



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 04:19 AM GMT

PDB ID : 2NTF  
Title : Crystal Structure of a Quorum-Quenching Antibody in Complex with an N-Acyl-L-Homoserine Lactone Analog  
Authors : Debler, E.W.; Wilson, I.A.  
Deposited on : 2006-11-07  
Resolution : 3.18 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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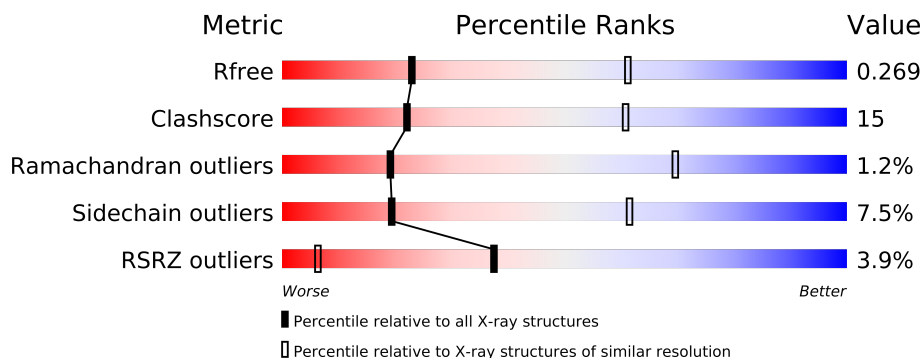
The following versions of software and data (see [references](#)) were used in the production of this report:

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 3.18 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	1472 (3.26-3.10)
Clashscore	79885	1024 (3.24-3.12)
Ramachandran outliers	78287	1002 (3.24-3.12)
Sidechain outliers	78261	1001 (3.24-3.12)
RSRZ outliers	66119	1473 (3.26-3.10)

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	211	
1	L	211	
2	B	222	
2	H	222	

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 6652 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.

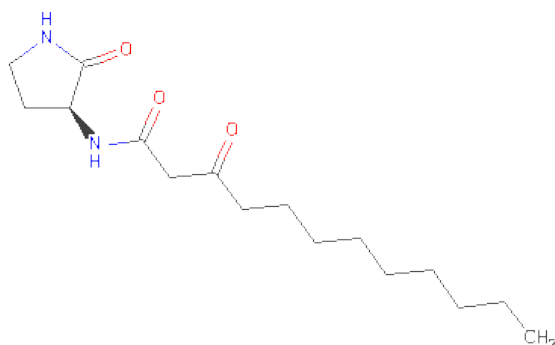
- Molecule 1 is a protein called Murine Antibody Fab RS2-1G9 Lambda Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	211	Total	C	N	O	S	0	0	0
			1606	1005	272	323	6			
1	A	211	Total	C	N	O	S	0	0	0
			1606	1005	272	323	6			

- Molecule 2 is a protein called Murine Antibody Fab RS2-1G9 IGG1 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	222	Total	C	N	O	S	0	0	0
			1699	1084	276	333	6			
2	B	222	Total	C	N	O	S	0	0	0
			1699	1084	276	333	6			

- Molecule 3 is 3-OXO-N-[(3S)-2-OXOPYRROLIDIN-3-YL]DODECANAMIDE (three-letter code: OHM) (formula: C<sub>16</sub>H<sub>28</sub>N<sub>2</sub>O<sub>3</sub>).

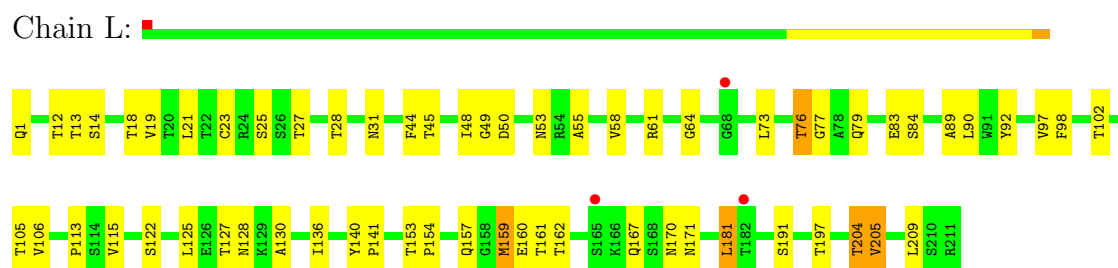


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	H	1	Total	C	N	O	0	0
			21	16	2	3		
3	B	1	Total	C	N	O	0	0
			21	16	2	3		

