



# Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 03:08 PM GMT

PDB ID : 2G20  
Title : Ketopiperazine-Based Renin Inhibitors: Optimization of the C Ring  
Authors : Holsworth, D.D.; Jalaiea, M.; Zhanga, E.; Mcconnella, P.  
Deposited on : 2006-02-15  
Resolution : 2.40 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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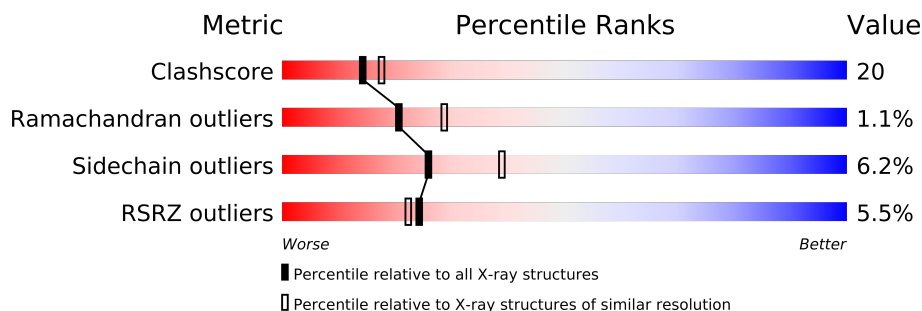
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.40 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))
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

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	333	
1	B	333	

## 2 Entry composition i

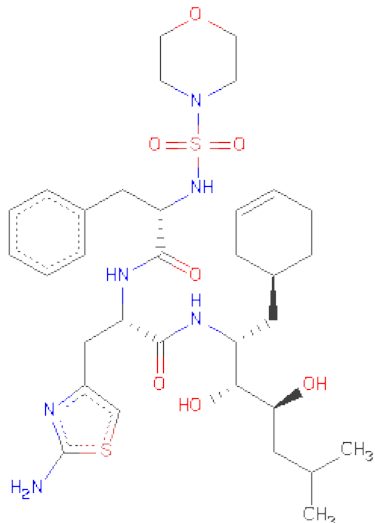
There are 3 unique types of molecules in this entry. The entry contains 5343 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Renin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	333	Total	C	N	O	S	0	0	0
			2572	1642	416	500	14			
1	B	333	Total	C	N	O	S	0	0	0
			2572	1642	416	500	14			

- Molecule 2 is N-(MORPHOLIN-4-YLSULFONYL)-L-PHENYLALANYL-3-(2-AMINO-1,3-THIAZOL-4-YL)-N-[(1R,2R,3S)-1-[(1R)-CYCLOHEX-3-EN-1-YLMETHYL]-2,3-DIHYDROXY-5-METHYLHEXYL]-L-ALANINAMIDE (three-letter code: L1A) (formula:  $C_{33}H_{50}N_6O_7S_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			48	33	6	7	2		
2	B	1	Total	C	N	O	S	0	0
			48	33	6	7	2		

- Molecule 3 is water.

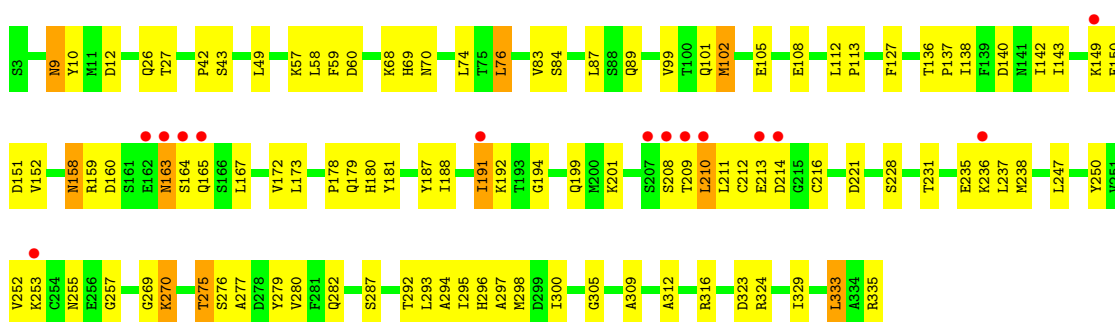
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	61	Total 61	O 61	0	0
3	B	42	Total 42	O 42	0	0

### 3 Residue-property plots

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.

