



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:06 PM GMT

PDB ID : 5AIR  
Title : Structural analysis of mouse GSK3beta fused with LRP6 peptide.  
Authors : Kim, K.L.  
Deposited on : 2015-02-17  
Resolution : 2.53 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

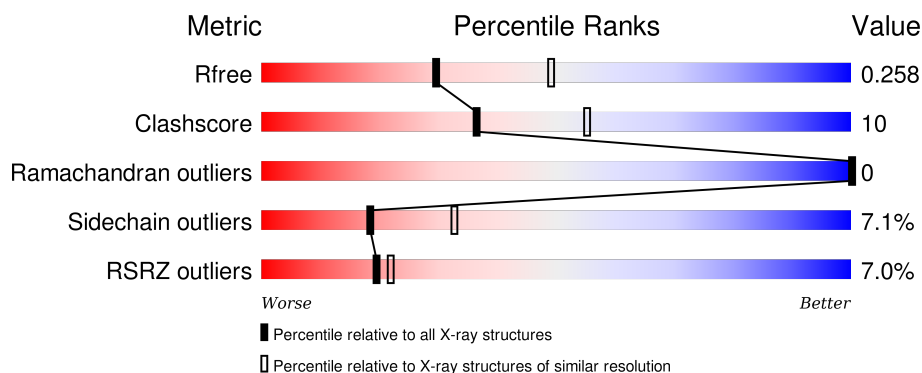
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.53 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))
$R_{free}$	91344	4241 (2.54-2.50)
Clashscore	102246	4968 (2.54-2.50)
Ramachandran outliers	100387	4873 (2.54-2.50)
Sidechain outliers	100360	4875 (2.54-2.50)
RSRZ outliers	91569	4253 (2.54-2.50)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	430	<div> <div>5%</div> <div> <div></div> <div>69%</div> <div>11%</div> <div>•</div> <div>18%</div> </div> </div>
1	B	430	<div> <div>7%</div> <div> <div></div> <div>65%</div> <div>17%</div> <div>•</div> <div>16%</div> </div> </div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5724 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.

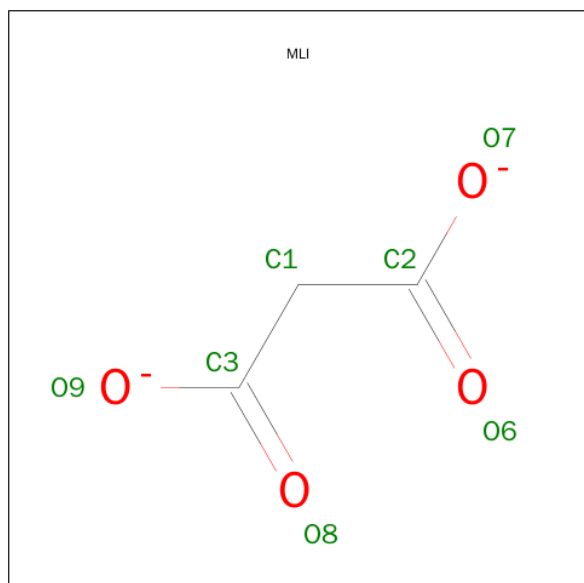
- Molecule 1 is a protein called LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 6, GLYCOGEN SYNTHASE KINASE-3 BETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	353	Total	C	N	O	S	0	0	0
			2818	1810	484	512	12			
1	B	361	Total	C	N	O	S	0	0	0
			2869	1841	493	523	12			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	MET	-	INITIATING METHIONINE	UNP Q9WV60
A	3	SER	-	LINKER	UNP Q9WV60
A	30	ILE	ARG	CONFLICT	UNP Q9WV60
B	-9	MET	-	INITIATING METHIONINE	UNP Q9WV60
B	3	SER	-	LINKER	UNP Q9WV60
B	30	ILE	ARG	CONFLICT	UNP Q9WV60

