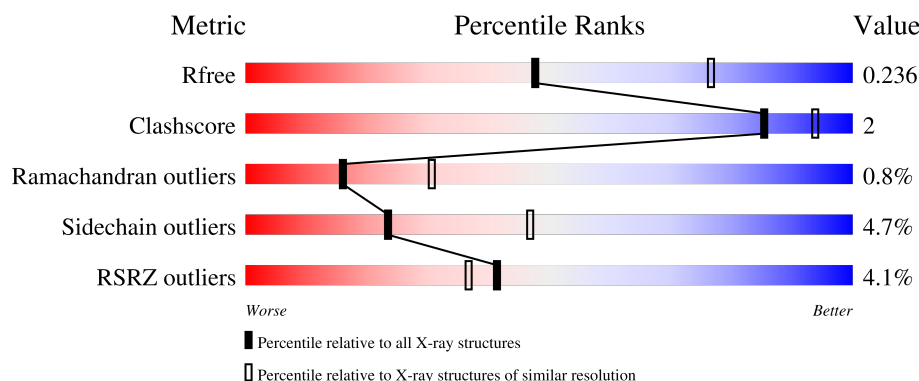
1 Overall quality at a glance

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	366	2% 81% 9% • 8%
1	B	366	3% 82% 10% • 8%
1	C	366	4% 84% 7% • 8%
1	D	366	6% 78% 11% • 8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11453 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 Mitogen-activated protein kinase 14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	S	0	0	0
			2720	1746	465	497	12			
1	B	338	Total	C	N	O	S	0	0	0
			2720	1746	465	497	12			
1	C	338	Total	C	N	O	S	0	0	0
			2720	1746	465	497	12			
1	D	338	Total	C	N	O	S	0	0	0
			2720	1746	465	497	12			

There are 28 discrepancies between the modelled and reference sequences:

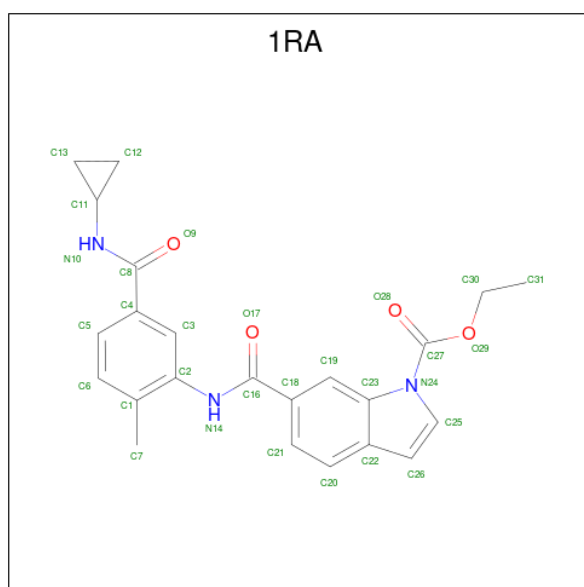
Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	expression tag	UNP Q16539
A	-4	ALA	-	expression tag	UNP Q16539
A	-3	HIS	-	expression tag	UNP Q16539
A	-2	HIS	-	expression tag	UNP Q16539
A	-1	HIS	-	expression tag	UNP Q16539
A	0	HIS	-	expression tag	UNP Q16539
A	1	HIS	-	expression tag	UNP Q16539
B	-5	MET	-	expression tag	UNP Q16539
B	-4	ALA	-	expression tag	UNP Q16539
B	-3	HIS	-	expression tag	UNP Q16539
B	-2	HIS	-	expression tag	UNP Q16539
B	-1	HIS	-	expression tag	UNP Q16539
B	0	HIS	-	expression tag	UNP Q16539
B	1	HIS	-	expression tag	UNP Q16539
C	-5	MET	-	expression tag	UNP Q16539
C	-4	ALA	-	expression tag	UNP Q16539
C	-3	HIS	-	expression tag	UNP Q16539
C	-2	HIS	-	expression tag	UNP Q16539
C	-1	HIS	-	expression tag	UNP Q16539
C	0	HIS	-	expression tag	UNP Q16539
C	1	HIS	-	expression tag	UNP Q16539

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-5	MET	-	expression tag	UNP Q16539
D	-4	ALA	-	expression tag	UNP Q16539
D	-3	HIS	-	expression tag	UNP Q16539
D	-2	HIS	-	expression tag	UNP Q16539
D	-1	HIS	-	expression tag	UNP Q16539
D	0	HIS	-	expression tag	UNP Q16539
D	1	HIS	-	expression tag	UNP Q16539

- Molecule 2 is ethyl 6-{{5-(cyclopropylcarbamoyl)-2-methylphenyl}carbamoyl}-1H-indole-1-carboxylate (CCD ID: 1RA) (formula: C₂₃H₂₃N₃O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			30	23	3	4		
2	B	1	Total	C	N	O	0	0
			30	23	3	4		
2	C	1	Total	C	N	O	0	0
			30	23	3	4		
2	D	1	Total	C	N	O	0	0
			30	23	3	4		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	146	Total	O	0	0
			146	146		

