



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 10:09 AM UTC

PDB ID : 2BDE / pdb\_00002bde  
Title : Crystal Structure of the cytosolic IMP-GMP specific 5'-nucleotidase (lpg0095) from Legionella pneumophila, Northeast Structural Genomics Target LgR1  
Authors : Forouhar, F.; Abashidze, M.; Ho, C.K.; Conover, K.; Acton, T.B.; Montelione, G.T.; Hunt, J.F.; Tong, L.; Northeast Structural Genomics Consortium (NESG)  
Deposited on : 2005-10-20  
Resolution : 2.90 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

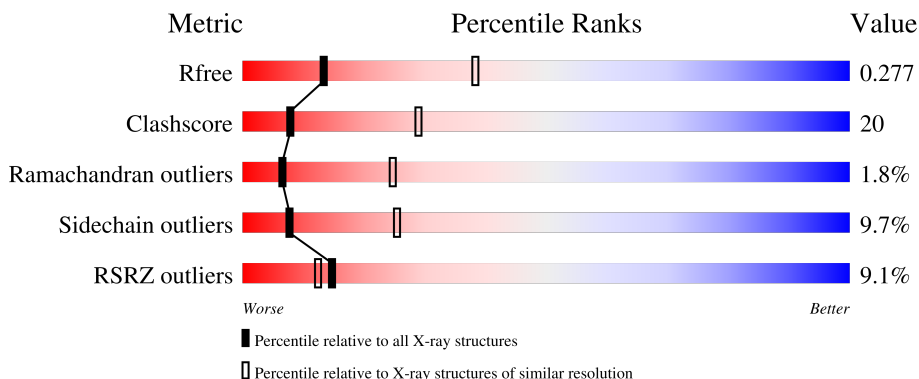
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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))
$R_{free}$	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	470	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	471	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3839 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 cytosolic IMP-GMP specific 5'-nucleotidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	458	3758	2415	633	697	5	8	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP Q5ZZB6
A	14	MSE	MET	modified residue	UNP Q5ZZB6
A	24	MSE	MET	modified residue	UNP Q5ZZB6
A	122	MSE	MET	modified residue	UNP Q5ZZB6
A	150	MSE	MET	modified residue	UNP Q5ZZB6
A	267	MSE	MET	modified residue	UNP Q5ZZB6
A	348	MSE	MET	modified residue	UNP Q5ZZB6
A	431	MSE	MET	modified residue	UNP Q5ZZB6
A	443	MSE	MET	modified residue	UNP Q5ZZB6
A	460	ALA	-	cloning artifact	UNP Q5ZZB6
A	461	ALA	-	cloning artifact	UNP Q5ZZB6
A	462	ALA	-	cloning artifact	UNP Q5ZZB6
A	463	LEU	-	cloning artifact	UNP Q5ZZB6
A	464	GLU	-	cloning artifact	UNP Q5ZZB6
A	465	HIS	-	expression tag	UNP Q5ZZB6
A	466	HIS	-	expression tag	UNP Q5ZZB6
A	467	HIS	-	expression tag	UNP Q5ZZB6
A	468	HIS	-	expression tag	UNP Q5ZZB6
A	469	HIS	-	expression tag	UNP Q5ZZB6
A	470	HIS	-	expression tag	UNP Q5ZZB6

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S).