- Molecule 2 is MALONATE ION (three-letter code: MLI) (formula:  $C_3H_2O_4$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	7	0
			7	3	4		
2	B	1	Total	C	O	7	0
			7	3	4		

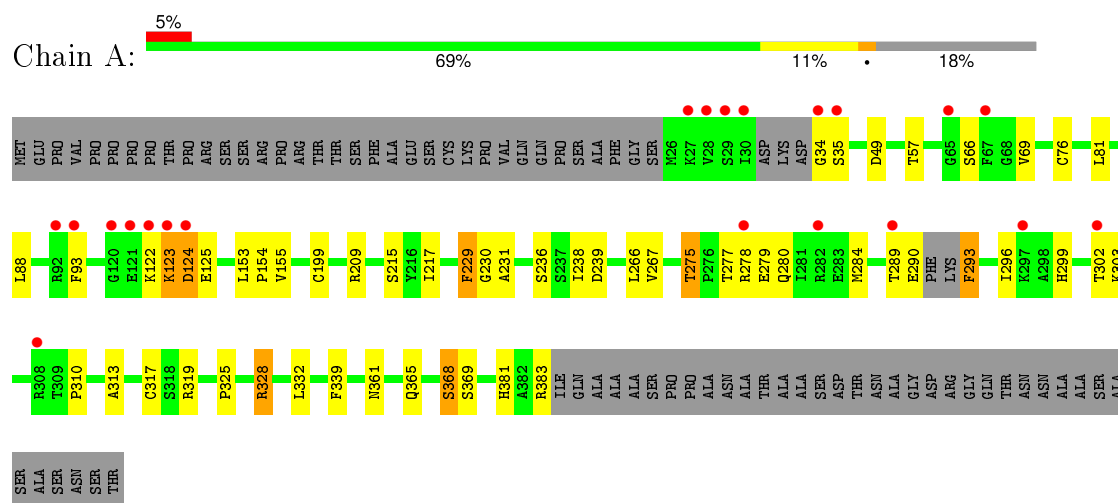
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	14	Total	O	0	0
			14	14		
3	B	9	Total	O	0	0
			9	9		

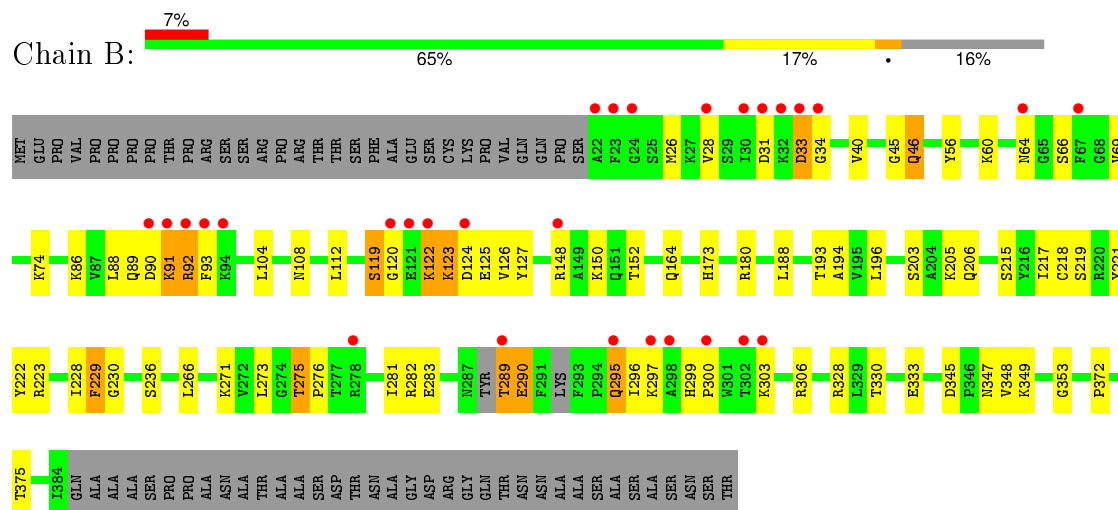
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 6, GLYCOGEN SYNTHASE KINASE-3 BETA



