



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 04:36 AM GMT

PDB ID : 4L02  
Title : Crystal Structure of SphK1 with inhibitor  
Authors : Min, X.; Walker, N.; Wang, Z.  
Deposited on : 2013-05-30  
Resolution : 2.75 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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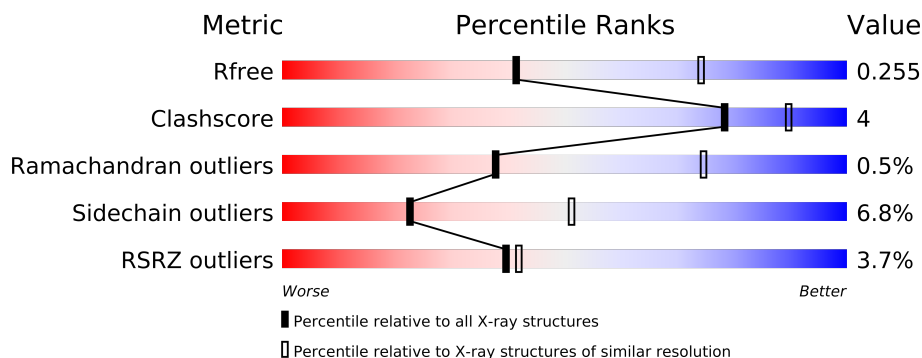
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.75 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))
$R_{free}$	66092	2406 (2.80-2.72)
Clashscore	79885	2995 (2.80-2.72)
Ramachandran outliers	78287	2941 (2.80-2.72)
Sidechain outliers	78261	2944 (2.80-2.72)
RSRZ outliers	66119	2409 (2.80-2.72)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	384	
1	B	384	
1	C	384	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	1V2	C	401	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8318 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Sphingosine kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	360	Total	C	N	O	S	0	2	0
			2806	1795	498	491	22			
1	B	340	Total	C	N	O	S	0	1	0
			2668	1711	470	467	20			
1	C	345	Total	C	N	O	S	0	0	0
			2693	1724	477	471	21			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q9NYA1
A	-18	SER	-	EXPRESSION TAG	UNP Q9NYA1
A	-17	TYR	-	EXPRESSION TAG	UNP Q9NYA1
A	-16	TYR	-	EXPRESSION TAG	UNP Q9NYA1
A	-15	HIS	-	EXPRESSION TAG	UNP Q9NYA1
A	-14	HIS	-	EXPRESSION TAG	UNP Q9NYA1
A	-13	HIS	-	EXPRESSION TAG	UNP Q9NYA1
A	-12	HIS	-	EXPRESSION TAG	UNP Q9NYA1
A	-11	HIS	-	EXPRESSION TAG	UNP Q9NYA1
A	-10	HIS	-	EXPRESSION TAG	UNP Q9NYA1
A	-9	ASP	-	EXPRESSION TAG	UNP Q9NYA1
A	-8	TYR	-	EXPRESSION TAG	UNP Q9NYA1
A	-7	ASP	-	EXPRESSION TAG	UNP Q9NYA1
A	-6	ILE	-	EXPRESSION TAG	UNP Q9NYA1
A	-5	PRO	-	EXPRESSION TAG	UNP Q9NYA1
A	-4	THR	-	EXPRESSION TAG	UNP Q9NYA1
A	-3	THR	-	EXPRESSION TAG	UNP Q9NYA1
A	-2	GLU	-	EXPRESSION TAG	UNP Q9NYA1
A	-1	ASN	-	EXPRESSION TAG	UNP Q9NYA1
A	0	LEU	-	EXPRESSION TAG	UNP Q9NYA1
A	1	TYR	-	EXPRESSION TAG	UNP Q9NYA1
A	2	PHE	-	EXPRESSION TAG	UNP Q9NYA1
A	3	GLN	-	EXPRESSION TAG	UNP Q9NYA1

