



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2024 – 03:39 PM EST

PDB ID : 3PTG
Title : Design and Synthesis of a Novel, Orally Efficacious Tri-substituted Thiophene Based JNK Inhibitor
Authors : Bowers, S.; Truong, A.P.; Neitz, J.; Neitzel, M.; Probst, G.D.; Hom, R.K.; Konradi, A.W.; Sham, H.L.; Toth, G.; Pan, H.; Yao, N.; Artis, D.R.; Brigham, E.F.; Quinn, K.P.; Sauer, J.; Powell, K.; Ruslim, L.; Bard, F.; Yednock, T.A.; Griswold-Prenner, I.
Deposited on : 2010-12-02
Resolution : 2.43 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)

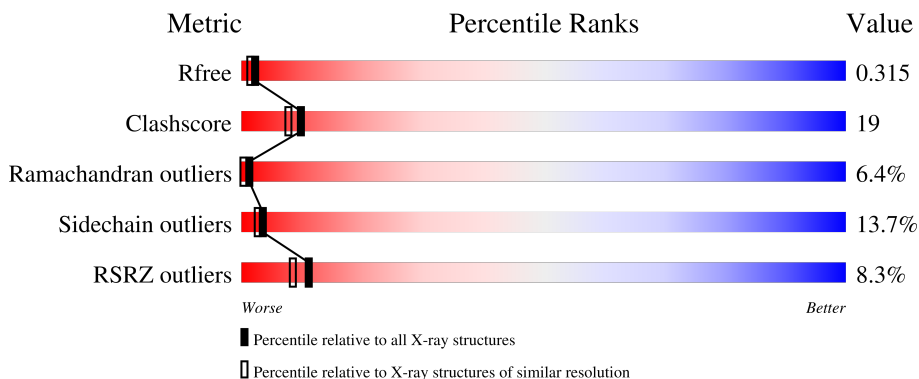
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.43 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}	130704	1564 (2.46-2.42)
Clashscore	141614	1631 (2.46-2.42)
Ramachandran outliers	138981	1617 (2.46-2.42)
Sidechain outliers	138945	1617 (2.46-2.42)
RSRZ outliers	127900	1547 (2.46-2.42)

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	363	
2	J	11	

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
 Validation Pipeline (wwPDB-VP) : 2.36

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2895 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 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	340	2757	1769	470	499	19	0	0	0

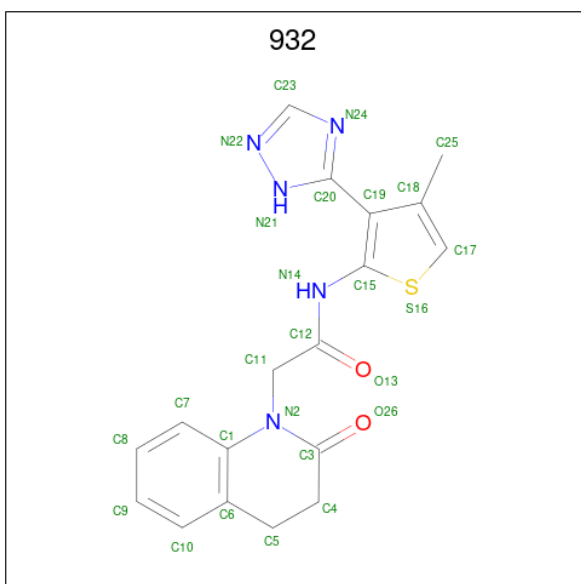
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	39	ALA	-	expression tag	UNP P53779

- Molecule 2 is a protein called C-Jun-amino-terminal kinase-interacting protein 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	J	10	84	55	15	14	0	0	0

- Molecule 3 is N-[4-methyl-3-(1H-1,2,4-triazol-5-yl)thiophen-2-yl]-2-(2-oxo-3,4-dihydroquinolin-1(2H)-yl)acetamide (three-letter code: 932) (formula: C₁₈H₁₇N₅O₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			26	18	5	2	1		

