



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:50 PM GMT

PDB ID : 1M9S  
Title : Crystal structure of Internalin B (InlB), a *Listeria monocytogenes* virulence protein containing SH3-like domains.  
Authors : Marino, M.; Banerjee, M.; Jonquieres, R.; Cossart, P.; Ghosh, P.  
Deposited on : 2002-07-29  
Resolution : 2.65 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

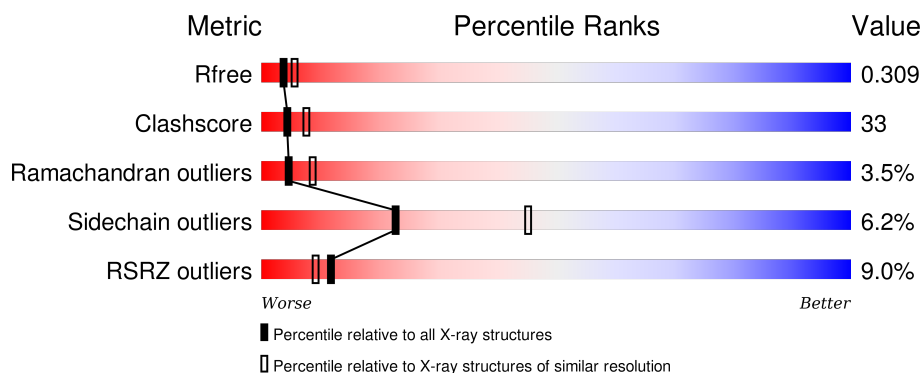
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.65 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	3152 (2.70-2.62)
Clashscore	102246	3524 (2.70-2.62)
Ramachandran outliers	100387	3469 (2.70-2.62)
Sidechain outliers	100360	3469 (2.70-2.62)
RSRZ outliers	91569	3161 (2.70-2.62)

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	605	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4247 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 Internalin B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	523	Total	C	N	O	S	0	0	0
			4170	2648	731	785	6			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	34	MET	-	CLONING ARTIFACT	UNP P25147
A	35	GLY	-	CLONING ARTIFACT	UNP P25147
A	41	SER	PRO	Variant	UNP P25147
A	49	PRO	SER	Variant	UNP P25147
A	117	THR	ALA	Variant	UNP P25147
A	132	ILE	VAL	Variant	UNP P25147
A	396	THR	ALA	Variant	UNP P25147
A	631	LEU	-	EXPRESSION TAG	UNP P25147
A	632	GLU	-	EXPRESSION TAG	UNP P25147
A	633	HIS	-	EXPRESSION TAG	UNP P25147
A	634	HIS	-	EXPRESSION TAG	UNP P25147
A	635	HIS	-	EXPRESSION TAG	UNP P25147
A	636	HIS	-	EXPRESSION TAG	UNP P25147
A	637	HIS	-	EXPRESSION TAG	UNP P25147
A	638	HIS	-	EXPRESSION TAG	UNP P25147

- Molecule 2 is TERBIUM(III) ION (three-letter code: Tb) (formula: Tb).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	7	Total	Tb	0	0
			7	7		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		