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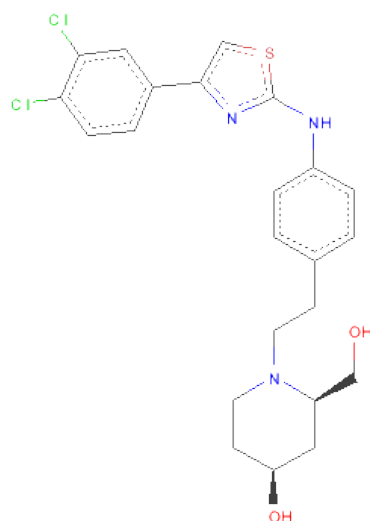
Chain	Residue	Modelled	Actual	Comment	Reference
A	4	GLY	-	EXPRESSION TAG	UNP Q9NYA1
A	5	ALA	-	EXPRESSION TAG	UNP Q9NYA1
A	6	MET	-	EXPRESSION TAG	UNP Q9NYA1
A	7	GLY	-	EXPRESSION TAG	UNP Q9NYA1
A	8	SER	-	EXPRESSION TAG	UNP Q9NYA1
B	-19	MET	-	EXPRESSION TAG	UNP Q9NYA1
B	-18	SER	-	EXPRESSION TAG	UNP Q9NYA1
B	-17	TYR	-	EXPRESSION TAG	UNP Q9NYA1
B	-16	TYR	-	EXPRESSION TAG	UNP Q9NYA1
B	-15	HIS	-	EXPRESSION TAG	UNP Q9NYA1
B	-14	HIS	-	EXPRESSION TAG	UNP Q9NYA1
B	-13	HIS	-	EXPRESSION TAG	UNP Q9NYA1
B	-12	HIS	-	EXPRESSION TAG	UNP Q9NYA1
B	-11	HIS	-	EXPRESSION TAG	UNP Q9NYA1
B	-10	HIS	-	EXPRESSION TAG	UNP Q9NYA1
B	-9	ASP	-	EXPRESSION TAG	UNP Q9NYA1
B	-8	TYR	-	EXPRESSION TAG	UNP Q9NYA1
B	-7	ASP	-	EXPRESSION TAG	UNP Q9NYA1
B	-6	ILE	-	EXPRESSION TAG	UNP Q9NYA1
B	-5	PRO	-	EXPRESSION TAG	UNP Q9NYA1
B	-4	THR	-	EXPRESSION TAG	UNP Q9NYA1
B	-3	THR	-	EXPRESSION TAG	UNP Q9NYA1
B	-2	GLU	-	EXPRESSION TAG	UNP Q9NYA1
B	-1	ASN	-	EXPRESSION TAG	UNP Q9NYA1
B	0	LEU	-	EXPRESSION TAG	UNP Q9NYA1
B	1	TYR	-	EXPRESSION TAG	UNP Q9NYA1
B	2	PHE	-	EXPRESSION TAG	UNP Q9NYA1
B	3	GLN	-	EXPRESSION TAG	UNP Q9NYA1
B	4	GLY	-	EXPRESSION TAG	UNP Q9NYA1
B	5	ALA	-	EXPRESSION TAG	UNP Q9NYA1
B	6	MET	-	EXPRESSION TAG	UNP Q9NYA1
B	7	GLY	-	EXPRESSION TAG	UNP Q9NYA1
B	8	SER	-	EXPRESSION TAG	UNP Q9NYA1
C	-19	MET	-	EXPRESSION TAG	UNP Q9NYA1
C	-18	SER	-	EXPRESSION TAG	UNP Q9NYA1
C	-17	TYR	-	EXPRESSION TAG	UNP Q9NYA1
C	-16	TYR	-	EXPRESSION TAG	UNP Q9NYA1
C	-15	HIS	-	EXPRESSION TAG	UNP Q9NYA1
C	-14	HIS	-	EXPRESSION TAG	UNP Q9NYA1
C	-13	HIS	-	EXPRESSION TAG	UNP Q9NYA1
C	-12	HIS	-	EXPRESSION TAG	UNP Q9NYA1
C	-11	HIS	-	EXPRESSION TAG	UNP Q9NYA1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-10	HIS	-	EXPRESSION TAG	UNP Q9NYA1
C	-9	ASP	-	EXPRESSION TAG	UNP Q9NYA1
C	-8	TYR	-	EXPRESSION TAG	UNP Q9NYA1
C	-7	ASP	-	EXPRESSION TAG	UNP Q9NYA1
C	-6	ILE	-	EXPRESSION TAG	UNP Q9NYA1
C	-5	PRO	-	EXPRESSION TAG	UNP Q9NYA1
C	-4	THR	-	EXPRESSION TAG	UNP Q9NYA1
C	-3	THR	-	EXPRESSION TAG	UNP Q9NYA1
C	-2	GLU	-	EXPRESSION TAG	UNP Q9NYA1
C	-1	ASN	-	EXPRESSION TAG	UNP Q9NYA1
C	0	LEU	-	EXPRESSION TAG	UNP Q9NYA1
C	1	TYR	-	EXPRESSION TAG	UNP Q9NYA1
C	2	PHE	-	EXPRESSION TAG	UNP Q9NYA1
C	3	GLN	-	EXPRESSION TAG	UNP Q9NYA1
C	4	GLY	-	EXPRESSION TAG	UNP Q9NYA1
C	5	ALA	-	EXPRESSION TAG	UNP Q9NYA1
C	6	MET	-	EXPRESSION TAG	UNP Q9NYA1
C	7	GLY	-	EXPRESSION TAG	UNP Q9NYA1
C	8	SER	-	EXPRESSION TAG	UNP Q9NYA1