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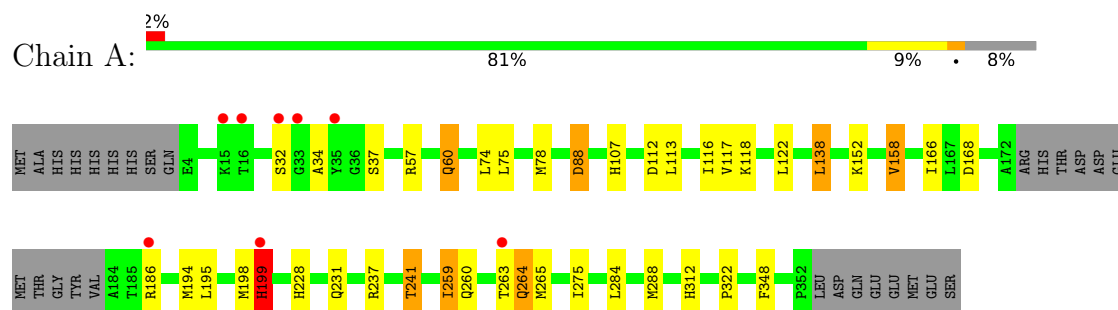
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	121	Total 121	O 121	0	0
3	C	111	Total 111	O 111	0	0
3	D	75	Total 75	O 75	0	0

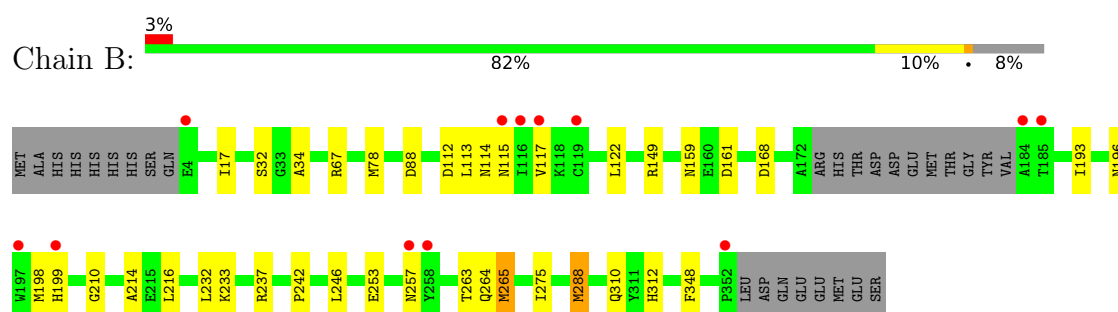
3 Residue-property plots [i](#)

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.

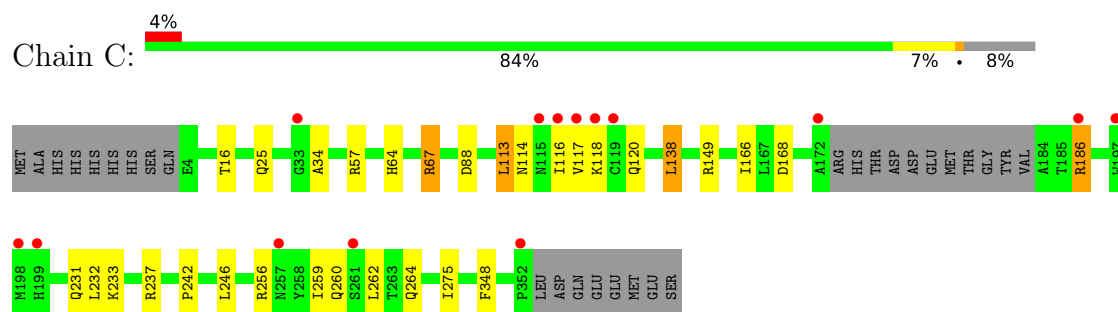
- Molecule 1: Mitogen-activated protein kinase 14



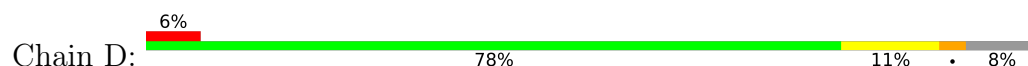
- Molecule 1: Mitogen-activated protein kinase 14

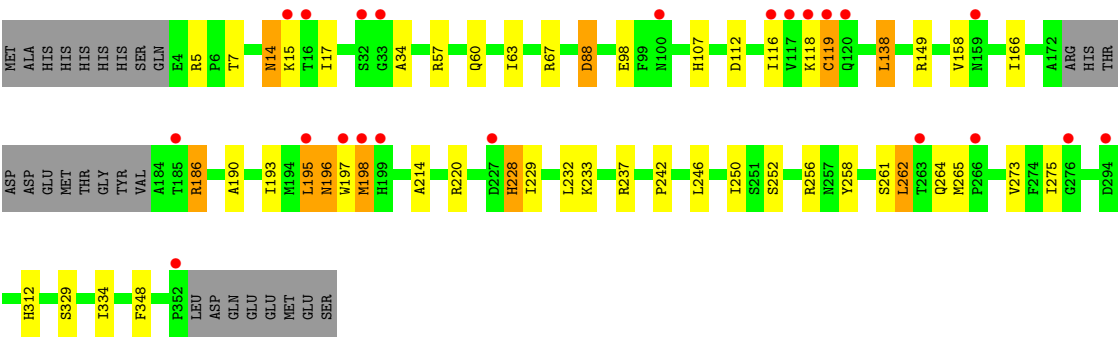


- Molecule 1: Mitogen-activated protein kinase 14



- Molecule 1: Mitogen-activated protein kinase 14





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	101.00Å 73.54Å 100.57Å 90.00° 96.66° 90.00°	Depositor
Resolution (Å)	42.88 – 2.50 42.88 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.6 (42.88-2.50) 96.6 (42.88-2.50)	Depositor EDS
R_{merge}	0.02	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	12.87 (at 2.51Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.184 , 0.228 0.189 , 0.236	Depositor DCC
R_{free} test set	2489 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	33.6	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.069 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11453	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 33.14 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 8.3944e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: 1RA