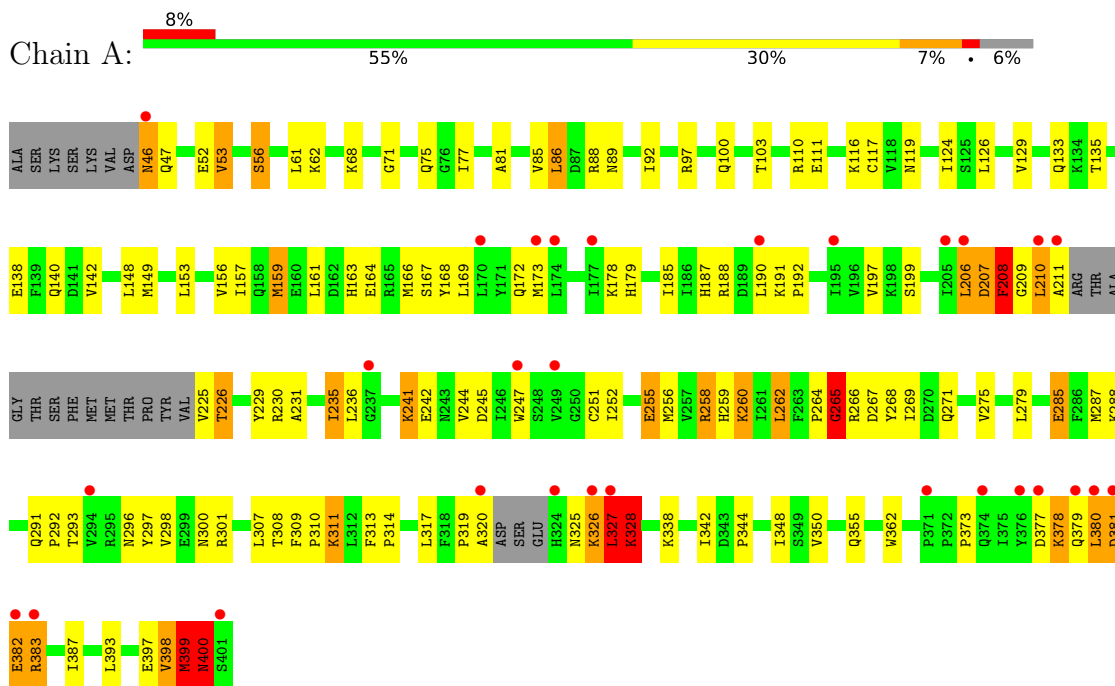
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	27	Total	O	0	0
			27	27		
4	J	1	Total	O	0	0
			1	1		

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: Mitogen-activated protein kinase 10



- Molecule 2: C-Jun-amino-terminal kinase-interacting protein 1



4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.77Å 80.43Å 83.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.21 – 2.43 34.21 – 2.43	Depositor EDS
% Data completeness (in resolution range)	88.2 (34.21-2.43) 88.3 (34.21-2.43)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 2.42Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.244 , 0.316 0.240 , 0.315	Depositor DCC
R_{free} test set	701 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	55.0	Xtrriage
Anisotropy	0.133	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 37.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	0.011 for -h,l,k	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2895	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.11% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 932

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	0/2819	0.93	7/3814 (0.2%)
2	J	0.72	0/86	0.91	0/114
All	All	0.80	0/2905	0.92	7/3928 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	153	LEU	CA-CB-CG	7.11	131.66	115.30
1	A	236	LEU	CA-CB-CG	6.14	129.43	115.30
1	A	328	LYS	N-CA-C	-6.08	94.58	111.00
1	A	327	LEU	C-N-CA	5.40	135.19	121.70
1	A	258	ARG	NE-CZ-NH1	-5.25	117.67	120.30
1	A	190	LEU	CA-CB-CG	5.03	126.88	115.30
1	A	245	ASP	CB-CG-OD1	5.02	122.82	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	265	GLY	Peptide

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	2757	0	2769	108	0
2	J	84	0	91	2	0
3	A	26	0	17	3	0
4	A	27	0	0	3	0
4	J	1	0	0	0	0
All	All	2895	0	2877	110	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 19.