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

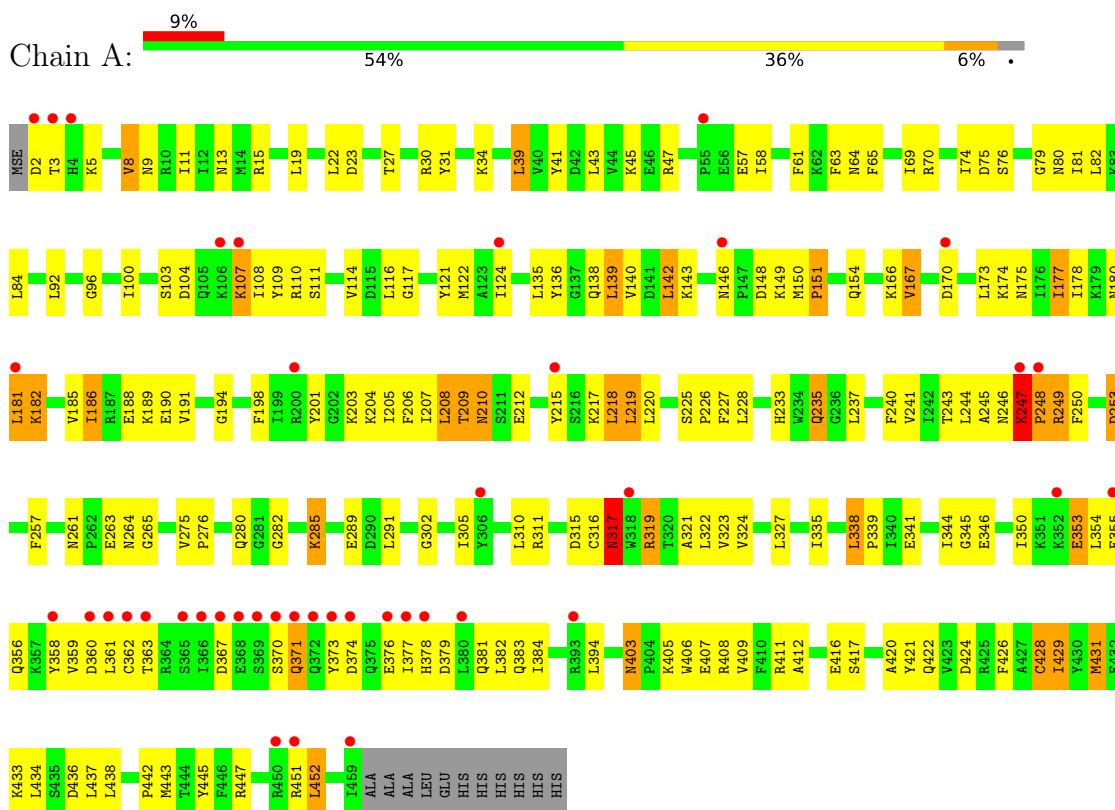
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	71	Total	O	0	0
			71	71		

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

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: cytosolic IMP-GMP specific 5'-nucleotidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	152.54Å 152.54Å 188.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.12 – 2.90 30.12 – 2.90	Depositor EDS
% Data completeness (in resolution range)	94.0 (30.12-2.90) 96.1 (30.12-2.90)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.48 (at 2.91Å)	Xtrriage
Refinement program	CNS 1.1, XTALVIEW	Depositor
R, $R_{free}$	0.221 , 0.267 0.233 , 0.277	Depositor DCC
$R_{free}$ test set	4594 reflections (9.76%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.3	Xtrriage
Anisotropy	0.289	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 45.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	3839	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.64% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: 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	0.50	0/3829	0.89	9/5148 (0.2%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	8	VAL	N-CA-C	6.26	117.32	108.36
1	A	426	PHE	N-CA-C	6.01	119.08	111.69
1	A	265	GLY	N-CA-C	-5.54	107.45	115.27
1	A	117	GLY	N-CA-C	-5.41	107.95	114.66
1	A	428	CYS	N-CA-C	-5.19	106.46	112.89
1	A	246	ASN	N-CA-C	-5.13	104.34	111.52
1	A	409	VAL	N-CA-C	5.06	115.83	110.72
1	A	317	ASN	CA-C-N	-5.00	114.82	122.87
1	A	317	ASN	C-N-CA	-5.00	114.82	122.87

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	3758	0	3755	149	0
2	A	10	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	71	0	0	3	0
All	All	3839	0	3755	149	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 20.