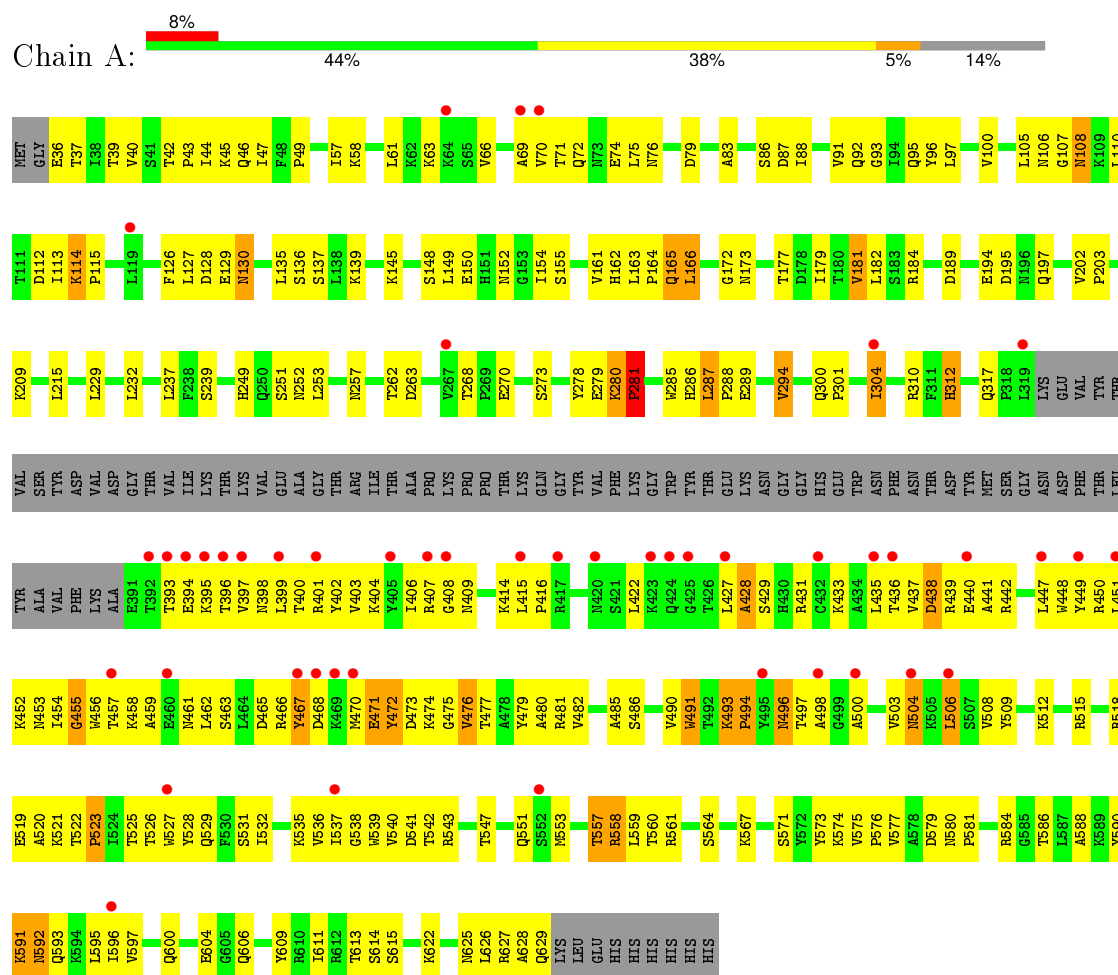
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	65	Total	O	0	0
			65	65		

### 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: Internalin B



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	48.50Å 330.90Å 182.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.65 47.19 – 2.65	Depositor EDS
% Data completeness (in resolution range)	85.8 (50.00-2.65) 86.3 (47.19-2.65)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.04 (at 2.65Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.273 , 0.302 0.276 , 0.309	Depositor DCC
$R_{free}$ test set	1706 reflections (4.78%)	DCC
Wilson B-factor (Å <sup>2</sup> )	69.0	Xtriage
Anisotropy	0.497	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 81.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 37408 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	4247	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TB, SO4

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	0.35	0/4246	0.65	1/5750 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	493	LYS	C-N-CD	-7.06	105.06	120.60

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	4170	0	4270	277	0
2	A	7	0	0	0	0
3	A	5	0	0	0	0
4	A	65	0	0	6	0
All	All	4247	0	4270	277	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 33.