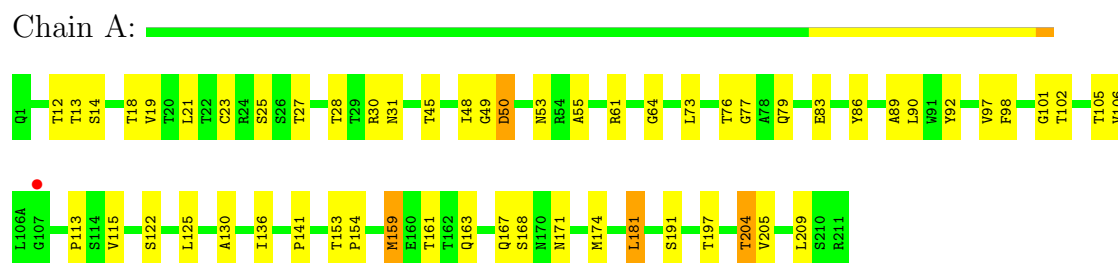
### 3 Residue-property plots

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.

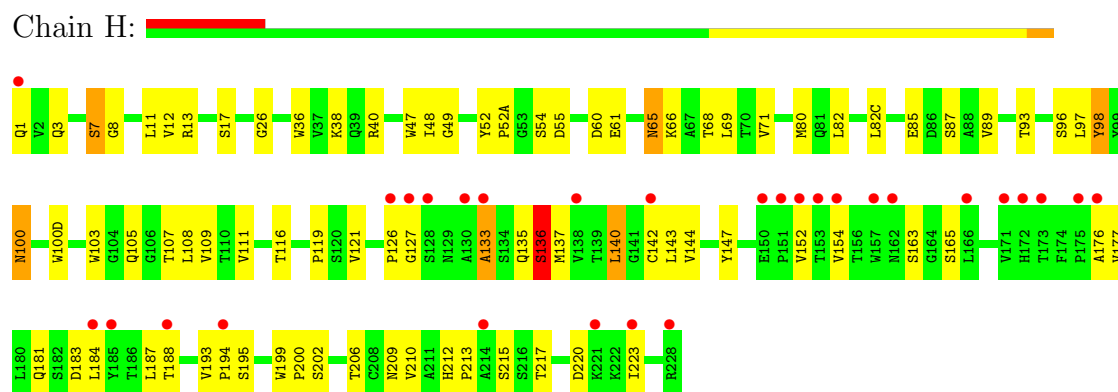
- Molecule 1: Murine Antibody Fab RS2-1G9 Lambda Light Chain



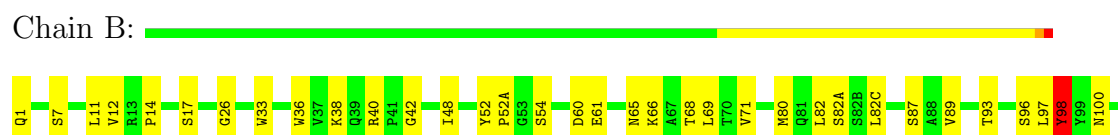
- Molecule 1: Murine Antibody Fab RS2-1G9 Lambda Light Chain