- Molecule 1: LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 6, 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, $\alpha$ , $\beta$ , $\gamma$	82.90Å 85.88Å 177.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.53 19.97 – 2.53	Depositor EDS
% Data completeness (in resolution range)	98.6 (20.00-2.53) 98.9 (19.97-2.53)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.08 (at 2.53Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, $R_{free}$	0.212 , 0.260 0.217 , 0.258	Depositor DCC
$R_{free}$ test set	2105 reflections (5.24%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.3	Xtriage
Anisotropy	0.076	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 30.7	EDS
Estimated twinning fraction	0.039 for k,h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 42326 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5724	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.60% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: MLI

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	0.73	0/2886	0.87	1/3922 (0.0%)
1	B	0.74	0/2937	0.86	4/3990 (0.1%)
All	All	0.74	0/5823	0.86	5/7912 (0.1%)

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	B	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	120	GLY	N-CA-C	-5.55	99.21	113.10
1	B	328	ARG	NE-CZ-NH2	-5.48	117.56	120.30
1	B	180	ARG	NE-CZ-NH2	-5.47	117.56	120.30
1	B	328	ARG	NE-CZ-NH1	5.40	123.00	120.30
1	A	319	ARG	NE-CZ-NH2	-5.16	117.72	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	119	SER	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	2818	0	2848	34	0
1	B	2869	0	2892	76	0
2	A	7	0	2	0	0
2	B	7	0	2	0	0
3	A	14	0	0	0	0
3	B	9	0	0	0	0
All	All	5724	0	5744	109	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 10.