All (110) 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:287:MET:HE2	1:A:298:VAL:HG12	1.22	1.12
1:A:398:VAL:O	1:A:399:MET:HG2	1.50	1.10
1:A:308:THR:HG22	1:A:310:PRO:HD2	1.36	1.05
1:A:287:MET:CE	1:A:298:VAL:HG12	1.88	1.01
1:A:86:LEU:HD12	1:A:86:LEU:O	1.71	0.89
1:A:52:GLU:O	1:A:56:SER:O	1.93	0.85
1:A:97:ARG:HH11	1:A:100:GLN:NE2	1.78	0.81
1:A:258:ARG:HD2	1:A:313:PHE:CE1	2.21	0.76
1:A:258:ARG:HH12	1:A:260:LYS:NZ	1.86	0.73
1:A:142:VAL:HG13	1:A:398:VAL:HG21	1.70	0.72
1:A:119:ASN:H	1:A:179:HIS:HE1	1.35	0.72
1:A:381:ASP:N	1:A:382:GLU:HB3	2.06	0.71
1:A:126:LEU:HD11	1:A:129:VAL:HG12	1.71	0.70
1:A:226:THR:HG23	1:A:230:ARG:NH1	2.07	0.69
1:A:185:ILE:HG21	1:A:208:PHE:HB2	1.77	0.67
1:A:314:PRO:HD2	1:A:317:LEU:HD12	1.76	0.66
1:A:86:LEU:HG	1:A:88:ARG:HD2	1.77	0.66
1:A:398:VAL:O	1:A:398:VAL:HG12	1.98	0.64
1:A:191:LYS:HE2	1:A:226:THR:OG1	1.98	0.64
1:A:258:ARG:HH12	1:A:260:LYS:HZ1	1.43	0.63
1:A:149:MET:HB2	3:A:1:932:O13	1.98	0.63
1:A:379:GLN:HA	1:A:380:LEU:C	2.19	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:LEU:HA	1:A:211:ALA:HB2	1.81	0.62
1:A:129:VAL:HG23	1:A:398:VAL:HA	1.81	0.62
1:A:229:TYR:OH	1:A:255:GLU:OE1	2.16	0.62
1:A:258:ARG:NH1	1:A:260:LYS:NZ	2.49	0.60
1:A:326:LYS:HA	1:A:327:LEU:O	2.02	0.60
1:A:206:LEU:O	4:A:7:HOH:O	2.17	0.60
1:A:92:ILE:HD12	1:A:92:ILE:N	2.17	0.60
1:A:307:LEU:HB3	1:A:311:LYS:HD2	1.83	0.60
1:A:129:VAL:CG2	1:A:398:VAL:HA	2.31	0.59
1:A:47:GLN:HG2	1:A:62:LYS:HE2	1.84	0.59
1:A:117:CYS:O	1:A:373:PRO:HD2	2.03	0.59
1:A:320:ALA:HB3	1:A:325:ASN:CB	2.32	0.59
1:A:381:ASP:H	1:A:382:GLU:HB3	1.67	0.58
1:A:97:ARG:HH11	1:A:100:GLN:HE22	1.51	0.58
1:A:258:ARG:NH1	1:A:260:LYS:HZ2	1.99	0.58
1:A:381:ASP:N	1:A:382:GLU:O	2.36	0.58
1:A:116:LYS:HE2	1:A:126:LEU:HD23	1.85	0.58
1:A:169:LEU:O	1:A:173:MET:HG3	2.04	0.58
1:A:362:TRP:O	2:J:156:ARG:NH2	2.36	0.57
1:A:168:TYR:O	1:A:172:GLN:HG3	2.03	0.57
1:A:178:LYS:HB2	1:A:350:VAL:HG11	1.86	0.57
1:A:381:ASP:H	1:A:382:GLU:CB	2.18	0.57
1:A:81:ALA:HB3	1:A:92:ILE:HD11	1.87	0.56
1:A:135:THR:OG1	1:A:138:GLU:HG2	2.05	0.56
1:A:209:GLY:HA3	1:A:210:LEU:CB	2.36	0.56
1:A:326:LYS:HA	1:A:327:LEU:C	2.25	0.56
1:A:119:ASN:H	1:A:179:HIS:CE1	2.22	0.56
1:A:398:VAL:C	1:A:399:MET:HG2	2.26	0.55
1:A:163:HIS:O	1:A:167:SER:HB3	2.06	0.55
1:A:285:GLU:HA	1:A:288:LYS:HD2	1.89	0.55
1:A:320:ALA:HB3	1:A:325:ASN:HB3	1.89	0.55
1:A:81:ALA:HB3	1:A:92:ILE:CD1	2.39	0.53
1:A:86:LEU:O	1:A:86:LEU:CD1	2.53	0.53
1:A:226:THR:HA	4:A:2:HOH:O	2.09	0.51
1:A:231:ALA:HA	1:A:247:TRP:CD1	2.45	0.51