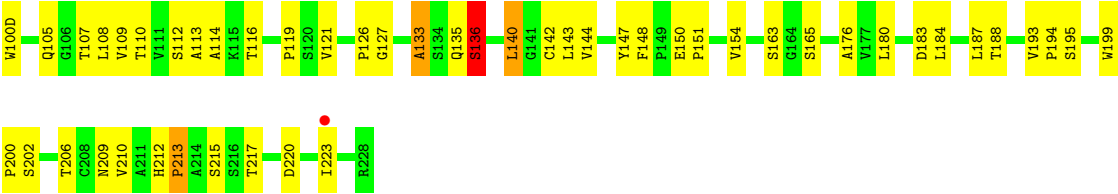


- Molecule 2: Murine Antibody Fab RS2-1G9 IGG1 Heavy Chain



- Molecule 2: Murine Antibody Fab RS2-1G9 IGG1 Heavy Chain





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	118.66Å 118.66Å 176.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.02 – 3.18 44.01 – 3.18	Depositor EDS
% Data completeness (in resolution range)	89.1 (44.02-3.18) 89.2 (44.01-3.18)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.35 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.3.0017	Depositor
R, $R_{free}$	0.210 , 0.265 0.212 , 0.269	Depositor DCC
$R_{free}$ test set	992 reflections (5.37%)	DCC
Wilson B-factor (Å <sup>2</sup> )	80.6	Xtriage
Anisotropy	0.120	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 108.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 19449 reflections	Xtriage
$F_o, F_c$ correlation	0.74	EDS
Total number of atoms	6652	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.60% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 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: OHM

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	0/1646	0.77	0/2250
1	L	0.75	0/1646	0.79	0/2250
2	B	0.67	1/1749 (0.1%)	0.74	1/2395 (0.0%)
2	H	0.70	0/1749	0.75	1/2395 (0.0%)
All	All	0.71	1/6790 (0.0%)	0.76	2/9290 (0.0%)

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
2	B	0	2
2	H	0	2
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	98	TYR	CD2-CE2	5.35	1.47	1.39

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	127	GLY	N-CA-C	-5.87	98.43	113.10
2	H	127	GLY	N-CA-C	-5.58	99.15	113.10

There are no chirality outliers.

All (4) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
2	B	126	PRO	Peptide
2	B	54	SER	Peptide
2	H	126	PRO	Peptide
2	H	54	SER	Peptide

## 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	1606	0	1543	48	0
1	L	1606	0	1543	54	0
2	B	1699	0	1646	58	0
2	H	1699	0	1646	54	1
3	B	21	0	28	2	0
3	H	21	0	28	0	0
All	All	6652	0	6434	196	1

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 15.