All (109) 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:91:LYS:NZ	1:B:125:GLU:OE1	1.72	1.20
1:B:275:THR:OG1	1:B:296:ILE:O	1.74	1.06
1:B:123:LYS:HE3	1:B:124:ASP:H	1.31	0.93
1:B:123:LYS:HE3	1:B:124:ASP:N	1.88	0.87
1:A:123:LYS:HG3	1:A:125:GLU:HB2	1.58	0.83
1:B:349:LYS:NZ	1:B:353:GLY:O	2.12	0.82
1:B:296:ILE:HG22	1:B:297:LYS:N	1.98	0.78
1:A:57:THR:HG23	1:A:76:CYS:SG	2.23	0.78
1:B:295:GLN:HE21	1:B:296:ILE:N	1.84	0.75
1:B:229:PHE:CD1	1:B:229:PHE:N	2.52	0.74
1:B:86:LYS:HE2	1:B:127:TYR:HD2	1.54	0.73
1:B:90:ASP:OD1	1:B:92:ARG:N	2.22	0.72
1:B:229:PHE:N	1:B:229:PHE:HD1	1.86	0.70
1:B:123:LYS:CE	1:B:124:ASP:H	2.02	0.69
1:B:91:LYS:CE	1:B:125:GLU:OE1	2.41	0.68
1:B:46:GLN:NE2	1:B:104:LEU:O	2.26	0.68
1:B:271:LYS:O	1:B:299:HIS:HB2	1.93	0.68
1:B:295:GLN:C	1:B:296:ILE:HD12	2.14	0.68
1:B:229:PHE:HE1	1:B:266:LEU:HD11	1.58	0.68
1:A:229:PHE:N	1:A:229:PHE:HD1	1.93	0.66
1:B:296:ILE:HG22	1:B:297:LYS:H	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:218:CYS:HB3	1:B:223:ARG:HG2	1.79	0.63
1:A:229:PHE:CD1	1:A:229:PHE:N	2.64	0.62
1:B:123:LYS:CG	1:B:124:ASP:H	2.12	0.61
1:A:293:PHE:HD1	1:A:293:PHE:N	1.99	0.61
1:B:86:LYS:CE	1:B:127:TYR:HD2	2.14	0.60
1:B:123:LYS:HG3	1:B:124:ASP:H	1.65	0.60
1:A:293:PHE:N	1:A:293:PHE:CD1	2.70	0.59
1:B:228:ILE:C	1:B:229:PHE:HD1	2.06	0.59
1:A:290:GLU:HB3	1:A:293:PHE:HE1	1.67	0.58
1:B:152:THR:HG21	1:B:306:ARG:NH1	2.18	0.58
1:A:123:LYS:HD2	1:A:124:ASP:N	2.20	0.57
1:B:296:ILE:CG2	1:B:297:LYS:N	2.66	0.57
1:B:289:THR:OG1	1:B:290:GLU:HA	2.04	0.57
1:B:229:PHE:CE1	1:B:266:LEU:HD11	2.38	0.57
1:B:221:TYR:HB2	1:B:222:TYR:CE2	2.40	0.56
1:B:173:HIS:CE1	1:B:236:SER:HB3	2.40	0.56
1:B:300:PRO:HB2	1:B:303:LYS:HG2	1.88	0.56
1:B:90:ASP:OD1	1:B:92:ARG:CB	2.54	0.56
1:B:108:ASN:HD21	1:B:164:GLN:HG2	1.71	0.55
1:B:295:GLN:HE21	1:B:296:ILE:CA	2.19	0.55
1:A:275:THR:OG1	1:A:296:ILE:O	2.26	0.53
1:A:365:GLN:O	1:A:368:SER:OG	2.27	0.52
1:A:290:GLU:HB3	1:A:293:PHE:CE1	2.44	0.52
1:B:296:ILE:CG2	1:B:297:LYS:H	2.22	0.52
1:B:219:SER:O	1:B:223:ARG:HG3	2.09	0.51
1:A:313:ALA:HB2	1:A:339:PHE:CE1	2.46	0.51
1:B:108:ASN:ND2	1:B:164:GLN:HG2	2.26	0.51
1:A:383:ARG:NH1	1:A:383:ARG:HB2	2.26	0.51
1:B:89:GLN:HB3	1:B:126:VAL:HG23	1.93	0.50
1:B:275:THR:HG21	1:B:295:GLN:HG2	1.93	0.50
1:A:123:LYS:CG	1:A:125:GLU:HB2	2.36	0.50
1:B:92:ARG:HB2	1:B:93:PHE:CD2	2.47	0.49
1:B:273:LEU:N	1:B:273:LEU:HD12	2.26	0.49
1:B:295:GLN:O	1:B:296:ILE:HG13	2.12	0.49
1:A:229:PHE:HE1	1:A:266:LEU:HD11	1.77	0.49