All (149) 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:225:SER:HA	1:A:228:LEU:HD23	1.56	0.87
1:A:373:TYR:HB3	1:A:376:GLU:HB3	1.63	0.80
1:A:8:VAL:HG22	1:A:429:ILE:HD11	1.63	0.79
1:A:261:ASN:ND2	1:A:264:ASN:H	1.82	0.77
1:A:96:GLY:HA2	1:A:140:VAL:CG2	2.17	0.75
1:A:96:GLY:HA2	1:A:140:VAL:HG21	1.70	0.74
1:A:233:HIS:HB3	1:A:235:GLN:HE21	1.53	0.73
1:A:358:TYR:O	1:A:362:CYS:HB2	1.89	0.72
1:A:104:ASP:O	1:A:108:ILE:HG13	1.89	0.72
1:A:186:ILE:HG13	1:A:186:ILE:O	1.89	0.71
1:A:319:ARG:HA	2:A:471:SO4:O3	1.95	0.66
1:A:311:ARG:HG3	1:A:315:ASP:OD1	1.97	0.65
1:A:407:GLU:OE1	1:A:408:ARG:HG2	1.96	0.65
1:A:257:PHE:CE1	1:A:282:GLY:HA3	2.33	0.64
1:A:377:ILE:HD12	1:A:378:HIS:N	2.13	0.63
1:A:31:TYR:HE1	1:A:177:ILE:HD12	1.64	0.63
1:A:23:ASP:O	1:A:27:THR:HB	1.99	0.62
1:A:261:ASN:HD22	1:A:264:ASN:H	1.47	0.62
1:A:247:LYS:O	1:A:248:PRO:C	2.43	0.61
1:A:178:ILE:HD11	1:A:218:LEU:HB3	1.82	0.60
1:A:45:LYS:HD2	1:A:58:ILE:O	2.02	0.60
1:A:135:LEU:HG	1:A:139:LEU:HD22	1.82	0.60
1:A:174:LYS:HG2	3:A:534:HOH:O	2.02	0.60
1:A:22:LEU:HB2	1:A:207:ILE:HG22	1.84	0.59
1:A:142:LEU:HD12	1:A:150:MSE:SE	2.53	0.59
1:A:205:ILE:HD12	1:A:205:ILE:N	2.18	0.58
1:A:80:ASN:ND2	1:A:100:ILE:HD11	2.20	0.57
1:A:354:LEU:HD23	1:A:354:LEU:O	2.05	0.57
1:A:180:ASN:O	1:A:182:LYS:N	2.38	0.56
1:A:215:TYR:CE2	1:A:219:LEU:HD22	2.41	0.56
1:A:319:ARG:HH11	1:A:319:ARG:HB3	1.69	0.56
1:A:76:SER:HB2	1:A:154:GLN:HA	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:VAL:O	1:A:327:LEU:HB2	2.06	0.56
1:A:305:ILE:CD1	1:A:422:GLN:HB3	2.36	0.55
1:A:136:TYR:O	1:A:140:VAL:HG22	2.06	0.55
1:A:30:ARG:HG2	1:A:30:ARG:HH11	1.71	0.54
1:A:75:ASP:HB3	1:A:121:TYR:CD2	2.42	0.54
1:A:208:LEU:O	1:A:247:LYS:HE3	2.08	0.54
1:A:173:LEU:O	1:A:177:ILE:HG22	2.08	0.53
1:A:371:GLN:OE1	1:A:374:ASP:HB2	2.08	0.53
1:A:74:ILE:HG22	1:A:81:ILE:HG12	1.89	0.53
1:A:79:GLY:HA2	1:A:136:TYR:OH	2.08	0.53
1:A:225:SER:HA	1:A:228:LEU:CD2	2.35	0.53
1:A:431:MSE:HE3	1:A:434:LEU:HA	1.89	0.53
1:A:41:TYR:CE1	1:A:63:PHE:HB2	2.43	0.52
1:A:408:ARG:HG3	1:A:411:ARG:HB2	1.92	0.52
1:A:104:ASP:O	1:A:107:LYS:HG3	2.10	0.52
1:A:346:GLU:O	1:A:350:ILE:HG12	2.09	0.52
1:A:104:ASP:HA	1:A:107:LYS:HG2	1.92	0.52