All (196) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:H:48:ILE:HG21	2:H:80:MET:HE1	1.44	0.99
1:L:154:PRO:HG2	1:A:27:THR:HG21	1.47	0.96
2:B:48:ILE:HG21	2:B:80:MET:HE1	1.51	0.88
2:B:143:LEU:HA	2:B:188:THR:HG22	1.55	0.88
2:H:52(A):PRO:HA	2:H:71:VAL:HG11	1.56	0.84
2:H:48:ILE:HG21	2:H:80:MET:CE	2.07	0.84
2:B:52(A):PRO:HA	2:B:71:VAL:HG11	1.58	0.83
2:H:143:LEU:HA	2:H:188:THR:HG22	1.60	0.82
1:L:154:PRO:CG	1:A:27:THR:HG21	2.11	0.80
1:L:27:THR:HG21	1:A:154:PRO:HG2	1.65	0.79
2:B:48:ILE:HG21	2:B:80:MET:CE	2.17	0.74
1:L:27:THR:HG22	1:L:27:THR:O	1.89	0.72
1:L:209:LEU:HD12	1:L:209:LEU:O	1.89	0.71
2:H:187:LEU:HD12	2:H:188:THR:N	2.05	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:197:THR:OG1	1:A:204:THR:CG2	2.39	0.71
1:A:197:THR:OG1	1:A:204:THR:HG23	1.91	0.70
2:H:12:VAL:HG11	2:H:82(C):LEU:CD1	2.22	0.69
1:A:159:MET:HE2	1:A:159:MET:H	1.58	0.69
1:A:27:THR:O	1:A:27:THR:HG22	1.92	0.68
1:A:48:ILE:HD12	1:A:73:LEU:HD13	1.76	0.67
1:A:76:THR:HG22	1:A:77:GLY:N	2.10	0.67
1:L:28:THR:OG1	1:A:153:THR:CG2	2.43	0.66
1:A:13:THR:HB	1:A:19:VAL:HG11	1.76	0.66
1:L:76:THR:HG22	1:L:77:GLY:N	2.10	0.66
1:L:89:ALA:C	1:L:90:LEU:HD23	2.17	0.65
1:A:209:LEU:O	1:A:209:LEU:HD12	1.96	0.65
1:L:27:THR:HG21	1:A:154:PRO:CG	2.27	0.65
2:H:154:VAL:HG22	2:H:210:VAL:HG22	1.78	0.65
1:L:28:THR:OG1	1:A:153:THR:HG22	1.97	0.64
2:H:87:SER:OG	2:H:111:VAL:HG23	1.98	0.64
1:L:13:THR:HB	1:L:19:VAL:HG11	1.79	0.63
2:H:12:VAL:HG11	2:H:82(C):LEU:HD13	1.80	0.63
1:L:153:THR:CG2	1:A:28:THR:OG1	2.47	0.63
1:L:48:ILE:HD13	1:L:64:GLY:HA3	1.80	0.63
2:H:140:LEU:HD13	2:H:223:ILE:HG21	1.81	0.62
2:B:121:VAL:HG22	2:B:144:VAL:HG22	1.81	0.62
2:B:143:LEU:HD12	2:B:188:THR:CG2	2.30	0.62
2:H:36:TRP:CD1	2:H:69:LEU:HD21	2.35	0.62
2:B:140:LEU:HD13	2:B:223:ILE:HG21	1.81	0.62
1:L:159:MET:HE2	1:L:159:MET:H	1.62	0.62
2:B:12:VAL:HG11	2:B:82(C):LEU:CD1	2.29	0.62
2:B:12:VAL:HG11	2:B:82(C):LEU:HD13	1.80	0.61
2:B:11:LEU:HD11	2:B:148:PHE:HZ	1.66	0.61
2:B:112:SER:OG	2:B:114:ALA:CB	2.48	0.61
1:L:27:THR:CG2	1:L:27:THR:O	2.49	0.60
1:L:197:THR:OG1	1:L:204:THR:HG23	2.01	0.60
2:B:100(D):TRP:C	3:B:1002:OHM:H42	2.21	0.60
1:L:197:THR:OG1	1:L:204:THR:CG2	2.50	0.59
1:A:12:THR:HG22	1:A:105:THR:HB	1.84	0.59
2:H:11:LEU:C	2:H:11:LEU:HD23	2.22	0.59
1:A:130:ALA:HB3	1:A:181:LEU:CD1	2.33	0.59
1:L:130:ALA:HB3	1:L:181:LEU:CD1	2.33	0.59
1:L:21:LEU:HD12	1:L:21:LEU:N	2.19	0.58
1:L:153:THR:HG22	1:A:28:THR:HG21	1.86	0.58
2:B:36:TRP:CD1	2:B:69:LEU:HD21	2.38	0.58
2:B:147:TYR:OH	2:B:187:LEU:HD23	2.04	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:82:LEU:HB3	2:B:82(C):LEU:HD21	1.87	0.56
2:B:11:LEU:C	2:B:11:LEU:HD23	2.26	0.56
2:B:52:TYR:OH	2:B:98:TYR:CD1	2.57	0.56
1:A:27:THR:O	1:A:27:THR:CG2	2.54	0.55
1:A:89:ALA:HB2	1:A:98:PHE:CD1	2.41	0.55
2:B:187:LEU:HD12	2:B:188:THR:N	2.22	0.55
1:L:55:ALA:O	1:L:58:VAL:HG23	2.08	0.54
2:H:135:GLN:O	2:H:195:SER:OG	2.24	0.54