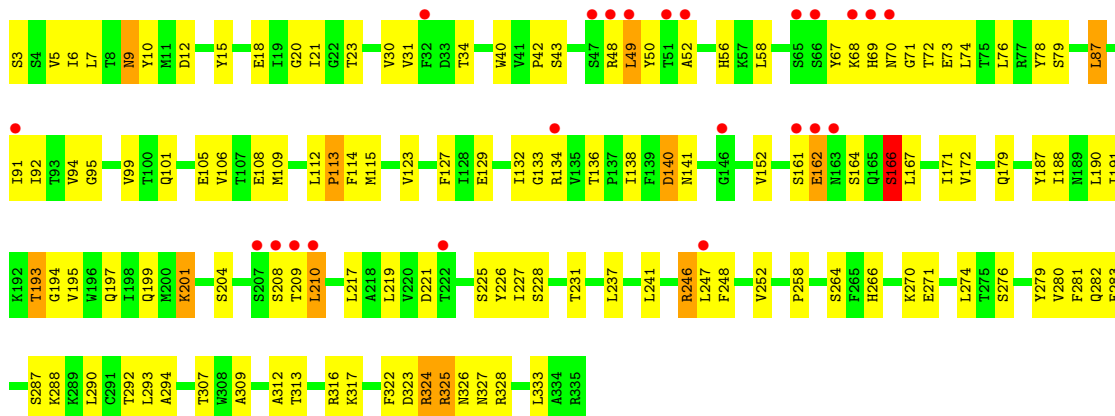
#### • Molecule 1: Renin

Chain A:



#### • Molecule 1: Renin

Chain B:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	141.33Å 141.33Å 141.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.40 33.31 – 2.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.40) 81.4 (33.31-2.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.05 (at 2.39Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.210 , 0.260 0.222 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	45.0	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 33.7	EDS
Estimated twinning fraction	0.016 for l,-k,h	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.36$	Xtriage
Outliers	0 of 35305 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5343	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.15% 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: L1A

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	0.36	0/2632	0.67	0/3568
1	B	0.35	0/2632	0.67	0/3568
All	All	0.35	0/5264	0.67	0/7136

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	2572	0	2501	94	0
1	B	2572	0	2501	109	0
2	A	48	0	50	3	0
2	B	48	0	50	5	0
3	A	61	0	0	8	0
3	B	42	0	0	7	0
All	All	5343	0	5102	203	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 20.