1:A:189:LYS:HB3	1:A:227:PHE:CD1	2.46	0.51
1:A:47:ARG:NH1	1:A:166:LYS:HD2	2.25	0.51
1:A:302:GLY:O	1:A:322:LEU:HD12	2.10	0.51
1:A:174:LYS:HB3	1:A:215:TYR:CE1	2.45	0.51
1:A:194:GLY:HA3	1:A:438:LEU:HB3	1.92	0.51
1:A:355:GLU:OE1	1:A:384:ILE:HD11	2.11	0.51
1:A:344:ILE:HG22	1:A:394:LEU:HB3	1.92	0.50
1:A:341:GLU:O	1:A:344:ILE:HG12	2.11	0.50
1:A:249:ARG:HB3	1:A:253:ASP:HB2	1.92	0.50
1:A:3:THR:HA	3:A:522:HOH:O	2.12	0.50
1:A:188:GLU:HG3	1:A:191:VAL:HG23	1.94	0.50
1:A:206:PHE:HB2	1:A:240:PHE:HB2	1.94	0.50
1:A:19:LEU:HD23	1:A:204:LYS:HB2	1.94	0.49
1:A:335:ILE:O	1:A:338:LEU:HB2	2.11	0.49
1:A:5:LYS:HB3	1:A:436:ASP:HB3	1.94	0.49
1:A:110:ARG:O	1:A:111:SER:HB2	2.12	0.49
1:A:244:LEU:HB2	1:A:280:GLN:HG3	1.94	0.49
1:A:285:LYS:HD2	1:A:289:GLU:OE2	2.13	0.49
1:A:403:ASN:HD22	1:A:406:TRP:H	1.61	0.48
1:A:210:ASN:OD1	1:A:247:LYS:HB2	2.13	0.48
1:A:15:ARG:HG2	1:A:443:MSE:HB2	1.96	0.48
1:A:57:GLU:OE1	1:A:57:GLU:N	2.37	0.47
1:A:363:THR:O	1:A:367:ASP:HB2	2.14	0.47
1:A:275:VAL:O	1:A:276:PRO:C	2.57	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:403:ASN:ND2	1:A:405:LYS:H	2.11	0.47
1:A:225:SER:HB2	1:A:226:PRO:HD3	1.95	0.47
1:A:92:LEU:HD12	1:A:92:LEU:O	2.15	0.47
1:A:43:LEU:HB3	1:A:167:VAL:HG21	1.96	0.47
1:A:166:LYS:O	1:A:170:ASP:HB2	2.14	0.47
1:A:175:ASN:HA	1:A:178:ILE:HG22	1.96	0.47
1:A:344:ILE:HG13	1:A:345:GLY:N	2.30	0.47
1:A:178:ILE:HA	1:A:181:LEU:HD21	1.96	0.47
1:A:190:GLU:H	1:A:190:GLU:CD	2.23	0.47
1:A:319:ARG:NH1	2:A:471:SO4:O4	2.48	0.47
1:A:261:ASN:HD21	1:A:263:GLU:HB2	1.79	0.46
1:A:323:VAL:HG13	1:A:323:VAL:O	2.15	0.46
1:A:323:VAL:CG2	1:A:433:LYS:HA	2.46	0.46
1:A:354:LEU:HD11	1:A:383:GLN:HG2	1.97	0.46
1:A:30:ARG:NE	1:A:188:GLU:OE2	2.49	0.46
1:A:431:MSE:CE	1:A:434:LEU:HA	2.46	0.46
1:A:45:LYS:HD2	1:A:61:PHE:HB2	1.98	0.46
1:A:302:GLY:O	1:A:323:VAL:HG12	2.15	0.46
1:A:316:CYS:O	1:A:317:ASN:HB3	2.14	0.46
1:A:2:ASP:CG	1:A:3:THR:H	2.24	0.45
1:A:201:TYR:CD1	1:A:442:PRO:HG2	2.51	0.45
1:A:261:ASN:ND2	1:A:264:ASN:ND2	2.64	0.45
1:A:64:ASN:C	1:A:64:ASN:HD22	2.24	0.45
1:A:198:PHE:CE2	1:A:438:LEU:HA	2.52	0.45
1:A:257:PHE:CD1	1:A:282:GLY:HA3	2.51	0.45
1:A:173:LEU:C	1:A:173:LEU:HD13	2.41	0.45
1:A:359:VAL:HG23	1:A:360:ASP:N	2.31	0.45