2:H:133:ALA:C	2:H:135:GLN:H	2.11	0.54
1:A:105:THR:HG21	1:A:141:PRO:HB3	1.89	0.54
2:B:133:ALA:C	2:B:135:GLN:H	2.11	0.54
2:B:154:VAL:HG22	2:B:210:VAL:HG22	1.89	0.54
1:L:48:ILE:HD12	1:L:73:LEU:HD13	1.90	0.53
2:H:82:LEU:HB3	2:H:82(C):LEU:HD21	1.90	0.53
2:H:52:TYR:OH	2:H:98:TYR:CD1	2.61	0.53
1:L:154:PRO:CG	1:A:27:THR:CG2	2.85	0.53
1:L:89:ALA:O	1:L:90:LEU:HD23	2.09	0.53
2:H:89:VAL:HG22	2:H:108:LEU:HD13	1.91	0.53
2:B:97:LEU:HD23	2:B:98:TYR:HB2	1.90	0.53
1:L:157:GLN:NE2	2:B:61:GLU:HB2	2.24	0.52
1:A:122:SER:HA	1:A:125:LEU:HD12	1.92	0.52
1:A:89:ALA:O	1:A:90:LEU:HD23	2.09	0.52
1:L:48:ILE:HD13	1:L:64:GLY:CA	2.38	0.52
2:H:121:VAL:HG22	2:H:144:VAL:HG22	1.91	0.52
1:L:153:THR:HG22	1:A:28:THR:OG1	2.10	0.52
1:L:115:VAL:HG21	1:L:205:VAL:HG12	1.92	0.52
1:A:18:THR:HG22	1:A:19:VAL:N	2.24	0.52
1:L:89:ALA:HB2	1:L:98:PHE:CD1	2.45	0.51
2:H:143:LEU:HD12	2:H:188:THR:CG2	2.41	0.51
2:H:8:GLY:O	2:H:107:THR:HA	2.09	0.51
2:H:97:LEU:HD23	2:H:98:TYR:HB2	1.93	0.50
1:A:21:LEU:HD23	1:A:102:THR:HB	1.94	0.50
2:B:193:VAL:HG23	2:B:194:PRO:O	2.12	0.50
1:A:167:GLN:O	1:A:171:ASN:N	2.43	0.50
2:B:112:SER:HG	2:B:114:ALA:HB2	1.76	0.50
1:L:18:THR:O	1:L:19:VAL:HG13	2.12	0.50
2:H:215:SER:O	2:H:217:THR:HG23	2.12	0.49
2:H:183:ASP:C	2:H:184:LEU:HD23	2.32	0.49
1:A:48:ILE:HD13	1:A:64:GLY:HA3	1.93	0.49
1:L:49:GLY:O	1:L:50:ASP:C	2.51	0.49
2:B:206:THR:HG21	2:B:220:ASP:HB3	1.94	0.49
1:A:25:SER:OG	1:A:92:TYR:OH	2.29	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:89:ALA:C	1:A:90:LEU:HD23	2.33	0.49
1:L:122:SER:HA	1:L:125:LEU:HD12	1.95	0.49
1:L:209:LEU:HD12	1:L:209:LEU:C	2.33	0.48
2:H:7:SER:O	2:H:107:THR:HG23	2.13	0.48
2:B:1:GLN:O	2:B:26:GLY:HA3	2.13	0.48
1:L:153:THR:HG22	1:A:28:THR:CG2	2.43	0.48
2:B:112:SER:OG	2:B:114:ALA:HB2	2.14	0.48
2:B:38:LYS:NZ	2:B:40:ARG:NH1	2.62	0.48
2:B:183:ASP:C	2:B:184:LEU:HD23	2.34	0.48
2:H:206:THR:HG21	2:H:220:ASP:HB3	1.94	0.48
1:L:162:THR:HG22	2:H:177:VAL:CG1	2.44	0.48
2:B:89:VAL:HG22	2:B:108:LEU:HD13	1.96	0.48
2:H:17:SER:HB3	2:H:82:LEU:O	2.14	0.47
1:L:159:MET:CE	1:L:159:MET:H	2.28	0.47
1:A:21:LEU:HD12	1:A:21:LEU:N	2.29	0.47
2:B:33:TRP:CG	3:B:1002:OHM:H101	2.50	0.47
2:H:193:VAL:HG23	2:H:194:PRO:O	2.14	0.47
2:H:1:GLN:O	2:H:26:GLY:HA3	2.13	0.47
2:H:147:TYR:CE1	2:H:152:VAL:HG13	2.50	0.47
1:L:160:GLU:HG3	2:H:181:GLN:OE1	2.14	0.47
2:H:187:LEU:HD12	2:H:188:THR:CA	2.44	0.47
1:A:48:ILE:CD1	1:A:73:LEU:HD13	2.44	0.47
1:L:21:LEU:HD23	1:L:102:THR:HB	1.97	0.47
1:A:83:GLU:OE1	1:A:106:VAL:N	2.46	0.47
1:L:140:TYR:HA	1:L:141:PRO:C	2.35	0.47
2:H:140:LEU:HD12	2:H:223:ILE:HD12	1.97	0.47
2:B:119:PRO:HB2	2:B:144:VAL:HG13	1.96	0.47
2:H:12:VAL:CG1	2:H:82(C):LEU:HD13	2.45	0.46
1:L:25:SER:OG	1:L:27:THR:HB	2.16	0.46
2:B:135:GLN:O	2:B:195:SER:OG	2.33	0.46
1:L:167:GLN:O	1:L:171:ASN:N	2.47	0.46
2:H:87:SER:HA	2:H:109:VAL:O	2.15	0.46
1:A:18:THR:O	1:A:19:VAL:HG13	2.16	0.46
2:H:147:TYR:OH	2:H:187:LEU:HD23	2.15	0.46