All (203) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:52:ALA:HA	1:B:115:MET:HE3	1.40	1.02
1:B:217:LEU:HB2	1:B:307:THR:HG22	1.39	1.01
1:B:197:GLN:OE1	1:B:307:THR:HG21	1.70	0.90
1:A:276:SER:O	1:A:280:VAL:HG12	1.72	0.89
1:A:160:ASP:HB3	3:A:934:HOH:O	1.72	0.88
1:A:158:ASN:HD22	1:A:159:ARG:H	1.24	0.81
1:A:158:ASN:ND2	1:A:159:ARG:H	1.82	0.78
1:B:42:PRO:HG3	1:B:109:MET:HE1	1.65	0.77
1:A:275:THR:HG22	1:A:277:ALA:H	1.50	0.77
1:A:163:ASN:H	1:A:163:ASN:HD22	1.30	0.76
1:A:152:VAL:HG12	1:A:323:ASP:HA	1.68	0.76
1:B:201:LYS:HE3	1:B:266:HIS:CD2	2.20	0.76
1:B:193:THR:HG23	1:B:327:ASN:HD21	1.48	0.76
1:A:99:VAL:HG21	1:A:142:ILE:HG12	1.67	0.75
1:B:252:VAL:HG23	3:B:891:HOH:O	1.86	0.74
1:B:208:SER:O	1:B:210:LEU:HD22	1.87	0.74
1:B:193:THR:HG23	1:B:327:ASN:ND2	2.03	0.74
1:B:43:SER:HB2	1:B:105:GLU:HB3	1.69	0.73
1:B:247:LEU:HD23	1:B:248:PHE:HB2	1.70	0.73
1:B:201:LYS:HB2	1:B:266:HIS:HD2	1.55	0.72
1:B:9:ASN:C	1:B:9:ASN:HD22	1.94	0.71
1:B:161:SER:HB3	1:B:164:SER:HB3	1.71	0.70
1:B:52:ALA:HA	1:B:115:MET:CE	2.18	0.70
1:A:26:GLN:HE22	1:A:60:ASP:H	1.39	0.70
1:B:9:ASN:HD21	1:B:12:ASP:H	1.38	0.69
1:B:270:LYS:HG2	3:B:900:HOH:O	1.94	0.68
1:B:152:VAL:HG12	1:B:323:ASP:HA	1.76	0.67
1:A:158:ASN:HD22	1:A:159:ARG:N	1.93	0.67
1:A:275:THR:HG22	1:A:277:ALA:N	2.11	0.66
1:A:43:SER:HB2	1:A:105:GLU:HB3	1.78	0.66
1:A:151:ASP:O	1:A:324:ARG:HB2	1.96	0.66
1:B:74:LEU:HD22	1:B:87:LEU:HD13	1.78	0.66
1:B:9:ASN:HD22	1:B:10:TYR:N	1.94	0.65
1:B:276:SER:HA	1:B:279:TYR:CE2	2.31	0.65
1:A:9:ASN:HD21	1:A:12:ASP:H	1.43	0.65
1:A:210:LEU:HB2	1:A:236:LYS:NZ	2.12	0.64
1:A:158:ASN:ND2	1:A:159:ARG:N	2.46	0.64
1:B:161:SER:O	1:B:162:GLU:HB2	1.95	0.64
1:B:217:LEU:HB2	1:B:307:THR:CG2	2.23	0.63
1:B:201:LYS:HE3	1:B:266:HIS:HD2	1.63	0.62
1:A:163:ASN:H	1:A:163:ASN:ND2	1.97	0.62
1:B:21:ILE:HG12	1:B:92:ILE:HG12	1.82	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:226:TYR:HB3	1:B:294:ALA:O	2.00	0.60
1:B:6:ILE:HG23	1:B:167:LEU:CD1	2.31	0.60
1:A:68:LYS:HB2	1:A:89:GLN:HB3	1.83	0.60
1:A:210:LEU:HB2	1:A:236:LYS:HZ1	1.66	0.59
1:A:191:ILE:HG22	1:A:192:LYS:N	2.18	0.59
1:B:227:ILE:HG13	1:B:313:THR:HB	1.84	0.58
1:B:247:LEU:CD2	1:B:248:PHE:HB2	2.34	0.58
1:B:70:ASN:ND2	3:B:895:HOH:O	2.37	0.58