1:A:380:LEU:HA	1:A:382:GLU:HG2	1.92	0.51
1:A:398:VAL:O	1:A:398:VAL:CG1	2.58	0.50
1:A:275:VAL:HG12	1:A:342:ILE:HD11	1.92	0.50
1:A:296:ASN:O	1:A:300:ASN:ND2	2.42	0.49
1:A:52:GLU:O	1:A:53:VAL:HB	2.11	0.49
1:A:47:GLN:CG	1:A:62:LYS:HE2	2.42	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:MET:HE3	1:A:298:VAL:HG12	1.88	0.49
1:A:320:ALA:HB3	1:A:325:ASN:HB2	1.94	0.48
1:A:381:ASP:H	1:A:382:GLU:CA	2.25	0.48
1:A:209:GLY:CA	1:A:210:LEU:CB	2.92	0.48
1:A:124:ILE:HG13	1:A:206:LEU:HD12	1.96	0.48
1:A:209:GLY:HA3	1:A:210:LEU:HB2	1.94	0.48
1:A:382:GLU:O	1:A:383:ARG:HB3	2.14	0.48
1:A:269:ILE:HG23	1:A:297:TYR:OH	2.14	0.48
1:A:187:HIS:CG	1:A:209:GLY:HA2	2.49	0.47
1:A:52:GLU:O	1:A:53:VAL:CB	2.62	0.47
1:A:241:LYS:HB2	1:A:242:GLU:H	1.58	0.47
1:A:46:ASN:HD22	1:A:46:ASN:N	2.13	0.47
1:A:89:ASN:HB3	1:A:148:LEU:HD23	1.96	0.47
1:A:133:GLN:HG2	1:A:138:GLU:O	2.15	0.47
1:A:397:GLU:HA	1:A:400:ASN:HB2	1.97	0.46
1:A:235:ILE:HG22	1:A:268:TYR:CE1	2.51	0.46
1:A:314:PRO:HD2	1:A:317:LEU:CD1	2.45	0.46
1:A:252:ILE:O	1:A:256:MET:HG3	2.15	0.45
1:A:255:GLU:O	1:A:255:GLU:HG3	2.16	0.45
1:A:156:VAL:HA	1:A:159:MET:HG2	1.99	0.45
1:A:381:ASP:H	1:A:382:GLU:C	2.20	0.45
1:A:86:LEU:HG	1:A:88:ARG:CD	2.47	0.44
1:A:191:LYS:HB2	1:A:192:PRO:CD	2.47	0.44
1:A:191:LYS:HB2	1:A:192:PRO:HD2	1.99	0.44
1:A:258:ARG:HD2	1:A:313:PHE:CD1	2.51	0.44
1:A:397:GLU:O	1:A:400:ASN:HB2	2.18	0.44
3:A:1:932:H25	3:A:1:932:HN21	1.83	0.44
1:A:85:VAL:CG1	1:A:85:VAL:O	2.65	0.44
1:A:46:ASN:ND2	1:A:61:LEU:HD22	2.33	0.43
1:A:206:LEU:HB3	1:A:207:ASP:H	1.73	0.43
1:A:297:TYR:CE2	1:A:301:ARG:HD2	2.53	0.43
1:A:265:GLY:HA2	1:A:266:ARG:CB	2.49	0.43
1:A:156:VAL:HG13	1:A:161:LEU:HD11	2.01	0.43
1:A:338:LYS:HD3	1:A:348:ILE:HD12	2.01	0.43
1:A:71:GLY:HA2	4:A:5:HOH:O	2.19	0.42
1:A:382:GLU:O	1:A:383:ARG:CB	2.67	0.42
1:A:163:HIS:O	1:A:167:SER:CB	2.67	0.42
1:A:265:GLY:HA2	1:A:266:ARG:HB3	2.02	0.42
1:A:241:LYS:O	1:A:244:VAL:HG12	2.19	0.42
1:A:251:CYS:HA	1:A:262:LEU:HD22	2.01	0.41
1:A:199:SER:O	2:J:160:LEU:N	2.49	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:MET:O	1:A:259:HIS:CE1	2.73	0.41
1:A:187:HIS:O	1:A:209:GLY:HA3	2.20	0.41
1:A:226:THR:CG2	1:A:230:ARG:NH1	2.82	0.41
1:A:308:THR:HG22	1:A:309:PHE:N	2.36	0.41
1:A:380:LEU:H	1:A:380:LEU:HG	1.68	0.40
3:A:1:932:O13	3:A:1:932:S16	2.80	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	334/363 (92%)	288 (86%)	24 (7%)	22 (7%)	1	0
2	J	8/11 (73%)	8 (100%)	0	0	100	100
All	All	342/374 (91%)	296 (86%)	24 (7%)	22 (6%)	1	0