All (277) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:475:GLY:HA2	1:A:518:ARG:HA	1.36	1.06
1:A:451:LEU:HB2	1:A:454:ILE:HB	1.48	0.94
1:A:280:LYS:HG3	1:A:281:PRO:HD3	1.50	0.93
1:A:161:VAL:HB	1:A:181:VAL:HG21	1.51	0.93
1:A:541:ASP:OD1	1:A:543:ARG:HG2	1.69	0.91
1:A:437:VAL:HG12	1:A:438:ASP:H	1.36	0.90
1:A:72:GLN:HE21	1:A:76:ASN:HD21	1.16	0.89
1:A:72:GLN:HE21	1:A:76:ASN:ND2	1.70	0.89
1:A:450:ARG:HG3	1:A:456:TRP:HE1	1.37	0.89
1:A:476:VAL:HG12	1:A:477:THR:H	1.37	0.86
1:A:39:THR:HG23	1:A:40:VAL:H	1.40	0.86
1:A:433:LYS:HD3	1:A:435:LEU:HD21	1.55	0.86
1:A:504:ASN:HB3	1:A:508:VAL:HG21	1.60	0.84
1:A:485:ALA:HB1	1:A:506:LEU:HB3	1.59	0.84
1:A:280:LYS:CG	1:A:281:PRO:HD3	2.09	0.83
1:A:86:SER:H	1:A:108:ASN:HD21	1.25	0.80
1:A:525:THR:HG22	1:A:526:THR:H	1.46	0.78
1:A:509:TYR:CE2	1:A:537:ILE:HD13	2.19	0.78
1:A:457:THR:HG22	1:A:461:ASN:HD22	1.48	0.78
1:A:457:THR:HG22	1:A:458:LYS:H	1.49	0.77
1:A:165:GLN:H	1:A:165:GLN:NE2	1.82	0.76
1:A:450:ARG:HG3	1:A:456:TRP:NE1	2.01	0.76
1:A:559:LEU:HD12	1:A:560:THR:H	1.51	0.76
1:A:161:VAL:HB	1:A:181:VAL:CG2	2.17	0.75
1:A:437:VAL:HG11	1:A:449:TYR:HD2	1.52	0.74
1:A:163:LEU:HB3	1:A:166:LEU:HD22	1.69	0.74
1:A:493:LYS:HA	1:A:539:TRP:CD1	2.23	0.73
1:A:404:LYS:HE3	1:A:407:ARG:HB3	1.70	0.73
1:A:400:THR:HA	1:A:435:LEU:O	1.89	0.72
1:A:564:SER:HB3	1:A:567:LYS:HB2	1.71	0.72
1:A:294:VAL:HG12	1:A:317:GLN:HB3	1.71	0.72
1:A:399:LEU:O	1:A:436:THR:HA	1.89	0.72
1:A:414:LYS:HB3	1:A:422:LEU:HD11	1.71	0.71
1:A:567:LYS:HG3	1:A:625:ASN:HA	1.73	0.71
1:A:476:VAL:HG12	1:A:477:THR:N	2.06	0.71
1:A:591:LYS:HE3	1:A:592:ASN:HD22	1.54	0.71
1:A:493:LYS:HD2	1:A:498:ALA:O	1.91	0.71
1:A:110:LEU:H	1:A:130:ASN:ND2	1.90	0.70
1:A:437:VAL:HG12	1:A:438:ASP:N	2.05	0.70
1:A:625:ASN:C	1:A:626:LEU:HD12	2.13	0.69
1:A:415:LEU:HB2	1:A:422:LEU:HD21	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:437:VAL:HG11	1:A:449:TYR:CD2	2.27	0.69
1:A:86:SER:H	1:A:108:ASN:ND2	1.91	0.69
1:A:467:TYR:CE1	1:A:523:PRO:HD2	2.28	0.68
1:A:471:GLU:O	1:A:472:TYR:HB3	1.93	0.68
1:A:83:ALA:HB3	1:A:105:LEU:HD23	1.74	0.68
1:A:112:ASP:OD1	1:A:114:LYS:HE3	1.93	0.68
1:A:280:LYS:HB3	1:A:281:PRO:CD	2.23	0.67
1:A:97:LEU:O	1:A:100:VAL:HG23	1.93	0.67
1:A:591:LYS:O	1:A:592:ASN:HB2	1.93	0.67
1:A:47:ILE:O	1:A:49:PRO:HD3	1.94	0.67
1:A:404:LYS:HE2	1:A:461:ASN:HA	1.76	0.67
1:A:527:TRP:HD1	1:A:539:TRP:HB3	1.59	0.67
1:A:627:ARG:HD2	1:A:629:GLN:HB2	1.75	0.67