1:B:42:PRO:HB2	1:B:58:LEU:HD23	1.85	0.57
1:A:84:SER:HB3	1:A:108:GLU:OE1	2.04	0.57
1:B:49:LEU:O	1:B:49:LEU:HD12	2.03	0.57
1:B:101:GLN:NE2	1:B:138:ILE:HA	2.19	0.57
1:B:99:VAL:HA	3:B:909:HOH:O	2.05	0.57
1:B:91:ILE:O	1:B:91:ILE:HG13	2.03	0.57
1:B:280:VAL:HG22	1:B:293:LEU:CD2	2.34	0.57
1:B:237:LEU:O	1:B:241:LEU:HD13	2.04	0.56
1:A:143:ILE:HD11	1:A:151:ASP:OD2	2.05	0.56
1:A:70:ASN:ND2	3:A:888:HOH:O	2.36	0.56
1:B:136:THR:HG21	1:B:141:ASN:ND2	2.21	0.56
1:A:208:SER:O	1:A:210:LEU:HG	2.06	0.55
1:B:161:SER:O	1:B:162:GLU:CB	2.55	0.55
1:B:195:VAL:HG12	1:B:197:GLN:HB2	1.88	0.55
1:A:74:LEU:HD13	1:A:87:LEU:HD21	1.87	0.55
1:B:42:PRO:HG3	1:B:109:MET:CE	2.35	0.55
1:B:129:GLU:OE1	1:B:129:GLU:N	2.36	0.55
1:B:246:ARG:HG2	1:B:247:LEU:N	2.22	0.54
1:B:221:ASP:OD1	2:B:886:L1A:O3	2.24	0.54
1:A:212:CYS:SG	1:A:212:CYS:O	2.64	0.54
1:A:191:ILE:HD11	1:A:199:GLN:HB2	1.90	0.54
1:A:228:SER:OG	1:A:309:ALA:HB3	2.07	0.54
1:A:9:ASN:HD21	1:A:12:ASP:N	2.05	0.54
1:B:247:LEU:HD23	1:B:248:PHE:N	2.21	0.54
1:A:89:GLN:HB2	1:A:102:MET:CE	2.37	0.54
1:B:217:LEU:CB	1:B:307:THR:HG22	2.27	0.54
1:A:201:LYS:HE2	1:A:269:GLY:H	1.73	0.54
1:B:225:SER:O	1:B:312:ALA:HB3	2.08	0.53
1:B:7:LEU:HD11	1:B:171:ILE:HG13	1.89	0.53
1:A:9:ASN:ND2	1:A:12:ASP:H	2.07	0.53
1:A:112:LEU:N	1:A:112:LEU:HD12	2.23	0.53
1:A:209:THR:HG22	1:A:209:THR:O	2.09	0.53
1:A:163:ASN:HD22	1:A:163:ASN:N	1.96	0.52
1:A:27:THR:O	1:A:57:LYS:HG2	2.09	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:213:GLU:O	1:A:214:ASP:HB2	2.09	0.52
1:B:9:ASN:C	1:B:9:ASN:ND2	2.61	0.52
1:A:180:HIS:C	1:A:335:ARG:HG2	2.30	0.52
1:B:274:LEU:CD2	1:B:317:LYS:HG2	2.40	0.52
1:B:179:GLN:HG2	3:B:898:HOH:O	2.10	0.51
1:B:12:ASP:O	1:B:316:ARG:NH1	2.44	0.51
1:A:42:PRO:HB2	1:A:58:LEU:HD23	1.92	0.51
1:A:127:PHE:CG	1:A:194:GLY:HA2	2.46	0.51
1:B:280:VAL:HG22	1:B:293:LEU:HD22	1.93	0.51
1:B:9:ASN:HD21	1:B:12:ASP:N	2.09	0.50
1:A:312:ALA:O	1:A:316:ARG:HB2	2.10	0.50
1:B:9:ASN:ND2	1:B:12:ASP:H	2.09	0.50
1:A:89:GLN:HB2	1:A:102:MET:HE2	1.94	0.50
1:B:67:TYR:CZ	1:B:69:HIS:HA	2.46	0.50
1:B:258:PRO:HD3	1:B:282:GLN:HE22	1.76	0.50
1:B:287:SER:OG	1:B:288:LYS:HE3	2.12	0.50
1:B:188:ILE:HD12	1:B:188:ILE:N	2.25	0.50
1:A:276:SER:O	1:A:280:VAL:CG1	2.55	0.49
1:A:309:ALA:HB3	2:A:885:L1A:HN41	1.77	0.49