1:B:33:ASP:N	1:B:34:GLY:HA2	2.26	0.49
1:B:275:THR:HG23	1:B:296:ILE:H	1.78	0.49
1:A:279:GLU:N	1:A:279:GLU:OE1	2.41	0.49
1:A:155:VAL:HG21	1:A:310:PRO:HG2	1.94	0.49
1:A:299:HIS:CE1	1:A:303:LYS:HB2	2.47	0.48
1:B:215:SER:CB	1:B:230:GLY:HA2	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:LYS:HE2	1:B:127:TYR:CD2	2.42	0.48
1:B:372:PRO:O	1:B:375:THR:HB	2.13	0.48
1:B:123:LYS:CG	1:B:124:ASP:N	2.76	0.48
1:B:345:ASP:O	1:B:348:VAL:HG12	2.13	0.48
1:B:289:THR:CB	1:B:290:GLU:HA	2.44	0.47
1:B:88:LEU:HD13	1:B:127:TYR:HE1	1.80	0.47
1:A:57:THR:CG2	1:A:76:CYS:SG	3.00	0.47
1:A:229:PHE:CE1	1:A:266:LEU:HD11	2.50	0.47
1:A:361:ASN:OD1	1:A:361:ASN:N	2.43	0.46
1:A:124:ASP:O	1:A:124:ASP:CG	2.54	0.46
1:A:267:VAL:HG11	1:B:66:SER:HB3	1.98	0.46
1:A:215:SER:OG	1:A:230:GLY:HA2	2.15	0.46
1:B:299:HIS:CE1	1:B:303:LYS:HB2	2.51	0.45
1:A:277:THR:OG1	1:A:280:GLN:HG3	2.16	0.45
1:B:193:THR:O	1:B:194:ALA:HB3	2.16	0.45
1:B:276:PRO:HB2	1:B:281:ILE:HG13	1.97	0.45
1:B:26:MET:HB3	1:B:40:VAL:HG12	1.99	0.45
1:B:273:LEU:N	1:B:273:LEU:CD1	2.80	0.45
1:B:125:GLU:OE1	1:B:125:GLU:HA	2.17	0.45
1:B:345:ASP:OD1	1:B:347:ASN:N	2.47	0.45
1:B:299:HIS:ND1	1:B:300:PRO:O	2.45	0.44
1:A:325:PRO:O	1:A:328:ARG:HG3	2.18	0.44
1:A:238:ILE:HG13	1:A:239:ASP:N	2.33	0.44
1:B:148:ARG:HH11	1:B:148:ARG:HG3	1.83	0.43
1:B:90:ASP:OD1	1:B:92:ARG:CA	2.67	0.43
1:A:381:HIS:CD2	1:A:381:HIS:H	2.34	0.43
1:B:299:HIS:HE1	1:B:303:LYS:HB2	1.83	0.43
1:A:332:LEU:HD12	1:A:332:LEU:HA	1.70	0.42
1:B:123:LYS:CD	1:B:124:ASP:H	2.32	0.42
1:A:215:SER:CB	1:A:230:GLY:HA2	2.49	0.42
1:B:205:LYS:HG2	1:B:206:GLN:N	2.35	0.42
1:B:122:LYS:HE3	1:B:122:LYS:HB2	1.65	0.41
1:B:330:THR:OG1	1:B:333:GLU:HG3	2.21	0.41
1:B:123:LYS:HD2	1:B:123:LYS:HA	1.76	0.41
1:A:34:GLY:HA3	1:A:35:SER:HA	1.92	0.41
1:B:215:SER:HB2	1:B:230:GLY:HA2	2.03	0.41
1:A:231:ALA:HB2	1:A:284:MET:O	2.21	0.41
1:B:88:LEU:HA	1:B:127:TYR:CD1	2.55	0.41
1:B:295:GLN:O	1:B:296:ILE:HD12	2.21	0.41
1:B:345:ASP:OD1	1:B:347:ASN:HB2	2.20	0.41
1:B:56:TYR:HA	1:B:74:LYS:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:295:GLN:NE2	1:B:296:ILE:CA	2.82	0.40
1:B:152:THR:HG21	1:B:306:ARG:CZ	2.51	0.40
1:A:153:LEU:HD12	1:A:154:PRO:HD2	2.02	0.40
1:B:188:LEU:O	1:B:196:LEU:HA	2.22	0.40
1:A:123:LYS:CD	1:A:124:ASP:N	2.83	0.40
1:B:45:GLY:HA3	1:B:112:LEU:O	2.21	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	347/430 (81%)	328 (94%)	19 (6%)	0	100	100
1	B	355/430 (83%)	327 (92%)	28 (8%)	0	100	100
All	All	702/860 (82%)	655 (93%)	47 (7%)	0	100	100