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	0.98	6/2783 (0.2%)	1.36	11/3778 (0.3%)
1	B	0.93	5/2783 (0.2%)	1.34	9/3778 (0.2%)
1	C	0.87	3/2783 (0.1%)	1.31	0/3778
1	D	0.90	3/2783 (0.1%)	1.38	18/3778 (0.5%)
All	All	0.92	17/11132 (0.2%)	1.35	38/15112 (0.3%)

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	312	HIS	ND1-CE1	6.26	1.38	1.32
1	A	228	HIS	ND1-CE1	5.99	1.38	1.32
1	C	57	ARG	CA-CB	5.68	1.56	1.52
1	A	260	GLN	CD-OE1	5.64	1.34	1.23
1	B	114	ASN	CG-OD1	5.63	1.34	1.23
1	B	199	HIS	ND1-CE1	5.59	1.38	1.32
1	A	107	HIS	ND1-CE1	5.54	1.38	1.32
1	B	196	ASN	CG-OD1	5.51	1.34	1.23
1	B	288	MET	SD-CE	-5.51	1.65	1.79
1	D	264	GLN	CD-OE1	5.29	1.33	1.23
1	D	107	HIS	ND1-CE1	5.27	1.37	1.32
1	B	312	HIS	ND1-CE1	5.25	1.37	1.32
1	A	264	GLN	CD-OE1	5.19	1.33	1.23
1	C	114	ASN	CG-OD1	5.18	1.33	1.23
1	A	312	HIS	ND1-CE1	5.14	1.37	1.32
1	A	60	GLN	CD-OE1	5.13	1.33	1.23
1	C	25	GLN	CD-OE1	5.12	1.33	1.23

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	186	ARG	CA-C-N	9.52	137.81	121.14
1	D	186	ARG	C-N-CA	9.52	137.81	121.14
1	A	198	MET	CA-C-N	7.95	136.73	121.54
1	A	198	MET	C-N-CA	7.95	136.73	121.54
1	D	14	ASN	CA-CB-CG	7.76	120.36	112.60
1	A	107	HIS	CB-CG-CD2	-7.74	121.14	131.20
1	B	312	HIS	CB-CG-CD2	-7.73	121.15	131.20
1	D	107	HIS	CB-CG-CD2	-7.61	121.31	131.20
1	A	312	HIS	CB-CG-CD2	-7.47	121.49	131.20
1	A	228	HIS	CB-CG-CD2	-7.46	121.51	131.20
1	D	312	HIS	CB-CG-CD2	-7.37	121.62	131.20
1	B	199	HIS	CB-CG-CD2	-7.32	121.69	131.20
1	D	195	LEU	CA-C-N	6.47	133.90	121.54
1	D	195	LEU	C-N-CA	6.47	133.90	121.54
1	A	199	HIS	N-CA-C	-6.39	97.19	110.80
1	B	214	ALA	CA-C-N	5.89	128.18	120.28
1	B	214	ALA	C-N-CA	5.89	128.18	120.28
1	B	198	MET	N-CA-C	-5.83	100.69	109.79
1	A	158	VAL	CA-C-N	5.79	131.35	121.29
1	A	158	VAL	C-N-CA	5.79	131.35	121.29
1	B	115	ASN	CA-C-N	5.62	127.75	120.56
1	B	115	ASN	C-N-CA	5.62	127.75	120.56
1	D	229	ILE	N-CA-C	-5.58	104.92	111.00
1	D	262	LEU	CA-C-N	5.57	132.18	121.54
1	D	262	LEU	C-N-CA	5.57	132.18	121.54
1	D	67	ARG	CA-C-N	5.45	127.52	120.44
1	D	67	ARG	C-N-CA	5.45	127.52	120.44
1	B	112	ASP	CA-CB-CG	5.32	117.92	112.60
1	A	88	ASP	CA-CB-CG	5.32	117.92	112.60
1	D	214	ALA	CA-C-N	5.25	127.83	120.28
1	D	214	ALA	C-N-CA	5.25	127.83	120.28
1	D	118	LYS	CA-C-N	5.18	131.43	121.54
1	D	118	LYS	C-N-CA	5.18	131.43	121.54
1	D	112	ASP	CA-CB-CG	5.09	117.69	112.60
1	A	241	THR	CB-CA-C	5.05	117.41	109.27
1	A	112	ASP	CA-CB-CG	5.04	117.64	112.60
1	D	88	ASP	CA-CB-CG	5.03	117.63	112.60
1	B	257	ASN	CA-CB-CG	5.01	117.61	112.60

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	2720	0	2718	17	0
1	B	2720	0	2718	9	0
1	C	2720	0	2718	10	0
1	D	2720	0	2718	16	0
2	A	30	0	23	2	0
2	B	30	0	23	1	0
2	C	30	0	23	1	0
2	D	30	0	23	0	0
3	A	146	0	0	0	0
3	B	121	0	0	1	0
3	C	111	0	0	0	0
3	D	75	0	0	1	0
All	All	11453	0	10964	49	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 2.