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	226	THR
1	A	293	THR
1	A	326	LYS
1	A	327	LEU
1	A	328	LYS
1	A	399	MET
1	A	381	ASP
1	A	159	MET
1	A	206	LEU
1	A	265	GLY
1	A	267	ASP
1	A	377	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	382	GLU
1	A	208	PHE
1	A	264	PRO
1	A	319	PRO
1	A	378	LYS
1	A	383	ARG
1	A	400	ASN
1	A	292	PRO
1	A	398	VAL
1	A	53	VAL

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	305/327 (93%)	267 (88%)	38 (12%)	4	3
2	J	10/11 (91%)	5 (50%)	5 (50%)	0	0
All	All	315/338 (93%)	272 (86%)	43 (14%)	3	3

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	ASN
1	A	56	SER
1	A	68	LYS
1	A	75	GLN
1	A	77	ILE
1	A	86	LEU
1	A	103	THR
1	A	110	ARG
1	A	111	GLU
1	A	140	GLN
1	A	157	ILE
1	A	164	GLU
1	A	166	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	188	ARG
1	A	197	VAL
1	A	207	ASP
1	A	208	PHE
1	A	210	LEU
1	A	225	VAL
1	A	235	ILE
1	A	241	LYS
1	A	255	GLU
1	A	260	LYS
1	A	262	LEU
1	A	271	GLN
1	A	279	LEU
1	A	285	GLU
1	A	291	GLN
1	A	311	LYS
1	A	328	LYS
1	A	344	PRO
1	A	355	GLN
1	A	378	LYS
1	A	380	LEU
1	A	387	ILE
1	A	393	LEU
1	A	399	MET
1	A	400	ASN
2	J	154	PRO
2	J	156	ARG
2	J	158	THR
2	J	161	ASN
2	J	163	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	ASN
1	A	100	GLN
1	A	102	GLN
1	A	140	GLN
1	A	179	HIS
1	A	278	GLN
1	A	296	ASN
1	A	331	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	355	GLN
1	A	400	ASN
2	J	161	ASN

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 monosaccharides 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	932	A	1	-	25,29,29	2.25	4 (16%)	22,41,41	1.76	5 (22%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	932	A	1	-	-	0/6/25/25	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1	932	C17-C18	7.86	1.41	1.37
3	A	1	932	C1-C6	5.10	1.47	1.40
3	A	1	932	C17-S16	4.45	1.77	1.70
3	A	1	932	C20-N21	-2.30	1.31	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1	932	C18-C17-S16	-4.39	108.92	112.68
3	A	1	932	O26-C3-C4	-2.33	115.93	121.32
3	A	1	932	C11-N2-C1	-2.33	117.79	120.23
3	A	1	932	C4-C5-C6	-2.27	107.22	112.03
3	A	1	932	C7-C1-C6	-2.13	116.71	119.87

There are no chirality outliers.