There are no Ramachandran outliers to report.

### 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	314/374 (84%)	291 (93%)	23 (7%)	17	31
1	B	318/374 (85%)	296 (93%)	22 (7%)	19	34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	632/748 (84%)	587 (93%)	45 (7%)	18	33

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	ASP
1	A	66	SER
1	A	69	VAL
1	A	81	LEU
1	A	88	LEU
1	A	93	PHE
1	A	122	LYS
1	A	123	LYS
1	A	124	ASP
1	A	199	CYS
1	A	209	ARG
1	A	217	ILE
1	A	229	PHE
1	A	236	SER
1	A	275	THR
1	A	278	ARG
1	A	289	THR
1	A	293	PHE
1	A	302	THR
1	A	317	CYS
1	A	328	ARG
1	A	368	SER
1	A	369	SER
1	B	28	VAL
1	B	31	ASP
1	B	33	ASP
1	B	46	GLN
1	B	60	LYS
1	B	64	ASN
1	B	69	VAL
1	B	91	LYS
1	B	92	ARG
1	B	119	SER
1	B	122	LYS
1	B	123	LYS
1	B	150	LYS
1	B	203	SER

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Mol	Chain	Res	Type
1	B	217	ILE
1	B	229	PHE
1	B	275	THR
1	B	282	ARG
1	B	283	GLU
1	B	289	THR
1	B	290	GLU
1	B	295	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	365	GLN
1	B	295	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 carbohydrates 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	MLI	A	1001	-	0,6,6	0.00	-	0,7,7	0.00	-
2	MLI	B	1002	-	0,6,6	0.00	-	0,7,7	0.00	-

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	MLI	A	1001	-	-	0/0/4/4	0/0/0/0
2	MLI	B	1002	-	-	0/0/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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, 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	353/430 (82%)	-0.07	21 (5%)	26 30	20, 37, 99, 123	0
1	B	361/430 (83%)	0.04	29 (8%)	15 16	21, 41, 113, 135	0
All	All	714/860 (83%)	-0.01	50 (7%)	19 22	20, 39, 107, 135	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	289	THR	8.3
1	A	120	GLY	7.3
1	A	30	ILE	7.1
1	B	23	PHE	6.7
1	A	122	LYS	6.1
1	A	34	GLY	5.8
1	B	32	LYS	5.4
1	A	35	SER	4.6
1	B	93	PHE	4.6
1	A	28	VAL	4.6
1	B	33	ASP	4.4
1	B	22	ALA	4.4
1	B	92	ARG	4.4
1	B	122	LYS	4.3
1	A	29	SER	4.2
1	A	124	ASP	4.1
1	A	92	ARG	3.7
1	B	28	VAL	3.7
1	B	30	ILE	3.6
1	A	93	PHE	3.5
1	B	120	GLY	3.2
1	B	31	ASP	3.1
1	B	297	LYS	3.1
1	B	302	THR	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	121	GLU	3.0
1	A	282	ARG	3.0
1	B	278	ARG	2.9
1	B	90	ASP	2.8
1	A	123	LYS	2.8
1	A	289	THR	2.8
1	B	91	LYS	2.7
1	B	34	GLY	2.7
1	B	24	GLY	2.6
1	A	278	ARG	2.5
1	B	67	PHE	2.4
1	A	121	GLU	2.4
1	A	67	PHE	2.4
1	A	302	THR	2.4
1	A	297	LYS	2.4
1	B	303	LYS	2.3
1	B	94	LYS	2.3
1	B	298	ALA	2.3
1	B	124	ASP	2.3
1	A	27	LYS	2.2
1	A	308	ARG	2.1
1	B	64	ASN	2.1
1	A	65	GLY	2.1
1	B	300	PRO	2.1
1	B	295	GLN	2.1
1	B	148	ARG	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 carbohydrates 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. 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	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MLI	B	1002	7/7	-	-	-	20,29,45,54	7
2	MLI	A	1001	7/7	-	-	-	15,21,25,30	7

## 6.5 Other polymers [i](#)

There are no such residues in this entry.