All (49) 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:113:LEU:O	1:B:117:VAL:HG22	1.84	0.77
1:C:113:LEU:O	1:C:117:VAL:HG22	1.97	0.63
1:D:232:LEU:HD23	1:D:258:TYR:HE2	1.64	0.62
1:D:116:ILE:HG13	1:D:158:VAL:HG11	1.86	0.58
1:A:116:ILE:HG13	1:A:158:VAL:HG13	1.85	0.57
1:B:210:GLY:HA2	1:B:288:MET:HE3	1.87	0.56
1:D:232:LEU:HD23	1:D:258:TYR:CE2	2.39	0.56
1:A:116:ILE:HG13	1:A:158:VAL:CG1	2.39	0.53
1:C:168:ASP:HA	2:C:401:1RA:H2	1.91	0.53
1:A:113:LEU:O	1:A:117:VAL:HG12	2.09	0.52
1:A:168:ASP:HA	2:A:401:1RA:H2	1.92	0.52
1:D:138:LEU:HD13	1:D:166:ILE:HD13	1.92	0.52
1:C:64:HIS:HA	1:C:67:ARG:HD2	1.92	0.51
1:A:322:PRO:HG3	1:D:220:ARG:HH12	1.76	0.51
1:A:138:LEU:HD13	1:A:166:ILE:HD13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:LEU:HD22	1:A:259:ILE:HG22	1.93	0.50
1:C:242:PRO:HB3	1:C:246:LEU:HD23	1.92	0.50
1:C:138:LEU:HD13	1:C:166:ILE:HD13	1.93	0.50
1:A:237:ARG:HA	1:A:265:MET:HG2	1.93	0.49
1:C:233:LYS:HE2	1:C:237:ARG:HH21	1.75	0.49
1:B:242:PRO:HB3	1:B:246:LEU:HD23	1.95	0.49
1:B:122:LEU:HD22	1:B:216:LEU:HD22	1.96	0.48
1:D:195:LEU:HD13	1:D:198:MET:HE1	1.96	0.47
1:D:197:TRP:HB2	1:D:252:SER:HB2	1.97	0.47
1:C:259:ILE:HA	1:C:262:LEU:HD12	1.96	0.47
1:D:237:ARG:HA	1:D:265:MET:HG2	1.96	0.46
1:B:237:ARG:HA	1:B:265:MET:HG2	1.97	0.46
1:D:190:ALA:HB3	1:D:193:ILE:HG12	1.96	0.46
1:A:322:PRO:HB3	1:D:220:ARG:HH22	1.81	0.45
1:A:74:LEU:O	1:A:78:MET:HG2	2.17	0.45
1:D:195:LEU:HD11	1:D:232:LEU:HD22	1.99	0.44
1:D:256:ARG:HD3	3:D:575:HOH:O	2.17	0.44
1:A:88:ASP:HA	1:A:348:PHE:CE2	2.53	0.44
1:A:284:LEU:HG	1:A:288:MET:HE2	2.00	0.44
1:B:168:ASP:HA	2:B:401:1RA:H2	1.99	0.44
1:D:242:PRO:HB3	1:D:246:LEU:HD23	2.00	0.44
1:A:57:ARG:HB3	1:A:60:GLN:HB2	1.99	0.44
1:D:57:ARG:HD3	1:D:60:GLN:NE2	2.33	0.44
1:A:32:SER:HA	1:A:37:SER:HA	2.01	0.43
1:C:88:ASP:HA	1:C:348:PHE:CE2	2.53	0.42
1:D:88:ASP:HA	1:D:348:PHE:CE2	2.54	0.42
1:A:75:LEU:HD11	2:A:401:1RA:H19	2.01	0.42
1:B:88:ASP:HA	1:B:348:PHE:CE2	2.55	0.42
1:A:194:MET:HE1	1:A:231:GLN:HG3	2.01	0.41
1:A:322:PRO:HG2	1:D:273:VAL:HG13	2.01	0.41
1:B:159:ASN:HB3	1:B:161:ASP:H	1.85	0.41
1:B:67:ARG:HG2	3:B:583:HOH:O	2.20	0.40
1:C:233:LYS:HE2	1:C:237:ARG:NH2	2.36	0.40
1:C:186:ARG:HD2	1:C:231:GLN:HG2	2.03	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	334/366 (91%)	317 (95%)	14 (4%)	3 (1%)	14	27
1	B	334/366 (91%)	315 (94%)	18 (5%)	1 (0%)	36	55
1	C	334/366 (91%)	318 (95%)	15 (4%)	1 (0%)	36	55
1	D	334/366 (91%)	313 (94%)	15 (4%)	6 (2%)	6	12
All	All	1336/1464 (91%)	1263 (94%)	62 (5%)	11 (1%)	16	31

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	119	CYS
1	D	196	ASN
1	D	228	HIS
1	A	199	HIS
1	A	34	ALA
1	A	263	THR
1	D	34	ALA
1	B	34	ALA
1	C	34	ALA
1	D	261	SER
1	D	5	ARG

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	297/325 (91%)	287 (97%)	10 (3%)	32	60
1	B	297/325 (91%)	284 (96%)	13 (4%)	25	50
1	C	297/325 (91%)	283 (95%)	14 (5%)	23	47
1	D	297/325 (91%)	278 (94%)	19 (6%)	16	33
All	All	1188/1300 (91%)	1132 (95%)	56 (5%)	23	47