1:B:20:GLY:O	1:B:92:ILE:HA	2.12	0.49
1:A:187:TYR:C	1:A:188:ILE:HD12	2.33	0.49
1:A:276:SER:HA	1:A:279:TYR:CE2	2.47	0.49
1:A:143:ILE:CD1	1:A:151:ASP:OD2	2.61	0.49
1:A:269:GLY:O	1:A:270:LYS:HB2	2.13	0.49
1:A:9:ASN:C	1:A:9:ASN:HD22	2.14	0.48
1:A:238:MET:HG3	1:A:250:TYR:CD2	2.47	0.48
1:B:309:ALA:HB3	2:B:886:L1A:HN41	1.77	0.48
1:B:140:ASP:CG	1:B:324:ARG:HH12	2.14	0.48
1:B:30:VAL:HG21	1:B:123:VAL:HG23	1.95	0.48
1:A:255:ASN:OD1	1:A:287:SER:HA	2.14	0.48
1:B:164:SER:C	1:B:166:SER:H	2.17	0.48
1:B:30:VAL:HG21	1:B:123:VAL:CG2	2.43	0.48
1:B:208:SER:O	1:B:210:LEU:N	2.46	0.48
1:A:252:VAL:HG12	1:A:253:LYS:N	2.28	0.48
1:A:9:ASN:HD22	1:A:10:TYR:N	2.12	0.47
1:B:101:GLN:HE22	1:B:138:ILE:HA	1.78	0.47
1:B:50:TYR:CZ	1:B:108:GLU:HG2	2.49	0.47
1:A:26:GLN:NE2	1:A:59:PHE:HA	2.29	0.47
1:B:71:GLY:O	1:B:72:THR:C	2.51	0.47
1:A:159:ARG:HH11	1:A:159:ARG:HG3	1.78	0.47
1:B:161:SER:CB	1:B:164:SER:HB3	2.43	0.47
1:B:270:LYS:HG2	1:B:271:GLU:H	1.79	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:300:ILE:O	1:A:305:GLY:HA3	2.15	0.47
1:B:113:PRO:HG2	2:B:886:L1A:H2	1.97	0.47
1:A:26:GLN:HE22	1:A:59:PHE:HA	1.80	0.47
1:B:48:ARG:HD2	1:B:48:ARG:N	2.31	0.46
1:B:40:TRP:CE3	1:B:106:VAL:HG21	2.51	0.46
1:A:163:ASN:ND2	1:A:163:ASN:O	2.49	0.46
1:B:127:PHE:HB2	1:B:194:GLY:HA2	1.97	0.46
1:A:294:ALA:C	1:A:295:ILE:HG13	2.36	0.46
1:A:99:VAL:HG21	1:A:142:ILE:CG1	2.42	0.46
1:B:210:LEU:H	1:B:210:LEU:CD2	2.28	0.46
1:A:210:LEU:CD1	1:A:211:LEU:HG	2.45	0.46
1:A:187:TYR:HA	1:A:329:ILE:O	2.14	0.46
1:A:210:LEU:HD13	1:A:211:LEU:HG	1.97	0.46
1:A:9:ASN:HD21	1:A:12:ASP:HA	1.80	0.46
1:A:221:ASP:OD1	2:A:885:L1A:O3	2.34	0.45
1:A:231:THR:O	1:A:235:GLU:HG3	2.15	0.45
1:B:246:ARG:HD2	3:B:887:HOH:O	2.15	0.45
1:B:6:ILE:HG23	1:B:167:LEU:HD11	1.97	0.45
1:B:127:PHE:HB3	1:B:129:GLU:OE1	2.17	0.45
1:B:228:SER:OG	1:B:309:ALA:HB3	2.17	0.45
1:A:298:MET:HG2	2:A:885:L1A:C11	2.47	0.45
1:B:133:GLY:C	1:B:134:ARG:HG3	2.36	0.45
1:B:15:TYR:O	1:B:31:VAL:HG22	2.17	0.45
1:B:326:ASN:HB2	1:B:328:ARG:HG2	1.99	0.45
1:A:101:GLN:NE2	1:A:138:ILE:HA	2.32	0.45
1:B:209:THR:O	1:B:209:THR:HG22	2.16	0.45
1:B:140:ASP:OD2	1:B:140:ASP:N	2.50	0.44
1:B:281:PHE:HD1	1:B:292:THR:HG23	1.80	0.44
1:B:78:TYR:HB3	2:B:886:L1A:H171	1.99	0.44