2:B:40:ARG:HH11	2:B:40:ARG:HG3	1.81	0.46
2:B:215:SER:O	2:B:217:THR:HG23	2.15	0.46
1:L:44:PHE:HB2	2:H:103:TRP:CG	2.50	0.46
1:L:127:THR:O	1:L:128:ASN:HB2	2.16	0.45
1:L:61:ARG:NH1	1:L:79:GLN:HB2	2.30	0.45
2:B:143:LEU:HD12	2:B:188:THR:HG23	1.95	0.45
2:B:150:GLU:OE1	2:B:151:PRO:HA	2.17	0.45
2:B:48:ILE:HD13	2:B:80:MET:CE	2.46	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:48:ILE:HD13	1:A:64:GLY:CA	2.46	0.45
2:H:65:ASN:OD1	2:H:65:ASN:N	2.50	0.45
2:H:40:ARG:HG3	2:H:40:ARG:HH11	1.81	0.45
2:B:163:SER:N	2:B:209:ASN:OD1	2.50	0.44
1:A:163:GLN:HG3	2:B:42:GLY:HA2	1.99	0.44
2:B:176:ALA:HA	2:B:187:LEU:HB3	1.99	0.44
2:B:112:SER:OG	2:B:114:ALA:HB3	2.17	0.44
1:L:113:PRO:HB2	1:L:136:ILE:HG23	1.99	0.44
2:H:199:TRP:CG	2:H:200:PRO:HA	2.53	0.44
1:L:18:THR:HG22	1:L:19:VAL:N	2.32	0.44
2:B:199:TRP:CG	2:B:200:PRO:HA	2.53	0.44
1:L:90:LEU:HD23	1:L:90:LEU:N	2.31	0.44
1:L:25:SER:OG	1:L:92:TYR:OH	2.34	0.44
2:B:140:LEU:HD12	2:B:223:ILE:HD12	1.99	0.44
1:A:55:ALA:HB2	2:B:100(D):TRP:CD1	2.53	0.44
1:L:12:THR:HG22	1:L:105:THR:HB	2.00	0.44
2:H:152:VAL:HG12	2:H:212:HIS:CD2	2.52	0.43
2:H:176:ALA:HA	2:H:187:LEU:HB3	1.99	0.43
1:A:130:ALA:HB3	1:A:181:LEU:HD13	2.00	0.43
2:H:89:VAL:HG22	2:H:108:LEU:CD1	2.48	0.43
2:H:119:PRO:HB2	2:H:144:VAL:HG13	2.01	0.43
2:H:135:GLN:O	2:H:136:SER:C	2.56	0.43
2:B:135:GLN:O	2:B:136:SER:C	2.56	0.43
2:H:47:TRP:CH2	2:H:49:GLY:HA2	2.54	0.43
2:H:137:MET:HA	2:H:194:PRO:HA	2.01	0.43
2:B:112:SER:HG	2:B:114:ALA:CB	2.31	0.43
2:H:152:VAL:HG12	2:H:212:HIS:HD2	1.83	0.43
2:H:11:LEU:HD23	2:H:12:VAL:N	2.34	0.43
1:A:49:GLY:O	1:A:50:ASP:C	2.56	0.43
1:L:31:ASN:HB3	1:L:90:LEU:HB3	2.00	0.42
1:L:167:GLN:HB2	1:L:170:ASN:OD1	2.19	0.42
2:B:14:PRO:HD2	2:B:113:ALA:HB2	2.01	0.42
2:B:82:LEU:HA	2:B:82:LEU:HD23	1.77	0.42
1:L:55:ALA:HB2	2:H:100(D):TRP:CD1	2.55	0.42
2:B:17:SER:HB3	2:B:82:LEU:O	2.20	0.42
2:H:38:LYS:NZ	2:H:40:ARG:NH1	2.68	0.42
1:A:115:VAL:HG21	1:A:205:VAL:HG12	2.02	0.42
2:B:60:ASP:O	2:B:61:GLU:C	2.58	0.42
2:B:87:SER:HA	2:B:109:VAL:O	2.20	0.42
2:B:89:VAL:HG22	2:B:108:LEU:CD1	2.50	0.42
1:A:31:ASN:HB3	1:A:90:LEU:HB3	2.01	0.41
1:A:167:GLN:OE1	1:A:174:MET:HB3	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:H:100:ASN:C	2:H:100:ASN:ND2	2.73	0.41
2:H:60:ASP:OD1	2:H:61:GLU:N	2.53	0.41
2:B:180:LEU:HD12	2:B:180:LEU:HA	1.92	0.41
1:A:209:LEU:C	1:A:209:LEU:HD12	2.40	0.41
2:B:7:SER:O	2:B:107:THR:HG23	2.19	0.41
1:L:83:GLU:OE1	1:L:106:VAL:N	2.49	0.41
1:L:130:ALA:HB3	1:L:181:LEU:HD13	2.02	0.41
1:A:61:ARG:NH1	1:A:79:GLN:HB2	2.36	0.41
2:B:212:HIS:HA	2:B:213:PRO:HD2	1.79	0.41
1:A:86:TYR:O	1:A:101:GLY:HA2	2.20	0.41
2:B:11:LEU:HD23	2:B:12:VAL:N	2.36	0.40
1:A:113:PRO:HB2	1:A:136:ILE:HG23	2.03	0.40
2:H:163:SER:N	2:H:209:ASN:OD1	2.55	0.40
2:B:69:LEU:HA	2:B:69:LEU:HD23	1.96	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:H:3:GLN:OE1	2:H:13:ARG:NH2[7_555]	2.12	0.08