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	118	LYS
1	A	122	LEU
1	A	138	LEU
1	A	152	LYS
1	A	186	ARG
1	A	199	HIS
1	A	241	THR
1	A	259	ILE
1	A	264	GLN
1	A	275	ILE
1	B	17	ILE
1	B	32	SER
1	B	78	MET
1	B	149	ARG
1	B	193	ILE
1	B	232	LEU
1	B	233	LYS
1	B	253	GLU
1	B	263	THR
1	B	264	GLN
1	B	265	MET
1	B	275	ILE
1	B	310	GLN
1	C	16	THR
1	C	67	ARG
1	C	113	LEU
1	C	116	ILE
1	C	118	LYS
1	C	120	GLN
1	C	138	LEU
1	C	149	ARG
1	C	186	ARG
1	C	232	LEU

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Mol	Chain	Res	Type
1	C	256	ARG
1	C	260	GLN
1	C	264	GLN
1	C	275	ILE
1	D	7	THR
1	D	14	ASN
1	D	15	LYS
1	D	17	ILE
1	D	63	ILE
1	D	98	GLU
1	D	119	CYS
1	D	138	LEU
1	D	149	ARG
1	D	186	ARG
1	D	196	ASN
1	D	198	MET
1	D	228	HIS
1	D	233	LYS
1	D	250	ILE
1	D	262	LEU
1	D	275	ILE
1	D	329	SER
1	D	334	ILE

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	100	ASN
1	A	115	ASN
1	A	155	ASN
1	A	196	ASN
1	B	120	GLN
1	C	11	GLN
1	C	14	ASN
1	C	100	ASN
1	C	115	ASN
1	C	120	GLN
1	C	128	GLN
1	C	264	GLN
1	D	228	HIS

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	1RA	B	401	-	33,33,33	0.41	0	46,47,47	0.71	1 (2%)
2	1RA	D	401	-	33,33,33	0.21	0	46,47,47	0.70	1 (2%)
2	1RA	C	401	-	33,33,33	0.29	0	46,47,47	0.65	1 (2%)
2	1RA	A	401	-	33,33,33	0.36	0	46,47,47	0.66	1 (2%)

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	1RA	B	401	-	-	2/23/25/25	0/4/4/4
2	1RA	D	401	-	-	3/23/25/25	0/4/4/4
2	1RA	C	401	-	-	2/23/25/25	0/4/4/4
2	1RA	A	401	-	-	0/23/25/25	0/4/4/4

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	D	401	1RA	C19-C23-C22	-3.11	119.72	122.29
2	B	401	1RA	C19-C23-C22	-2.90	119.89	122.29
2	C	401	1RA	C19-C23-C22	-2.42	120.29	122.29
2	A	401	1RA	C19-C23-C22	-2.27	120.41	122.29

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	401	1RA	C13-C11-N10-C8
2	D	401	1RA	C1-C2-N14-C16
2	B	401	1RA	C1-C2-N14-C16
2	C	401	1RA	C3-C2-N14-C16
2	C	401	1RA	C1-C2-N14-C16
2	B	401	1RA	C3-C2-N14-C16
2	D	401	1RA	C3-C2-N14-C16

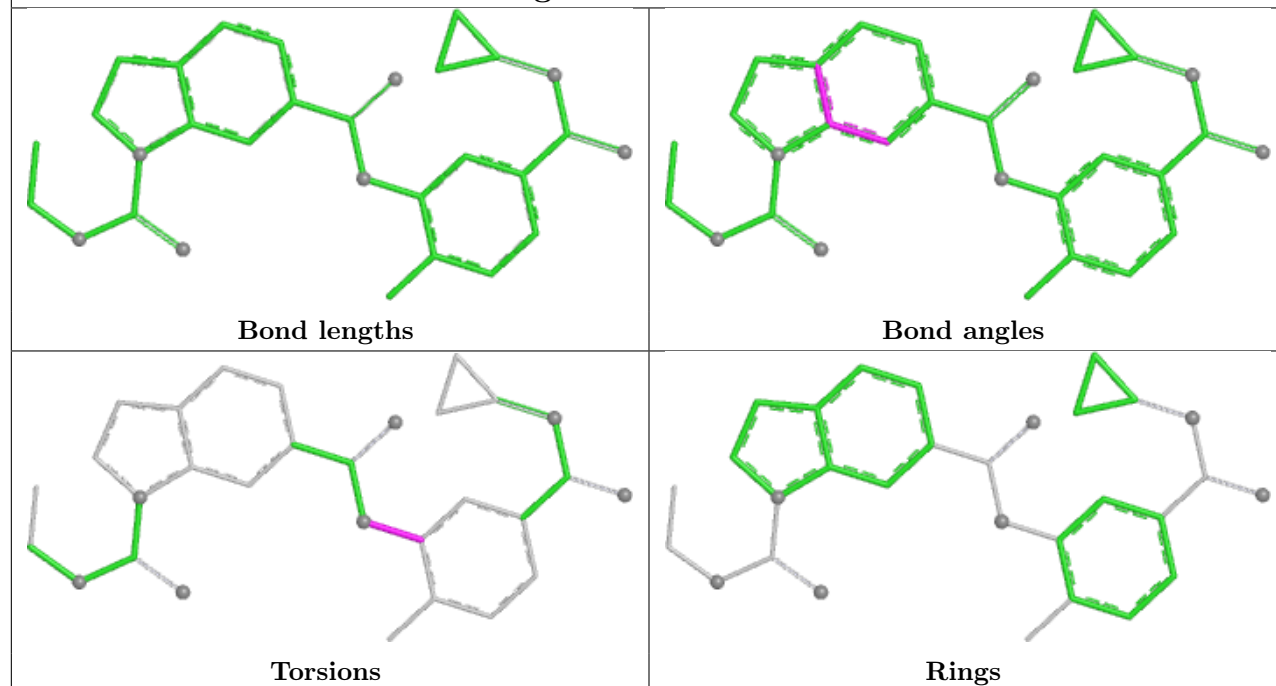
There are no ring outliers.