1:A:316:ARG:NH2	3:A:895:HOH:O	2.47	0.44
1:B:56:HIS:HE1	1:B:114:PHE:O	1.99	0.44
1:A:333:LEU:HA	1:A:333:LEU:HD23	1.69	0.44
1:A:252:VAL:HG12	1:A:253:LYS:O	2.18	0.44
1:A:191:ILE:HD11	1:A:199:GLN:CA	2.47	0.44
1:A:9:ASN:ND2	1:A:9:ASN:C	2.72	0.43
1:B:172:VAL:HG23	3:B:903:HOH:O	2.17	0.43
1:A:216:CYS:HB2	3:A:919:HOH:O	2.18	0.43
1:B:79:SER:OG	2:B:886:L1A:H132	2.19	0.43
1:A:238:MET:HG3	1:A:250:TYR:CE2	2.54	0.43
1:B:76:LEU:HD23	1:B:132:ILE:HD12	1.99	0.43
1:A:76:LEU:HB2	1:A:83:VAL:HG23	2.01	0.43
1:B:40:TRP:HZ3	1:B:109:MET:HE1	1.84	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:191:ILE:HD11	1:B:199:GLN:N	2.33	0.43
1:B:74:LEU:HD13	1:B:87:LEU:HD11	2.01	0.43
1:B:23:THR:OG1	1:B:91:ILE:HD11	2.18	0.43
1:A:149:LYS:HG2	1:A:150:GLU:HG3	2.00	0.43
1:A:163:ASN:O	1:A:165:GLN:N	2.48	0.43
1:B:201:LYS:HB2	1:B:266:HIS:CD2	2.44	0.43
1:A:252:VAL:CG1	1:A:253:LYS:N	2.81	0.43
1:A:136:THR:HA	1:A:137:PRO:HD3	1.87	0.42
1:A:275:THR:CG2	1:A:276:SER:N	2.82	0.42
1:B:324:ARG:NH2	1:B:324:ARG:HG3	2.34	0.42
1:A:167:LEU:HD23	1:A:167:LEU:N	2.34	0.42
1:A:178:PRO:HG3	3:A:902:HOH:O	2.18	0.42
1:A:9:ASN:HD21	1:A:12:ASP:CA	2.33	0.42
1:A:297:ALA:O	1:A:298:MET:HE2	2.20	0.42
1:A:26:GLN:NE2	3:A:939:HOH:O	2.52	0.41
1:B:140:ASP:OD2	1:B:324:ARG:NH1	2.40	0.41
1:B:34:THR:HG21	1:B:322:PHE:CZ	2.55	0.41
1:A:102:MET:HB2	3:A:925:HOH:O	2.19	0.41
1:B:69:HIS:CG	1:B:70:ASN:N	2.88	0.41
1:A:178:PRO:HA	1:A:181:TYR:CE1	2.55	0.41
1:A:172:VAL:HG23	3:A:889:HOH:O	2.19	0.41
1:B:325:ARG:HA	1:B:325:ARG:HD2	1.77	0.41
1:B:187:TYR:HB3	1:B:328:ARG:HD2	2.03	0.41
1:B:204:SER:HB2	1:B:264:SER:HB2	2.02	0.41
1:B:127:PHE:CB	1:B:194:GLY:HA2	2.50	0.41
1:A:270:LYS:HA	1:A:270:LYS:HD2	1.91	0.41
1:B:247:LEU:HD23	1:B:248:PHE:CB	2.47	0.41
1:A:69:HIS:CG	1:A:70:ASN:N	2.88	0.41
1:B:112:LEU:HA	1:B:113:PRO:HA	1.79	0.40
1:A:292:THR:HG22	1:A:293:LEU:N	2.36	0.40
1:B:190:LEU:HG	1:B:327:ASN:O	2.21	0.40
1:B:282:GLN:O	1:B:283:GLU:C	2.59	0.40
1:A:257:GLY:HA3	1:A:282:GLN:HE22	1.85	0.40
1:A:228:SER:HB2	1:A:298:MET:HB2	2.03	0.40
1:B:3:SER:OG	1:B:95:GLY:O	2.38	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	331/333 (99%)	314 (95%)	13 (4%)	4 (1%)	19	26
1	B	331/333 (99%)	309 (93%)	19 (6%)	3 (1%)	25	35
All	All	662/666 (99%)	623 (94%)	32 (5%)	7 (1%)	21	29