- Molecule 2 is (2R,4S)-1-[2-(4-{[4-(3,4-DICHLOROPHENYL)-1,3-THIAZOL-2-YL]AMINO}PHENYL)ETHYL]-2-(HYDROXYMETHYL)PIPERIDIN-4-OL (three-letter code: 1V2) (formula: C<sub>23</sub>H<sub>25</sub>Cl<sub>2</sub>N<sub>3</sub>O<sub>2</sub>S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	S	0	0
			31	23	2	3	2	1		

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	B	1	Total	C	Cl	N	O	S	0	0
			31	23	2	3	2	1		
2	C	1	Total	C	Cl	N	O	S	0	0
			31	23	2	3	2	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	22	Total	O	0	0
			22	22		
3	B	17	Total	O	0	0
			17	17		
3	C	19	Total	O	0	0
			19	19		



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.58Å 225.68Å 106.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.75 29.88 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.9 (30.00-2.75) 99.9 (29.88-2.75)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.69 (at 2.76Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.208 , 0.255 0.208 , 0.255	Depositor DCC
$R_{free}$ test set	1645 reflections (5.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	42.4	Xtriage
Anisotropy	0.090	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 9.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 32431 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	8318	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.13% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 1V2

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	0.28	0/2879	0.53	0/3906
1	B	0.29	0/2731	0.52	0/3702
1	C	0.28	0/2755	0.52	0/3735
All	All	0.28	0/8365	0.52	0/11343

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2806	0	2852	18	0
1	B	2668	0	2699	26	0
1	C	2693	0	2724	16	0
2	A	31	0	25	1	0
2	B	31	0	25	0	0
2	C	31	0	25	0	0
3	A	22	0	0	0	0
3	B	17	0	0	1	0
3	C	19	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8318	0	8350	60	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