3 monomers are involved in 4 short contacts:

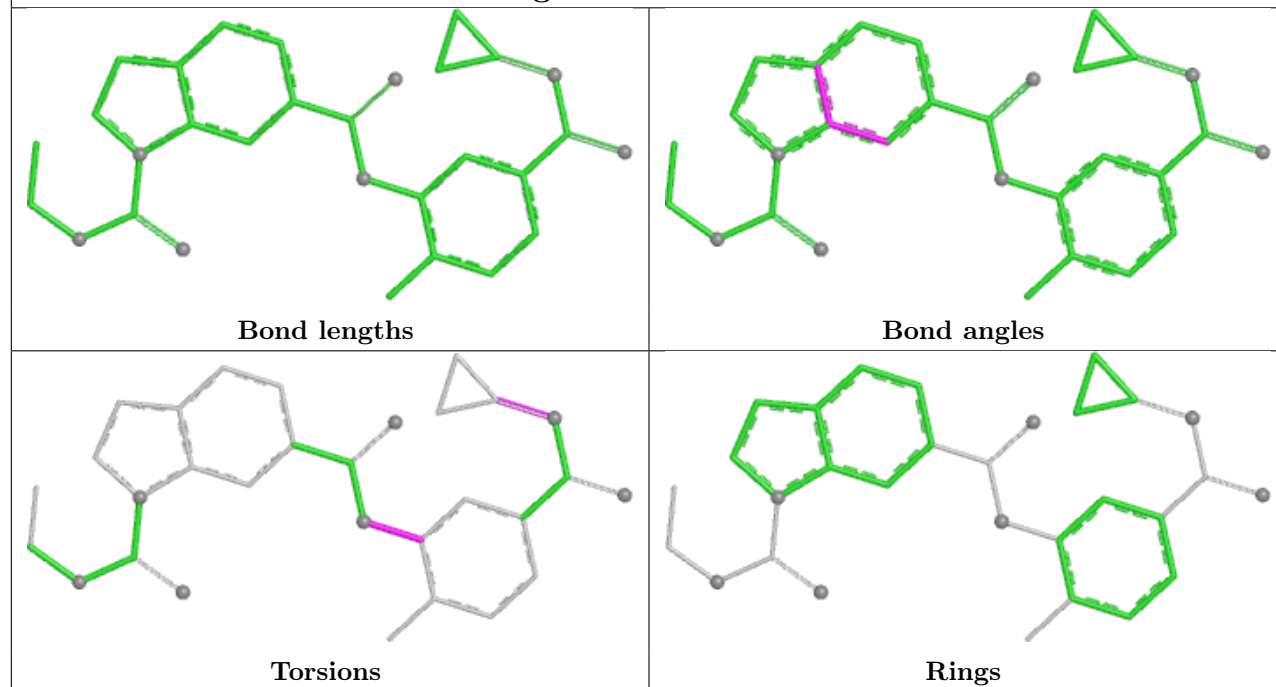
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	1RA	1	0
2	C	401	1RA	1	0
2	A	401	1RA	2	0