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	164	SER
1	A	191	ILE
1	A	247	LEU
1	A	270	LYS
1	B	162	GLU
1	B	166	SER
1	B	246	ARG

### 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	284/284 (100%)	269 (95%)	15 (5%)	32	48
1	B	284/284 (100%)	264 (93%)	20 (7%)	21	33
All	All	568/568 (100%)	533 (94%)	35 (6%)	26	39

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
1	A	49	LEU

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Mol	Chain	Res	Type
1	A	76	LEU
1	A	102	MET
1	A	113	PRO
1	A	140	ASP
1	A	158	ASN
1	A	163	ASN
1	A	173	LEU
1	A	179	GLN
1	A	210	LEU
1	A	237	LEU
1	A	275	THR
1	A	296	HIS
1	A	333	LEU
1	B	5	VAL
1	B	9	ASN
1	B	18	GLU
1	B	49	LEU
1	B	68	LYS
1	B	73	GLU
1	B	87	LEU
1	B	94	VAL
1	B	113	PRO
1	B	140	ASP
1	B	166	SER
1	B	193	THR
1	B	201	LYS
1	B	210	LEU
1	B	219	LEU
1	B	231	THR
1	B	290	LEU
1	B	324	ARG
1	B	325	ARG
1	B	333	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
1	A	26	GLN
1	A	101	GLN
1	A	141	ASN
1	A	145	GLN

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Mol	Chain	Res	Type
1	A	158	ASN
1	A	163	ASN
1	A	170	GLN
1	A	184	ASN
1	A	197	GLN
1	A	199	GLN
1	A	282	GLN
1	B	9	ASN
1	B	26	GLN
1	B	101	GLN
1	B	141	ASN
1	B	145	GLN
1	B	170	GLN
1	B	189	ASN
1	B	266	HIS
1	B	282	GLN
1	B	327	ASN

### 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 ⓘ

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	L1A	A	885	-	51,51,51	2.63	11 (21%)	68,70,70	2.22	17 (25%)
2	L1A	B	886	-	51,51,51	2.50	8 (15%)	68,70,70	2.24	19 (27%)

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	L1A	A	885	-	-	0/51/67/67	0/4/4/4
2	L1A	B	886	-	-	0/51/67/67	0/4/4/4

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	885	L1A	S2-N2	11.30	1.72	1.61
2	B	886	L1A	S2-N2	10.38	1.71	1.61
2	A	885	L1A	C32-C31	9.00	1.57	1.32
2	B	886	L1A	C32-C31	8.93	1.57	1.32
2	B	886	L1A	S2-N6	4.77	1.74	1.62
2	A	885	L1A	S2-N6	4.69	1.74	1.62
2	B	886	L1A	C15-N4	4.36	1.41	1.33
2	A	885	L1A	C15-N4	4.11	1.41	1.33
2	A	885	L1A	C12-N5	3.66	1.47	1.36
2	B	886	L1A	C12-N5	3.60	1.47	1.36
2	A	885	L1A	C18-C16	2.95	1.59	1.53
2	A	885	L1A	C16-N3	2.91	1.51	1.46
2	A	885	L1A	C10-N3	2.83	1.40	1.34
2	A	885	L1A	C30-C31	2.80	1.56	1.49
2	B	886	L1A	C30-C31	2.74	1.56	1.49
2	B	886	L1A	C33-C32	2.53	1.57	1.48
2	A	885	L1A	C33-C32	2.45	1.56	1.48
2	B	886	L1A	C18-C16	2.34	1.57	1.53
2	A	885	L1A	C11-C12	-2.00	1.33	1.37