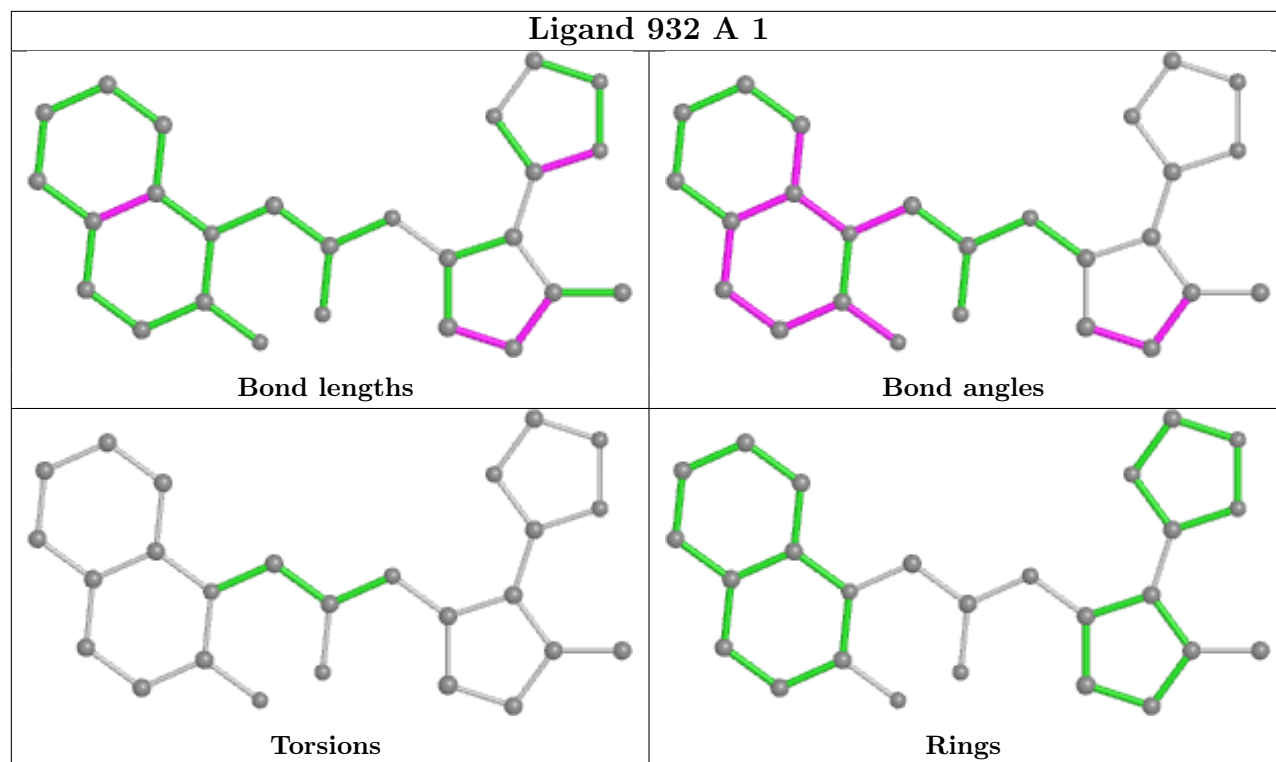
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1	932	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	340/363 (93%)	0.34	29 (8%) 10 8	30, 48, 74, 88	0
2	J	10/11 (90%)	0.56	0 100 100	51, 54, 66, 66	0
All	All	350/374 (93%)	0.35	29 (8%) 11 8	30, 49, 73, 88	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	327	LEU	8.4
1	A	380	LEU	5.9
1	A	382	GLU	5.4
1	A	401	SER	4.8
1	A	320	ALA	4.8
1	A	210	LEU	4.1
1	A	205	ILE	4.1
1	A	377	ASP	4.0
1	A	324	HIS	4.0
1	A	379	GLN	3.9
1	A	381	ASP	3.9
1	A	249	VAL	3.3
1	A	206	LEU	3.2
1	A	374	GLN	3.2
1	A	383	ARG	3.1
1	A	46	ASN	3.1
1	A	294	VAL	3.1
1	A	237	GLY	2.9
1	A	376	TYR	2.8
1	A	190	LEU	2.6
1	A	173	MET	2.5
1	A	326	LYS	2.4
1	A	211	ALA	2.3
1	A	371	PRO	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	177	ILE	2.1
1	A	247	TRP	2.1
1	A	195	ILE	2.1
1	A	174	LEU	2.0
1	A	170	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