## 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	209/211 (99%)	190 (91%)	18 (9%)	1 (0%)	38	85
1	L	209/211 (99%)	190 (91%)	19 (9%)	0	100	100
2	B	220/222 (99%)	192 (87%)	24 (11%)	4 (2%)	13	60
2	H	220/222 (99%)	196 (89%)	19 (9%)	5 (2%)	10	52
All	All	858/866 (99%)	768 (90%)	80 (9%)	10 (1%)	19	69

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	136	SER
2	B	136	SER
2	B	133	ALA
2	H	133	ALA
2	H	55	ASP
2	B	116	THR
1	A	50	ASP
2	B	213	PRO
2	H	116	THR
2	H	213	PRO

### 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	180/180 (100%)	168 (93%)	12 (7%)	23	66
1	L	180/180 (100%)	166 (92%)	14 (8%)	18	59
2	B	192/192 (100%)	177 (92%)	15 (8%)	18	59
2	H	192/192 (100%)	177 (92%)	15 (8%)	18	59
All	All	744/744 (100%)	688 (92%)	56 (8%)	19	61

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

Mol	Chain	Res	Type
1	L	1	GLN
1	L	14	SER
1	L	23	CYS
1	L	45	THR
1	L	53	ASN
1	L	76	THR
1	L	84	SER
1	L	97	VAL
1	L	159	MET
1	L	161	THR
1	L	181	LEU
1	L	191	SER
1	L	204	THR