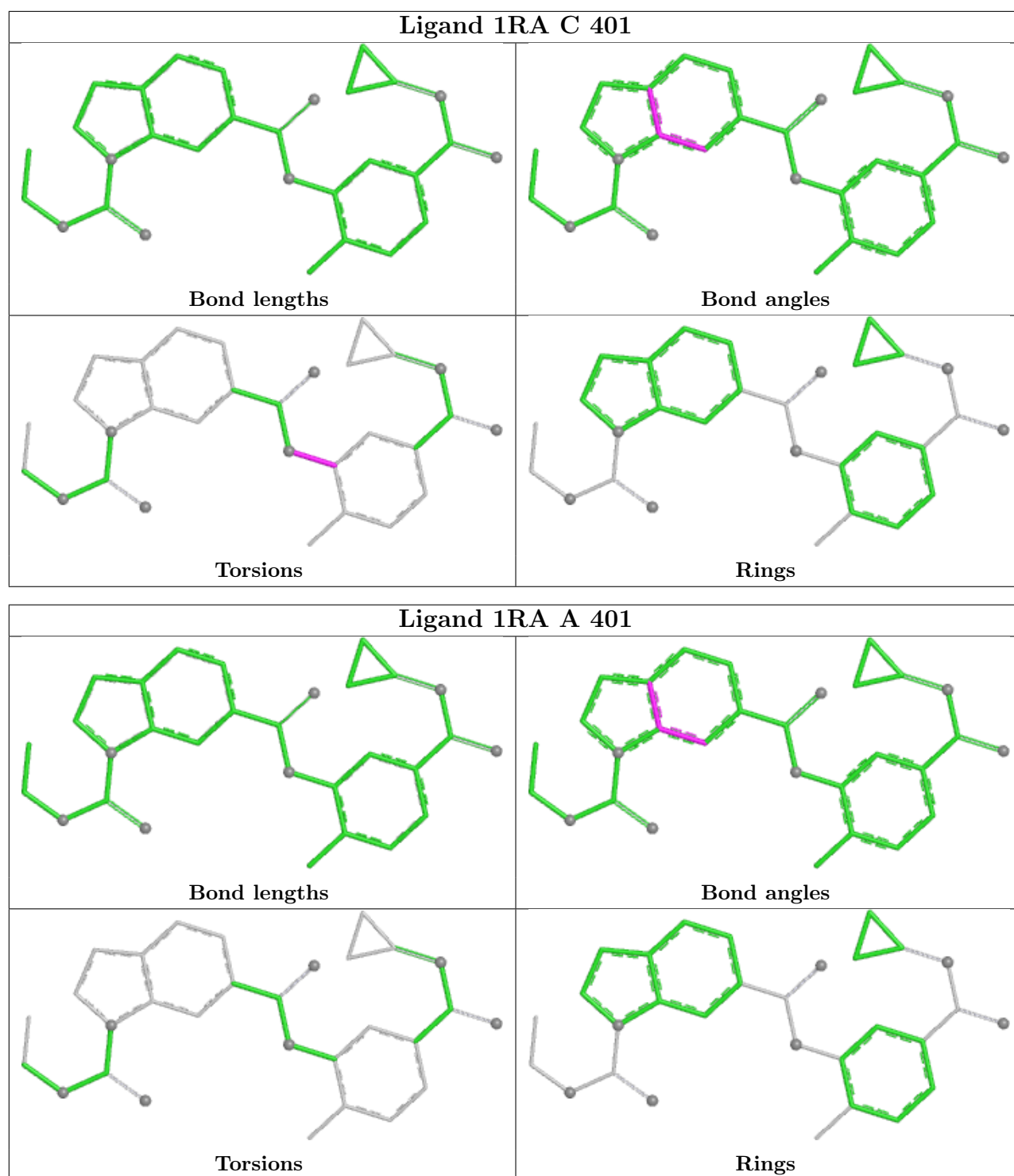
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

Ligand 1RA B 401



Ligand 1RA D 401





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

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	338/366 (92%)	-0.16	8 (2%) 59 55	15, 30, 59, 79	0
1	B	338/366 (92%)	0.04	12 (3%) 46 41	17, 32, 72, 93	0
1	C	338/366 (92%)	0.15	14 (4%) 41 37	21, 37, 75, 99	0
1	D	338/366 (92%)	0.38	22 (6%) 25 22	22, 42, 76, 102	0
All	All	1352/1464 (92%)	0.10	56 (4%) 41 37	15, 35, 71, 102	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	116	ILE	6.6
1	B	116	ILE	6.5
1	D	197	TRP	5.3
1	C	33	GLY	4.8
1	B	352	PRO	4.3
1	D	120	GLN	4.2
1	D	198	MET	4.1
1	A	33	GLY	4.1
1	B	185	THR	4.1
1	D	263	THR	3.5
1	C	119	CYS	3.5
1	C	352	PRO	3.4
1	C	199	HIS	3.3
1	C	198	MET	3.3
1	D	117	VAL	3.3
1	D	118	LYS	3.2
1	B	184	ALA	3.2
1	D	33	GLY	3.2
1	A	15	LYS	3.0
1	B	257	ASN	2.9
1	D	119	CYS	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	352	PRO	2.9
1	D	116	ILE	2.9
1	D	227	ASP	2.8
1	C	197	TRP	2.8
1	A	32	SER	2.7
1	D	195	LEU	2.7
1	C	115	ASN	2.6
1	B	199	HIS	2.6
1	A	35	TYR	2.6
1	A	16	THR	2.5
1	D	185	THR	2.5
1	C	257	ASN	2.5
1	D	100	ASN	2.5
1	D	159	ASN	2.5
1	D	32	SER	2.5
1	D	16	THR	2.4
1	D	15	LYS	2.4
1	D	276	GLY	2.4
1	A	199	HIS	2.4
1	B	197	TRP	2.3
1	B	4	GLU	2.2
1	B	115	ASN	2.2
1	B	119	CYS	2.2
1	C	186	ARG	2.2
1	C	117	VAL	2.2
1	C	172	ALA	2.2
1	A	186	ARG	2.2
1	C	118	LYS	2.1
1	B	117	VAL	2.1
1	B	258	TYR	2.1
1	D	294	ASP	2.1
1	C	261	SER	2.0
1	D	266	PRO	2.0
1	A	263	THR	2.0
1	D	199	HIS	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 [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

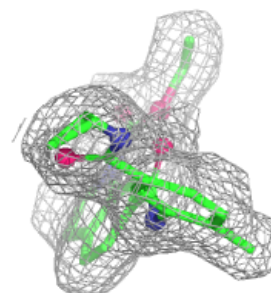
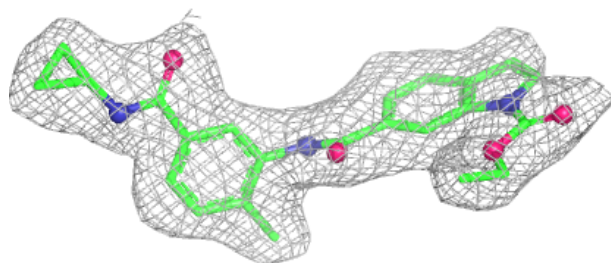
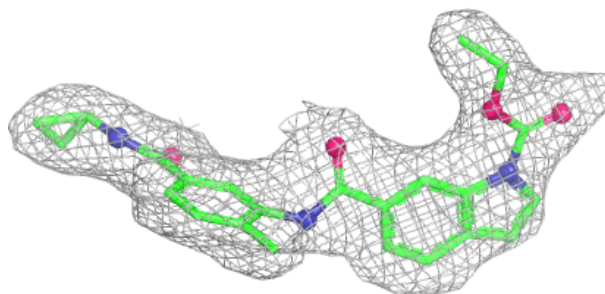
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	1RA	C	401	30/30	0.95	0.07	17,26,43,47	0
2	1RA	D	401	30/30	0.95	0.07	27,33,41,45	0
2	1RA	A	401	30/30	0.97	0.06	14,26,35,37	0
2	1RA	B	401	30/30	0.97	0.07	17,28,41,46	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.