1:A:591:LYS:HD3	1:A:591:LYS:O	1.96	0.66
1:A:561:ARG:NH1	1:A:628:ALA:HB2	2.10	0.66
1:A:88:ILE:HB	1:A:108:ASN:OD1	1.95	0.65
1:A:401:ARG:HB2	1:A:462:LEU:HD21	1.77	0.65
1:A:395:LYS:CB	1:A:439:ARG:HG2	2.26	0.65
1:A:591:LYS:HE3	1:A:592:ASN:ND2	2.11	0.65
1:A:526:THR:O	1:A:542:THR:HG23	1.96	0.64
1:A:39:THR:HG23	1:A:40:VAL:N	2.10	0.64
1:A:415:LEU:HD13	1:A:422:LEU:HD11	1.79	0.64
1:A:571:SER:HB3	4:A:669:HOH:O	1.97	0.64
1:A:520:ALA:HB3	1:A:527:TRP:HB2	1.78	0.64
1:A:252:ASN:HA	4:A:706:HOH:O	1.98	0.64
1:A:471:GLU:HG3	1:A:471:GLU:O	1.96	0.63
1:A:408:GLY:O	1:A:428:ALA:HB2	1.97	0.63
1:A:239:SER:H	1:A:312:HIS:CD2	2.16	0.63
1:A:531:SER:HB2	1:A:535:LYS:O	1.98	0.62
1:A:433:LYS:CD	1:A:435:LEU:HD21	2.27	0.62
1:A:521:LYS:HB2	1:A:526:THR:HG22	1.82	0.62
1:A:441:ALA:O	1:A:442:ARG:HG3	2.00	0.62
1:A:451:LEU:HD12	1:A:451:LEU:H	1.65	0.61
1:A:395:LYS:HB3	1:A:439:ARG:HG2	1.81	0.61
1:A:145:LYS:O	1:A:166:LEU:HD12	2.00	0.61
1:A:280:LYS:CB	1:A:281:PRO:HD3	2.30	0.61
1:A:590:TYR:HA	1:A:593:GLN:NE2	2.16	0.61
1:A:493:LYS:O	1:A:494:PRO:O	2.18	0.61
1:A:522:THR:HB	1:A:523:PRO:HD2	1.82	0.61
1:A:280:LYS:CB	1:A:281:PRO:CD	2.80	0.60
1:A:406:ILE:HD13	1:A:523:PRO:HB3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:493:LYS:HG3	1:A:493:LYS:O	2.01	0.60
1:A:106:ASN:HD21	1:A:126:PHE:HB3	1.66	0.60
1:A:451:LEU:HD12	1:A:451:LEU:N	2.17	0.59
1:A:162:HIS:C	1:A:163:LEU:HD22	2.22	0.59
1:A:613:THR:HG22	1:A:615:SER:H	1.67	0.59
1:A:474:LYS:HE2	1:A:519:GLU:HG2	1.83	0.59
1:A:525:THR:HG22	1:A:526:THR:N	2.18	0.59
1:A:503:VAL:O	1:A:504:ASN:O	2.21	0.59
1:A:92:GLN:NE2	1:A:95:GLN:HE22	2.01	0.59
1:A:148:SER:HB3	4:A:678:HOH:O	2.03	0.59
1:A:79:ASP:HA	1:A:100:VAL:HA	1.83	0.58
1:A:416:PRO:HB3	1:A:456:TRP:CE3	2.38	0.58
1:A:71:THR:OG1	1:A:74:GLU:HG3	2.02	0.58
1:A:482:VAL:HG13	1:A:506:LEU:HD12	1.84	0.58
1:A:518:ARG:HB2	1:A:529:GLN:HB3	1.87	0.57
1:A:485:ALA:CB	1:A:506:LEU:HB3	2.33	0.57
1:A:401:ARG:HB3	1:A:463:SER:O	2.05	0.57
1:A:527:TRP:HB3	1:A:539:TRP:HE3	1.69	0.57
1:A:286:HIS:HD1	1:A:288:PRO:HG3	1.68	0.57
1:A:179:ILE:HB	1:A:182:LEU:HD12	1.87	0.56
1:A:404:LYS:HG2	1:A:461:ASN:O	2.05	0.56
1:A:209:LYS:HB2	4:A:653:HOH:O	2.06	0.56
1:A:407:ARG:C	1:A:409:ASN:H	2.09	0.55
1:A:239:SER:H	1:A:312:HIS:HD2	1.54	0.55
1:A:508:VAL:HG12	1:A:508:VAL:O	2.06	0.55
1:A:403:VAL:HA	1:A:462:LEU:HD12	1.88	0.55
1:A:479:TYR:CE1	1:A:515:ARG:HG3	2.41	0.55
1:A:467:TYR:C	1:A:467:TYR:CD1	2.80	0.55
1:A:107:GLY:HA2	1:A:129:GLU:HB2	1.88	0.55