1:A:70:ARG:HD2	3:A:536:HOH:O	2.16	0.45
1:A:31:TYR:HE1	1:A:177:ILE:CD1	2.30	0.45
1:A:47:ARG:HH12	1:A:166:LYS:HD2	1.82	0.44
1:A:416:GLU:HB2	1:A:420:ALA:HB3	1.98	0.44
1:A:13:ASN:ND2	1:A:15:ARG:H	2.15	0.44
1:A:146:ASN:OD1	1:A:149:LYS:HG2	2.18	0.44
1:A:249:ARG:O	1:A:253:ASP:HB2	2.18	0.44
1:A:166:LYS:O	1:A:170:ASP:CB	2.66	0.44
1:A:96:GLY:HA2	1:A:140:VAL:HG23	1.94	0.43
1:A:175:ASN:O	1:A:178:ILE:HG22	2.19	0.43
1:A:9:ASN:OD1	1:A:424:ASP:HA	2.18	0.43
1:A:19:LEU:CD1	1:A:291:LEU:HD23	2.48	0.43
1:A:39:LEU:CD2	1:A:43:LEU:HG	2.48	0.43
1:A:92:LEU:HD12	1:A:92:LEU:C	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:ILE:HD11	1:A:122:MSE:SE	2.68	0.43
1:A:13:ASN:HD21	1:A:15:ARG:HG3	1.83	0.43
1:A:381:GLN:O	1:A:384:ILE:HG22	2.19	0.43
1:A:41:TYR:OH	1:A:61:PHE:HB3	2.19	0.43
1:A:64:ASN:HD22	1:A:65:PHE:N	2.16	0.43
1:A:412:ALA:HB2	1:A:417:SER:HA	2.00	0.43
1:A:243:THR:O	1:A:280:GLN:HA	2.19	0.42
1:A:353:GLU:HA	1:A:356:GLN:HB3	2.01	0.42
1:A:75:ASP:HB3	1:A:121:TYR:CE2	2.54	0.42
1:A:245:ALA:O	1:A:250:PHE:HB2	2.20	0.42
1:A:261:ASN:ND2	1:A:264:ASN:CG	2.77	0.42
1:A:316:CYS:O	1:A:317:ASN:CB	2.67	0.42
1:A:143:LYS:NZ	1:A:151:PRO:O	2.53	0.42
1:A:19:LEU:HD11	1:A:291:LEU:HD23	2.01	0.42
1:A:47:ARG:HH11	1:A:166:LYS:NZ	2.18	0.42
1:A:9:ASN:HD22	1:A:9:ASN:HA	1.65	0.41
1:A:109:TYR:O	1:A:110:ARG:C	2.62	0.41
1:A:310:LEU:HD22	1:A:310:LEU:O	2.20	0.41
1:A:84:LEU:HD21	1:A:114:VAL:HG21	2.02	0.41
1:A:428:CYS:O	1:A:429:ILE:HD12	2.20	0.41
1:A:445:TYR:HD2	1:A:447:ARG:HG2	1.86	0.41
1:A:138:GLN:HE21	1:A:138:GLN:HB2	1.69	0.41
1:A:321:ALA:HB1	1:A:429:ILE:HG22	2.02	0.41
1:A:451:ARG:O	1:A:452:LEU:CB	2.68	0.41
1:A:116:LEU:N	1:A:116:LEU:HD22	2.36	0.41
1:A:361:LEU:HD11	1:A:377:ILE:HG22	2.02	0.41
1:A:338:LEU:N	1:A:339:PRO:HD2	2.36	0.40
1:A:344:ILE:HG22	1:A:394:LEU:CB	2.51	0.40
1:A:39:LEU:HD13	1:A:173:LEU:HD22	2.03	0.40
1:A:378:HIS:O	1:A:382:LEU:HD13	2.21	0.40
1:A:74:ILE:CG2	1:A:81:ILE:HG12	2.50	0.40
1:A:209:THR:OG1	1:A:210:ASN:N	2.53	0.40
1:A:11:ILE:O	1:A:319:ARG:NH2	2.52	0.40
1:A:80:ASN:ND2	1:A:100:ILE:CD1	2.84	0.40
1:A:356:GLN:HE21	1:A:356:GLN:HA	1.86	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	456/470 (97%)	414 (91%)	34 (8%)	8 (2%)	6 25