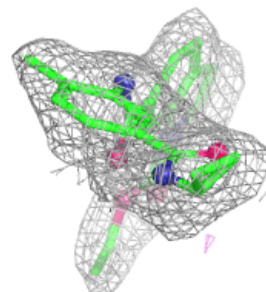
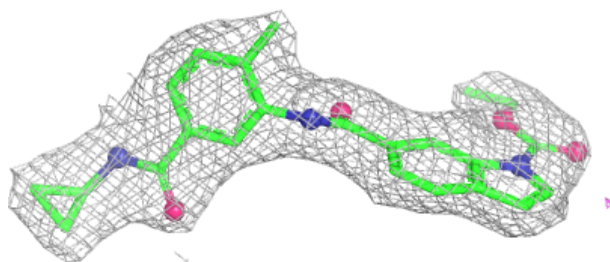
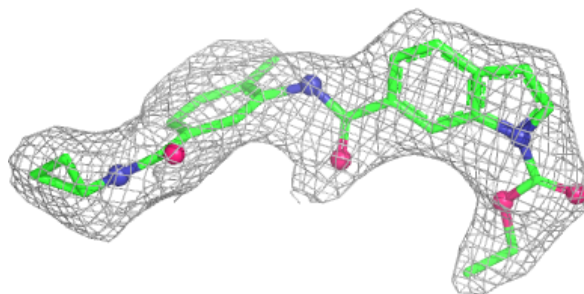
Electron density around 1RA C 401:

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

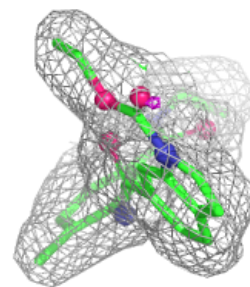
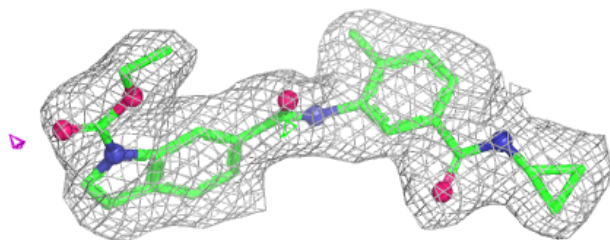
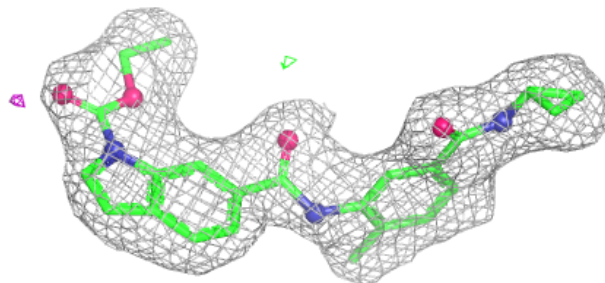


Electron density around 1RA D 401:

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

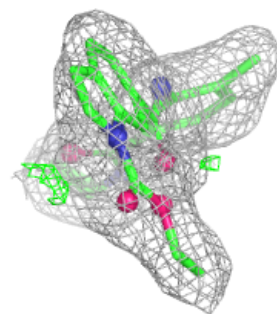
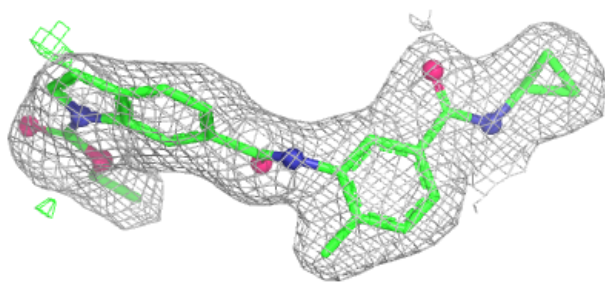
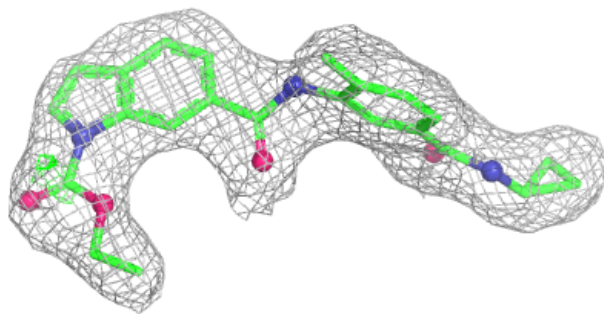
**Electron density around 1RA A 401:**

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



Electron density around 1RA B 401:

$2mF_o-DF_c$ (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.