1:A:163:LEU:N	1:A:163:LEU:HD22	2.22	0.55
1:A:202:VAL:N	1:A:203:PRO:HD2	2.21	0.55
1:A:470:MET:HA	1:A:522:THR:HG22	1.89	0.54
1:A:37:THR:HB	1:A:72:GLN:HG2	1.89	0.54
1:A:457:THR:HG22	1:A:461:ASN:ND2	2.20	0.54
1:A:437:VAL:CG1	1:A:438:ASP:H	2.16	0.54
1:A:439:ARG:CG	1:A:450:ARG:HD3	2.38	0.54
1:A:106:ASN:ND2	1:A:128:ASP:H	2.06	0.54
1:A:606:GLN:OE1	1:A:622:LYS:HE2	2.07	0.54
1:A:613:THR:C	1:A:615:SER:H	2.10	0.54
1:A:43:PRO:HA	1:A:69:ALA:HA	1.90	0.53
1:A:202:VAL:N	1:A:203:PRO:CD	2.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:ALA:HB3	1:A:105:LEU:CD2	2.39	0.52
1:A:480:ALA:HB2	1:A:547:THR:HG22	1.91	0.52
1:A:561:ARG:O	1:A:595:LEU:HB2	2.09	0.52
1:A:91:VAL:HG13	1:A:110:LEU:HD21	1.91	0.52
1:A:567:LYS:HD2	1:A:625:ASN:OD1	2.10	0.52
1:A:626:LEU:HD12	1:A:626:LEU:N	2.25	0.52
1:A:408:GLY:O	1:A:427:LEU:O	2.27	0.52
1:A:481:ARG:NH2	1:A:604:GLU:OE2	2.43	0.52
1:A:414:LYS:HB3	1:A:422:LEU:CD1	2.37	0.52
1:A:286:HIS:O	1:A:286:HIS:ND1	2.43	0.52
1:A:93:GLY:N	1:A:95:GLN:OE1	2.42	0.51
1:A:557:THR:CG2	1:A:600:GLN:HE21	2.23	0.51
1:A:36:GLU:O	1:A:96:TYR:HD2	1.92	0.51
1:A:557:THR:HG21	1:A:600:GLN:NE2	2.25	0.51
1:A:395:LYS:HB2	1:A:439:ARG:HG2	1.93	0.51
1:A:280:LYS:HB3	1:A:281:PRO:HD3	1.91	0.51
1:A:402:TYR:CD1	1:A:465:ASP:HA	2.46	0.51
1:A:75:LEU:HD13	1:A:96:TYR:HB3	1.92	0.51
1:A:39:THR:CG2	1:A:40:VAL:H	2.20	0.51
1:A:114:LYS:N	1:A:115:PRO:CD	2.73	0.51
1:A:63:LYS:HE2	1:A:70:VAL:HG12	1.93	0.51
1:A:92:GLN:HE22	1:A:95:GLN:HE22	1.59	0.50
1:A:468:ASP:OD1	1:A:497:THR:HA	2.11	0.50
1:A:574:LYS:HD2	1:A:584:ARG:NH2	2.26	0.50
1:A:37:THR:HA	1:A:96:TYR:CD2	2.45	0.50
1:A:528:TYR:HE1	1:A:547:THR:HG21	1.76	0.50
1:A:473:ASP:OD1	1:A:518:ARG:NH1	2.43	0.50
1:A:494:PRO:HA	1:A:527:TRP:CD1	2.47	0.50
1:A:401:ARG:HH11	1:A:401:ARG:HG2	1.76	0.50
1:A:127:LEU:HB2	1:A:149:LEU:HD23	1.94	0.50
1:A:521:LYS:HA	1:A:526:THR:HA	1.94	0.50
1:A:422:LEU:HG	1:A:422:LEU:O	2.12	0.49
1:A:613:THR:C	1:A:615:SER:N	2.64	0.49
1:A:437:VAL:HG13	1:A:450:ARG:O	2.12	0.49
1:A:399:LEU:HD22	1:A:399:LEU:N	2.27	0.49
1:A:559:LEU:HD12	1:A:560:THR:N	2.25	0.49
1:A:471:GLU:O	1:A:472:TYR:CB	2.59	0.49
1:A:414:LYS:HG2	1:A:415:LEU:HD12	1.94	0.49
1:A:559:LEU:HD21	1:A:561:ARG:NH2	2.28	0.49
1:A:127:LEU:N	4:A:678:HOH:O	2.45	0.48
1:A:72:GLN:OE1	1:A:75:LEU:HD12	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:452:LYS:O	1:A:453:ASN:HB2	2.14	0.48
1:A:270:GLU:HA	1:A:270:GLU:OE2	2.13	0.48