All (60) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:57:ARG:HG3	1:B:57:ARG:HH11	1.34	0.91
1:B:177:VAL:O	1:B:181:SER:HB2	1.92	0.69
1:B:203:LEU:HD12	1:B:296:ARG:HG2	1.77	0.66
1:C:335:LYS:HB3	1:C:346:VAL:HG12	1.81	0.61
1:B:57:ARG:NH1	1:B:57:ARG:HG3	2.08	0.59
1:A:286:HIS:HD2	1:A:321:TYR:OH	1.87	0.58
1:B:169:LEU:HD12	1:B:340:VAL:HG22	1.88	0.56
1:B:55:GLU:O	1:B:56:ARG:HB3	2.06	0.55
1:C:169:LEU:HD12	1:C:340:VAL:HG22	1.89	0.55
1:B:272:MET:HB3	1:B:306:MET:HE2	1.89	0.54
1:C:76:VAL:HB	1:C:106:CYS:HB3	1.90	0.54
1:A:153:LEU:HB3	1:A:165:SER:HB3	1.90	0.54
1:C:88:VAL:HG21	1:C:166:VAL:HG11	1.89	0.53
1:B:88:VAL:HG21	1:B:166:VAL:HG11	1.91	0.52
1:C:80:GLY:HA2	1:C:114:ASN:ND2	2.25	0.52
1:C:77:VAL:CG1	1:C:83:LEU:HB3	2.40	0.51
1:B:363:SER:HB2	3:B:517:HOH:O	2.10	0.51
1:B:286:HIS:HD2	1:B:321:TYR:OH	1.94	0.50
1:A:69:LEU:HB3	1:A:103:LYS:HE3	1.93	0.50
1:A:294:VAL:HG13	1:A:318:TYR:HB2	1.93	0.50
1:A:258:VAL:HG22	1:A:290:VAL:HB	1.94	0.50
1:A:207:ARG:HB3	1:A:332:LYS:HD2	1.92	0.50
1:A:170:ALA:HB3	1:A:339:ALA:HB3	1.94	0.49
1:B:205:THR:HG22	1:B:258:VAL:HG12	1.95	0.48
1:B:149:PRO:HB2	1:B:357:ASN:HB3	1.95	0.48
1:A:199:ARG:HD2	1:A:199:ARG:HA	1.72	0.47
1:A:328:ARG:HE	1:A:351:GLN:NE2	2.12	0.47
1:A:200:LEU:HD21	1:A:300:LEU:HB2	1.97	0.46
1:A:149:PRO:HB2	1:A:357:ASN:HB3	1.97	0.46
1:C:207:ARG:HB3	1:C:332:LYS:HE3	1.96	0.46
1:B:22:ASN:HD22	1:B:23:PRO:HD2	1.81	0.45
1:A:266:SER:HA	1:A:275:ALA:HB3	1.98	0.45
1:B:157:THR:OG1	1:B:161:LEU:HB3	2.17	0.45
1:A:169:LEU:HD12	1:A:340:VAL:HG22	1.98	0.45
1:B:179:LEU:HG	1:B:344:LEU:HG	1.98	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:115:ALA:HB3	1:C:167:LEU:HD21	1.99	0.44
1:A:112:SER:HB2	1:A:191:ARG:HH21	1.82	0.44
1:A:231:GLN:HG2	1:A:232:GLY:N	2.32	0.44
1:C:22:ASN:HD22	1:C:22:ASN:C	2.21	0.44
1:B:210:LEU:HD23	1:B:329:LEU:HD13	2.00	0.43
1:C:153:LEU:HB3	1:C:165:SER:HB3	1.99	0.43
1:B:57:ARG:NH1	1:B:57:ARG:CG	2.79	0.43
1:B:329:LEU:HD23	1:B:338:PHE:HE2	1.84	0.43
1:C:158:ALA:HB2	1:C:349:ALA:HB3	2.00	0.43
1:B:29:LYS:O	1:B:32:GLN:HG2	2.19	0.43
2:A:401:1V2:H8	2:A:401:1V2:N3	2.34	0.43
1:C:83:LEU:HA	1:C:83:LEU:HD23	1.91	0.42
1:A:19:VAL:HG22	1:A:76:VAL:HG22	2.01	0.42
1:B:193:THR:HG23	1:B:303:PHE:HE2	1.84	0.42
1:C:55:GLU:HB2	1:C:56:ARG:HD3	2.02	0.41
1:B:55:GLU:O	1:B:56:ARG:CB	2.69	0.41
1:B:201:ALA:HB1	1:C:300:LEU:HD21	2.00	0.41
1:B:193:THR:HG22	1:B:197:PHE:CZ	2.55	0.41
1:B:109:PRO:HG3	1:B:134:LEU:HG	2.02	0.41
1:A:99:THR:HA	1:A:102:GLN:HE21	1.86	0.41
1:B:103:LYS:HD3	1:B:104:PRO:HD2	2.04	0.40
1:C:157:THR:HG21	1:C:345:MET:HE1	2.03	0.40
1:A:196:THR:O	1:A:200:LEU:HB2	2.21	0.40
1:B:80:GLY:HA2	1:B:114:ASN:OD1	2.21	0.40
1:C:71:ARG:HD3	1:C:72:TRP:CE2	2.56	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	360/384 (94%)	349 (97%)	10 (3%)	1 (0%)	50	83
1	B	333/384 (87%)	322 (97%)	8 (2%)	3 (1%)	25	60
1	C	341/384 (89%)	331 (97%)	9 (3%)	1 (0%)	50	83