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	885	L1A	C24-C25-N6	9.26	114.55	108.22
2	B	886	L1A	C24-C25-N6	8.30	113.89	108.22
2	A	885	L1A	C19-C18-C16	7.53	124.92	113.61
2	B	886	L1A	C19-C18-C16	7.33	124.62	113.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	886	L1A	C27-C26-N6	6.45	112.63	108.22
2	A	885	L1A	C27-C26-N6	6.13	112.41	108.22
2	A	885	L1A	C16-N3-C10	4.36	131.46	123.24
2	B	886	L1A	C17-C16-N3	4.24	115.89	110.19
2	B	886	L1A	C16-N3-C10	3.88	130.55	123.24
2	B	886	L1A	C29-C17-C16	3.73	120.72	115.66
2	B	886	L1A	C30-C31-C32	-3.42	115.49	123.23
2	A	885	L1A	C30-C31-C32	-3.34	115.68	123.23
2	B	886	L1A	N2-S2-N6	2.91	112.34	105.85
2	A	885	L1A	N2-S2-N6	2.90	112.34	105.85
2	B	886	L1A	O3-C18-C16	-2.84	102.17	109.07
2	A	885	L1A	O3-C18-C16	-2.81	102.26	109.07
2	A	885	L1A	C21-C20-C19	2.76	119.29	115.08
2	A	885	L1A	C29-C17-C16	2.75	119.39	115.66
2	B	886	L1A	C21-C20-C19	2.70	119.21	115.08
2	A	885	L1A	C17-C29-C28	2.68	117.35	111.58
2	B	886	L1A	S1-C15-N4	2.60	127.36	123.23
2	A	885	L1A	C20-C19-C18	-2.51	107.58	112.06
2	A	885	L1A	S1-C15-N4	2.50	127.20	123.23
2	A	885	L1A	C13-C12-C11	-2.47	125.70	130.18
2	B	886	L1A	C8-N2-S2	-2.42	118.20	122.91
2	B	886	L1A	C13-C12-C11	-2.39	125.84	130.18
2	B	886	L1A	C17-C29-C28	2.38	116.70	111.58
2	A	885	L1A	C29-C30-C31	-2.37	110.46	113.01
2	A	885	L1A	C17-C16-C18	2.32	116.22	112.31
2	B	886	L1A	C18-C16-N3	-2.30	106.25	110.91
2	B	886	L1A	C13-C14-N1	-2.26	106.06	110.80
2	A	885	L1A	C18-C16-N3	-2.16	106.51	110.91
2	A	885	L1A	C33-C32-C31	-2.15	115.61	123.13
2	B	886	L1A	C33-C32-C31	-2.13	115.68	123.13
2	B	886	L1A	C29-C30-C31	-2.12	110.72	113.01
2	B	886	L1A	C20-C19-C18	-2.09	108.33	112.06

There are no chirality outliers.

There are no torsion outliers.

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	333/333 (100%)	0.01	14 (4%) 35 32	25, 39, 63, 84	0
1	B	333/333 (100%)	0.30	23 (6%) 17 15	27, 46, 69, 84	0
All	All	666/666 (100%)	0.16	37 (5%) 24 22	25, 43, 68, 84	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	209	THR	5.5
1	A	210	LEU	5.1
1	B	208	SER	4.3
1	B	207	SER	4.2
1	B	209	THR	4.1
1	A	165	GLN	3.8
1	B	162	GLU	3.5
1	B	210	LEU	3.3
1	B	49	LEU	3.3
1	A	214	ASP	3.1
1	A	163	ASN	3.1
1	B	66	SER	3.0
1	A	213	GLU	3.0
1	B	247	LEU	2.9
1	A	207	SER	2.6
1	B	91	ILE	2.6
1	B	163	ASN	2.6
1	A	236	LYS	2.5
1	B	48	ARG	2.5
1	A	253	LYS	2.5
1	B	47	SER	2.4
1	B	69	HIS	2.3
1	B	32	PHE	2.3
1	A	208	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	68	LYS	2.3
1	B	146	GLY	2.3
1	B	65	SER	2.3
1	B	70	ASN	2.2
1	B	161	SER	2.2
1	B	222	THR	2.1
1	A	164	SER	2.1
1	A	162	GLU	2.1
1	B	52	ALA	2.1
1	B	51	THR	2.1
1	B	134	ARG	2.0
1	A	149	LYS	2.0
1	A	191	ILE	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	L1A	A	885	48/48	0.14	0.23	25,33,37,37	0
2	L1A	B	886	48/48	0.17	-0.08	33,42,50,52	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.