1:A:451:LEU:CB	1:A:454:ILE:HB	2.34	0.48
1:A:447:LEU:HG	1:A:459:ALA:HB2	1.95	0.48
1:A:437:VAL:CG1	1:A:438:ASP:N	2.76	0.48
1:A:613:THR:HG22	1:A:614:SER:N	2.29	0.48
1:A:86:SER:O	1:A:88:ILE:HG13	2.14	0.48
1:A:173:ASN:HA	1:A:195:ASP:O	2.13	0.48
1:A:397:VAL:O	1:A:438:ASP:HA	2.14	0.48
1:A:490:VAL:HG22	1:A:540:VAL:CG2	2.44	0.48
1:A:72:GLN:NE2	1:A:76:ASN:HD21	1.98	0.48
1:A:395:LYS:HD3	1:A:439:ARG:CD	2.44	0.48
1:A:150:GLU:HB3	4:A:688:HOH:O	2.13	0.48
1:A:395:LYS:HD3	1:A:439:ARG:HD3	1.96	0.47
1:A:509:TYR:HD2	1:A:532:ILE:HD12	1.78	0.47
1:A:177:THR:HG22	1:A:197:GLN:HB2	1.97	0.47
1:A:42:THR:CG2	1:A:46:GLN:HG2	2.44	0.47
1:A:521:LYS:CB	1:A:526:THR:HG22	2.44	0.47
1:A:173:ASN:ND2	1:A:195:ASP:OD2	2.44	0.47
1:A:476:VAL:CG1	1:A:477:THR:H	2.07	0.47
1:A:611:ILE:HG21	1:A:626:LEU:HD21	1.95	0.47
1:A:286:HIS:ND1	1:A:288:PRO:HG3	2.30	0.47
1:A:229:LEU:O	1:A:304:ILE:HD11	2.15	0.47
1:A:396:THR:HG22	1:A:396:THR:O	2.15	0.47
1:A:580:ASN:HB3	1:A:581:PRO:HD3	1.97	0.47
1:A:215:LEU:HB2	1:A:237:LEU:HD23	1.95	0.46
1:A:86:SER:HB2	1:A:88:ILE:CD1	2.46	0.46
1:A:557:THR:CG2	1:A:600:GLN:NE2	2.79	0.46
1:A:112:ASP:CG	1:A:114:LYS:HE3	2.35	0.46
1:A:531:SER:HB3	1:A:536:VAL:HA	1.97	0.46
1:A:522:THR:HB	1:A:523:PRO:CD	2.45	0.46
1:A:557:THR:HG23	1:A:600:GLN:HE21	1.81	0.46
1:A:130:ASN:O	1:A:152:ASN:HA	2.15	0.46
1:A:106:ASN:ND2	1:A:126:PHE:HB3	2.30	0.46
1:A:491:TRP:N	1:A:491:TRP:CD1	2.83	0.46
1:A:519:GLU:HG3	1:A:520:ALA:N	2.30	0.46
1:A:232:LEU:HD12	1:A:304:ILE:HG13	1.98	0.45
1:A:304:ILE:O	1:A:304:ILE:HG13	2.14	0.45
1:A:268:THR:HG23	1:A:278:TYR:CE2	2.51	0.45
1:A:527:TRP:HB3	1:A:539:TRP:CE3	2.51	0.45
1:A:45:LYS:HG3	1:A:46:GLN:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:HIS:NE2	1:A:289:GLU:O	2.50	0.45
1:A:575:VAL:O	1:A:577:VAL:N	2.37	0.45
1:A:447:LEU:HD12	1:A:448:TRP:N	2.30	0.45
1:A:438:ASP:HB3	1:A:450:ARG:NH2	2.32	0.44
1:A:471:GLU:OE2	1:A:521:LYS:HD3	2.18	0.44
1:A:415:LEU:HD12	1:A:415:LEU:N	2.32	0.44
1:A:135:LEU:C	1:A:137:SER:H	2.19	0.44
1:A:439:ARG:HB2	1:A:450:ARG:HD3	2.00	0.44
1:A:416:PRO:HB3	1:A:456:TRP:CZ3	2.52	0.44
1:A:279:GLU:O	1:A:280:LYS:C	2.56	0.44
1:A:36:GLU:HG3	1:A:96:TYR:HE2	1.82	0.44
1:A:428:ALA:O	1:A:431:ARG:HG3	2.16	0.44
1:A:437:VAL:HG11	1:A:449:TYR:HB3	2.00	0.44
1:A:86:SER:O	1:A:87:ASP:C	2.56	0.43
1:A:407:ARG:C	1:A:409:ASN:N	2.71	0.43
1:A:494:PRO:HD3	1:A:539:TRP:CD2	2.53	0.43
1:A:61:LEU:HB3	1:A:63:LYS:HZ3	1.84	0.43
1:A:232:LEU:HD12	1:A:304:ILE:CG1	2.48	0.43