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1034/1152 (90%)	1002 (97%)	27 (3%)	5 (0%)	38 74

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	79	SER
1	A	79	SER
1	B	79	SER
1	B	56	ARG
1	B	189	GLU

### 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	301/322 (94%)	281 (93%)	20 (7%)	24 53
1	B	286/322 (89%)	267 (93%)	19 (7%)	24 53
1	C	287/322 (89%)	266 (93%)	21 (7%)	20 46
All	All	874/966 (90%)	814 (93%)	60 (7%)	22 50

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	31	LEU
1	A	35[A]	ARG
1	A	35[B]	ARG
1	A	57	ARG
1	A	76	VAL
1	A	83	LEU
1	A	98	GLU
1	A	105	LEU
1	A	132	GLU
1	A	152	LEU
1	A	153	LEU
1	A	162	ARG

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Mol	Chain	Res	Type
1	A	179	LEU
1	A	210	LEU
1	A	294	VAL
1	A	296	ARG
1	A	322	VAL
1	A	337	VAL
1	A	358	TYR
1	B	22	ASN
1	B	32	GLN
1	B	35	ARG
1	B	50	THR
1	B	57	ARG
1	B	105	LEU
1	B	147	LEU
1	B	152	LEU
1	B	153	LEU
1	B	169	LEU
1	B	179	LEU
1	B	185	ARG
1	B	199	ARG
1	B	242	GLU
1	B	273	PHE
1	B	277	MET
1	B	294	VAL
1	B	346	VAL
1	B	358	TYR
1	C	17	VAL
1	C	22	ASN
1	C	29	LYS
1	C	35	ARG
1	C	50	THR
1	C	56	ARG
1	C	57	ARG
1	C	71	ARG
1	C	76	VAL
1	C	83	LEU
1	C	105	LEU
1	C	147	LEU
1	C	152	LEU
1	C	153	LEU
1	C	162	ARG
1	C	210	LEU

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Mol	Chain	Res	Type
1	C	215	VAL
1	C	245	VAL
1	C	256	ASP
1	C	291	ARG
1	C	301	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	85	HIS
1	A	102	GLN
1	A	122	HIS
1	A	231	GLN
1	A	286	HIS
1	A	351	GLN
1	B	22	ASN
1	B	32	GLN
1	B	102	GLN
1	B	231	GLN
1	B	286	HIS
1	B	351	GLN
1	C	22	ASN
1	C	58	ASN
1	C	114	ASN
1	C	286	HIS
1	C	351	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

## 5.6 Ligand geometry

3 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	1V2	A	401	-	34,34,34	1.38	3 (8%)	45,47,47	1.42	4 (8%)
2	1V2	B	401	-	34,34,34	1.34	3 (8%)	45,47,47	1.35	4 (8%)
2	1V2	C	401	-	34,34,34	1.34	3 (8%)	45,47,47	1.44	5 (11%)