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Mol	Chain	Res	Type
1	L	205	VAL
2	H	7	SER
2	H	65	ASN
2	H	66	LYS
2	H	68	THR
2	H	85	GLU
2	H	93	THR
2	H	96	SER
2	H	98	TYR
2	H	100	ASN
2	H	105	GLN
2	H	136	SER
2	H	140	LEU
2	H	142	CYS
2	H	165	SER
2	H	202	SER
1	A	14	SER
1	A	23	CYS
1	A	30	ARG
1	A	45	THR
1	A	53	ASN
1	A	97	VAL
1	A	159	MET
1	A	161	THR
1	A	168	SER
1	A	181	LEU
1	A	191	SER
1	A	204	THR
2	B	65	ASN
2	B	66	LYS
2	B	68	THR
2	B	82(A)	SER
2	B	93	THR
2	B	96	SER
2	B	98	TYR
2	B	100	ASN
2	B	105	GLN
2	B	110	THR
2	B	136	SER
2	B	140	LEU
2	B	142	CYS
2	B	165	SER

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Mol	Chain	Res	Type
2	B	202	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	53	ASN
2	H	100	ASN
1	A	53	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	$\# Z  > 2$
3	OHM	B	1002	-	21,21,21	0.94	0	25,25,25	2.83	7 (28%)
3	OHM	H	1001	-	21,21,21	0.89	0	25,25,25	2.48	5 (20%)

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
3	OHM	B	1002	-	-	0/17/27/27	0/1/1/1
3	OHM	H	1001	-	-	0/17/27/27	0/1/1/1

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1002	OHM	C4-N3-C2	-10.04	108.46	114.17
3	H	1001	OHM	C4-N3-C2	-9.05	109.02	114.17
3	H	1001	OHM	C1-C2-N3	5.98	111.24	107.61
3	B	1002	OHM	C1-C2-N3	4.50	110.34	107.61
3	B	1002	OHM	O6-C2-C1	-4.20	122.97	126.25
3	B	1002	OHM	C5-C1-C2	-4.12	99.55	103.65
3	H	1001	OHM	C2-C1-N7	-3.63	106.33	111.51
3	B	1002	OHM	C10-C8-N7	3.42	120.72	116.00
3	B	1002	OHM	C4-C5-C1	-2.85	99.39	104.38
3	B	1002	OHM	C5-C1-N7	2.72	118.30	114.30
3	H	1001	OHM	O6-C2-C1	-2.62	124.20	126.25
3	H	1001	OHM	C5-C4-N3	2.05	104.59	102.80

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	211/211 (100%)	0.14	1 (0%) 88 43	53, 71, 93, 105	0
1	L	211/211 (100%)	0.83	3 (1%) 72 20	53, 71, 93, 105	0
2	B	222/222 (100%)	0.27	1 (0%) 88 43	48, 77, 93, 98	0
2	H	222/222 (100%)	1.05	29 (13%) 4 1	48, 77, 93, 98	0
All	All	866/866 (100%)	0.58	34 (3%) 37 6	48, 77, 93, 105	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	166	LEU	5.8
2	H	133	ALA	3.8
2	H	152	VAL	3.3
2	H	150	GLU	3.3
2	H	223	ILE	3.1
2	H	175	PRO	3.1
1	A	107	GLY	3.0
2	H	151	PRO	3.0
2	H	162	ASN	2.9
2	H	173	THR	2.9
2	H	154	VAL	2.8
2	H	194	PRO	2.8
2	H	127	GLY	2.8
2	H	157	TRP	2.8
2	H	130	ALA	2.7
2	H	126	PRO	2.7
2	H	176	ALA	2.6
2	H	138	VAL	2.6
2	H	1	GLN	2.5
2	H	172	HIS	2.5
1	L	68	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
2	H	188	THR	2.4
1	L	165	SER	2.3
1	L	182	THR	2.3
2	H	221	LYS	2.3
2	H	128	SER	2.2
2	H	142	CYS	2.1
2	H	185	TYR	2.1
2	H	153	THR	2.1
2	H	228	ARG	2.1
2	H	214	ALA	2.1
2	B	223	ILE	2.1
2	H	184	LEU	2.0
2	H	171	VAL	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
3	OHM	B	1002	21/21	0.27	-	54,58,71,73	0
3	OHM	H	1001	21/21	0.24	-	49,52,68,69	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.