1:A:512:LYS:HE3	1:A:532:ILE:HG21	2.00	0.43
1:A:397:VAL:HG22	1:A:398:ASN:N	2.34	0.43
1:A:579:ASP:OD2	1:A:581:PRO:HD2	2.18	0.43
1:A:397:VAL:HG11	1:A:440:GLU:OE2	2.18	0.43
1:A:401:ARG:HD2	1:A:462:LEU:CD2	2.48	0.43
1:A:415:LEU:H	1:A:422:LEU:HD21	1.83	0.43
1:A:150:GLU:HG2	1:A:172:GLY:N	2.32	0.43
1:A:162:HIS:C	1:A:164:PRO:HD2	2.39	0.43
1:A:531:SER:CB	1:A:536:VAL:HA	2.49	0.43
1:A:300:GLN:NE2	1:A:301:PRO:HD2	2.33	0.43
1:A:558:ARG:CZ	1:A:596:ILE:HG23	2.49	0.43
1:A:496:ASN:HD22	1:A:496:ASN:HA	1.55	0.42
1:A:597:VAL:HG13	1:A:609:TYR:HB3	2.01	0.42
1:A:44:ILE:HB	1:A:66:VAL:O	2.18	0.42
1:A:165:GLN:H	1:A:165:GLN:HE21	1.61	0.42
1:A:97:LEU:HB3	1:A:100:VAL:CG2	2.48	0.42
1:A:529:GLN:HA	1:A:538:GLY:O	2.20	0.42
1:A:441:ALA:CB	1:A:456:TRP:HZ3	2.32	0.42
1:A:462:LEU:HD12	1:A:463:SER:H	1.84	0.42
1:A:139:LYS:HE3	1:A:139:LYS:HB2	1.82	0.42
1:A:37:THR:HB	1:A:72:GLN:CD	2.40	0.42
1:A:393:THR:HG22	1:A:395:LYS:H	1.85	0.42
1:A:439:ARG:HD2	1:A:450:ARG:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:402:TYR:CD1	1:A:402:TYR:N	2.88	0.42
1:A:37:THR:HB	1:A:72:GLN:CG	2.50	0.42
1:A:415:LEU:HD13	1:A:422:LEU:HD21	2.02	0.42
1:A:573:TYR:CD1	1:A:573:TYR:N	2.88	0.42
1:A:482:VAL:HG22	1:A:506:LEU:CD1	2.50	0.41
1:A:112:ASP:OD1	1:A:113:ILE:N	2.53	0.41
1:A:439:ARG:HG3	1:A:450:ARG:HD3	2.02	0.41
1:A:509:TYR:HE2	1:A:537:ILE:HD13	1.77	0.41
1:A:591:LYS:CE	1:A:592:ASN:HD22	2.30	0.41
1:A:506:LEU:HD21	1:A:540:VAL:HG11	2.02	0.41
1:A:163:LEU:CD2	1:A:163:LEU:N	2.82	0.41
1:A:36:GLU:OE1	1:A:36:GLU:HA	2.21	0.41
1:A:561:ARG:HH11	1:A:628:ALA:HB2	1.83	0.41
1:A:493:LYS:O	1:A:493:LYS:CG	2.68	0.41
1:A:286:HIS:O	1:A:287:LEU:C	2.58	0.41
1:A:45:LYS:HB2	1:A:45:LYS:HE3	1.94	0.41
1:A:551:GLN:C	1:A:553:MET:N	2.72	0.41
1:A:300:GLN:HE21	1:A:301:PRO:HD2	1.85	0.41
1:A:57:ILE:O	1:A:58:LYS:C	2.58	0.41
1:A:280:LYS:HG3	1:A:281:PRO:CD	2.36	0.41
1:A:531:SER:HB2	1:A:535:LYS:C	2.42	0.41
1:A:93:GLY:C	1:A:95:GLN:H	2.24	0.41
1:A:154:ILE:HG22	1:A:155:SER:N	2.35	0.41
1:A:76:ASN:HD22	1:A:76:ASN:N	2.19	0.41
1:A:457:THR:HG22	1:A:458:LYS:N	2.27	0.40
1:A:285:TRP:HB3	1:A:287:LEU:HG	2.03	0.40
1:A:586:THR:HG22	1:A:588:ALA:H	1.86	0.40
1:A:145:LYS:C	1:A:166:LEU:HD12	2.42	0.40
1:A:415:LEU:CB	1:A:422:LEU:HD21	2.47	0.40
1:A:551:GLN:C	1:A:553:MET:H	2.24	0.40
1:A:454:ILE:HG22	1:A:455:GLY:N	2.37	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	519/605 (86%)	411 (79%)	90 (17%)	18 (4%)	4	9