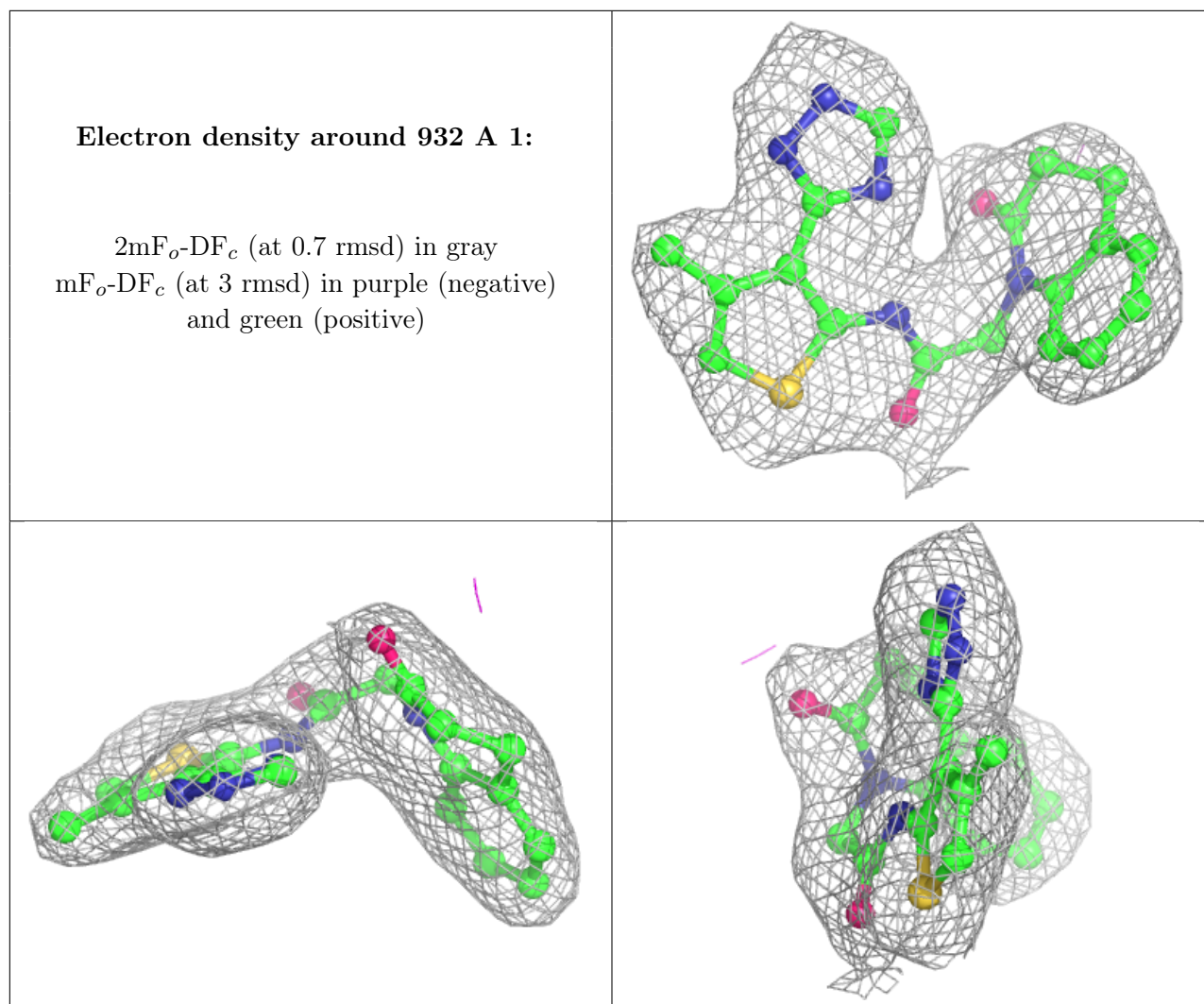
There are no monosaccharides in this entry.

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	932	A	1	26/26	0.97	0.17	31,39,43,45	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.