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	1V2	A	401	-	-	0/15/28/28	0/4/4/4
2	1V2	B	401	-	-	0/15/28/28	0/4/4/4
2	1V2	C	401	-	-	1/15/28/28	0/4/4/4

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	1V2	C12-C11	-5.64	1.39	1.48
2	A	401	1V2	C12-C11	-5.64	1.39	1.48
2	C	401	1V2	C12-C11	-5.53	1.39	1.48
2	A	401	1V2	C1-N1	-2.96	1.34	1.40
2	B	401	1V2	C1-N1	-2.87	1.34	1.40
2	C	401	1V2	C1-N1	-2.82	1.34	1.40
2	A	401	1V2	C9-S1	-2.41	1.66	1.74
2	B	401	1V2	C9-S1	-2.13	1.67	1.74
2	C	401	1V2	C9-S1	-2.13	1.67	1.74

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	1V2	C10-C11-C12	-4.88	122.75	129.39
2	B	401	1V2	C10-C11-C12	-4.67	123.03	129.39
2	A	401	1V2	C10-C11-C12	-4.62	123.10	129.39
2	A	401	1V2	C11-C10-S1	-4.06	107.23	111.97
2	B	401	1V2	C11-C10-S1	-4.01	107.29	111.97
2	C	401	1V2	C11-C10-S1	-3.64	107.72	111.97
2	A	401	1V2	C10-S1-C9	3.32	95.56	90.49
2	B	401	1V2	C10-S1-C9	3.17	95.33	90.49
2	B	401	1V2	C10-C11-N3	3.06	114.38	109.74
2	A	401	1V2	C10-C11-N3	3.00	114.29	109.74
2	C	401	1V2	C10-C11-N3	2.98	114.26	109.74
2	C	401	1V2	C10-S1-C9	2.92	94.94	90.49
2	C	401	1V2	C19-C18-N2	2.81	112.95	110.61

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	401	1V2	S1-C9-N1-C1

There are no ring outliers.

## 5.7 Other polymers ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	360/384 (93%)	-0.03	16 (4%) 33 35	22, 34, 65, 78	0
1	B	340/384 (88%)	0.06	11 (3%) 45 49	26, 41, 71, 84	0
1	C	345/384 (89%)	-0.00	12 (3%) 42 44	27, 41, 63, 86	0
All	All	1045/1152 (90%)	0.01	39 (3%) 39 42	22, 39, 67, 86	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	228	VAL	6.9
1	A	224	ALA	6.0
1	C	335	LYS	4.8
1	C	334	GLY	4.3
1	B	335	LYS	4.2
1	C	27	LYS	3.9
1	B	231	GLN	3.5
1	C	348	GLU	3.4
1	A	229	VAL	3.0
1	A	27	LYS	2.9
1	A	227	VAL	2.8
1	C	333	ASP	2.8
1	C	217	ARG	2.8
1	A	52	MET	2.8
1	A	230	GLN	2.7
1	C	57	ARG	2.6
1	C	186	ARG	2.5
1	B	197	PHE	2.5
1	A	333	ASP	2.5
1	C	247	SER	2.4
1	A	221	LYS	2.4
1	C	26	GLY	2.4
1	C	242	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	253	PRO	2.3
1	A	222	THR	2.3
1	B	184	TYR	2.3
1	B	242	GLU	2.2
1	B	95	PRO	2.2
1	A	334	GLY	2.2
1	A	223	PRO	2.2
1	C	24	ARG	2.2
1	A	57	ARG	2.1
1	A	315	GLU	2.1
1	A	5	ALA	2.1
1	B	360	TRP	2.1
1	A	56	ARG	2.1
1	B	52	MET	2.0
1	B	111	GLY	2.0
1	B	57	ARG	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	1V2	C	401	31/31	0.21	2.06	30,39,65,72	0
2	1V2	A	401	31/31	0.18	0.62	26,29,48,54	0
2	1V2	B	401	31/31	0.18	0.42	36,48,67,75	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.