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	253	LEU
1	A	280	LYS
1	A	472	TYR
1	A	494	PRO
1	A	504	ASN
1	A	428	ALA
1	A	455	GLY
1	A	476	VAL
1	A	486	SER
1	A	500	ALA
1	A	591	LYS
1	A	592	ASN
1	A	136	SER
1	A	438	ASP
1	A	281	PRO
1	A	287	LEU
1	A	466	ARG
1	A	576	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	465/535 (87%)	436 (94%)	29 (6%)	23	45

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	108	ASN

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Mol	Chain	Res	Type
1	A	114	LYS
1	A	130	ASN
1	A	165	GLN
1	A	166	LEU
1	A	181	VAL
1	A	184	ARG
1	A	189	ASP
1	A	194	GLU
1	A	251	SER
1	A	257	ASN
1	A	262	THR
1	A	263	ASP
1	A	273	SER
1	A	281	PRO
1	A	294	VAL
1	A	304	ILE
1	A	310	ARG
1	A	312	HIS
1	A	394	GLU
1	A	429	SER
1	A	467	TYR
1	A	471	GLU
1	A	491	TRP
1	A	496	ASN
1	A	506	LEU
1	A	523	PRO
1	A	557	THR
1	A	558	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	ASN
1	A	92	GLN
1	A	106	ASN
1	A	108	ASN
1	A	130	ASN
1	A	165	GLN
1	A	219	HIS
1	A	231	ASN
1	A	244	ASN
1	A	248	ASN

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Mol	Chain	Res	Type
1	A	257	ASN
1	A	300	GLN
1	A	312	HIS
1	A	453	ASN
1	A	461	ASN
1	A	496	ASN
1	A	502	HIS
1	A	592	ASN
1	A	593	GLN
1	A	600	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

Of 8 ligands modelled in this entry, 7 are monoatomic - leaving 1 for Mogul analysis.

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	SO4	A	646	-	4,4,4	0.16	0	6,6,6	0.08	0

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	SO4	A	646	-	-	0/0/0/0	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 ⓘ

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	523/605 (86%)	0.75	47 (8%) 12 9	23, 95, 149, 166	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	457	THR	6.3
1	A	468	ASP	5.7
1	A	396	THR	5.2
1	A	397	VAL	5.0
1	A	415	LEU	4.8
1	A	417	ARG	4.7
1	A	435	LEU	4.5
1	A	399	LEU	4.3
1	A	425	GLY	4.1
1	A	392	THR	3.9
1	A	469	LYS	3.9
1	A	527	TRP	3.9
1	A	394	GLU	3.8
1	A	420	ASN	3.3
1	A	423	LYS	3.2
1	A	449	TYR	3.1
1	A	395	LYS	2.9
1	A	64	LYS	2.8
1	A	393	THR	2.8
1	A	401	ARG	2.6
1	A	432	CYS	2.6
1	A	440	GLU	2.6
1	A	427	LEU	2.6
1	A	69	ALA	2.6
1	A	319	LEU	2.5
1	A	447	LEU	2.5
1	A	467	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	500	ALA	2.4
1	A	552	SER	2.3
1	A	119	LEU	2.3
1	A	451	LEU	2.3
1	A	407	ARG	2.3
1	A	537	ILE	2.3
1	A	408	GLY	2.3
1	A	436	THR	2.3
1	A	596	ILE	2.3
1	A	495	TYR	2.2
1	A	424	GLN	2.2
1	A	70	VAL	2.2
1	A	460	GLU	2.2
1	A	304	ILE	2.2
1	A	506	LEU	2.1
1	A	498	ALA	2.1
1	A	405	TYR	2.1
1	A	470	MET	2.1
1	A	504	ASN	2.0
1	A	267	VAL	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(Å <sup>2</sup> )	Q<0.9
2	TB	A	643	1/1	0.96	0.21	-	198,198,198,198	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	TB	A	642	1/1	0.77	0.10	-	201,201,201,201	0
2	TB	A	641	1/1	0.98	0.29	-	140,140,140,140	0
3	SO4	A	646	5/5	0.85	0.20	-	191,194,195,195	0
2	TB	A	645	1/1	0.80	0.21	-	201,201,201,201	0
2	TB	A	639	1/1	0.99	0.22	-	123,123,123,123	0
2	TB	A	640	1/1	0.97	0.26	-	144,144,144,144	0
2	TB	A	644	1/1	0.96	0.14	-	180,180,180,180	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.