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	181	LEU
1	A	182	LYS
1	A	370	SER
1	A	253	ASP
1	A	371	GLN
1	A	247	LYS
1	A	248	PRO
1	A	151	PRO

### 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	412/412 (100%)	372 (90%)	40 (10%)	8 25

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	LYS
1	A	39	LEU
1	A	69	ILE

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Mol	Chain	Res	Type
1	A	82	LEU
1	A	103	SER
1	A	107	LYS
1	A	124	ILE
1	A	139	LEU
1	A	142	LEU
1	A	148	ASP
1	A	167	VAL
1	A	177	ILE
1	A	185	VAL
1	A	186	ILE
1	A	203	LYS
1	A	208	LEU
1	A	209	THR
1	A	210	ASN
1	A	212	GLU
1	A	217	LYS
1	A	218	LEU
1	A	219	LEU
1	A	220	LEU
1	A	235	GLN
1	A	237	LEU
1	A	241	VAL
1	A	247	LYS
1	A	249	ARG
1	A	285	LYS
1	A	317	ASN
1	A	319	ARG
1	A	338	LEU
1	A	353	GLU
1	A	379	ASP
1	A	403	ASN
1	A	421	TYR
1	A	429	ILE
1	A	431	MSE
1	A	437	LEU
1	A	452	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	ASN

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Mol	Chain	Res	Type
1	A	64	ASN
1	A	78	ASN
1	A	99	GLN
1	A	138	GLN
1	A	161	GLN
1	A	168	HIS
1	A	175	ASN
1	A	235	GLN
1	A	246	ASN
1	A	261	ASN
1	A	264	ASN
1	A	334	GLN
1	A	356	GLN
1	A	390	GLN
1	A	403	ASN
1	A	440	HIS

### 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 oligosaccharides 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	SO4	A	471	-	4,4,4	0.33	0	6,6,6	0.16	0
2	SO4	A	472	-	4,4,4	0.28	0	6,6,6	0.10	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.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	471	SO4	2	0

## 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	450/470 (95%)	0.41	41 (9%) <b>15</b> <b>12</b>	20, 45, 87, 106	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	THR	6.9
1	A	4	HIS	5.2
1	A	361	LEU	5.1
1	A	377	ILE	4.4
1	A	2	ASP	3.6
1	A	459	ILE	3.6
1	A	367	ASP	3.5
1	A	369	SER	3.3
1	A	370	SER	3.3
1	A	368	GLU	3.2
1	A	451	ARG	3.0
1	A	363	THR	3.0
1	A	380	LEU	2.9
1	A	124	ILE	2.9
1	A	371	GLN	2.9
1	A	247	LYS	2.8
1	A	107	LYS	2.7
1	A	372	GLN	2.6
1	A	181	LEU	2.6
1	A	55	PRO	2.6
1	A	352	LYS	2.5
1	A	318	TRP	2.5
1	A	373	TYR	2.5
1	A	215	TYR	2.4
1	A	200	ARG	2.4
1	A	374	ASP	2.4
1	A	355	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	450	ARG	2.3
1	A	360	ASP	2.2
1	A	376	GLU	2.2
1	A	146	ASN	2.2
1	A	106	LYS	2.2
1	A	378	HIS	2.2
1	A	306	TYR	2.2
1	A	358	TYR	2.2
1	A	365	SER	2.2
1	A	362	CYS	2.1
1	A	248	PRO	2.1
1	A	170	ASP	2.1
1	A	393	ARG	2.1
1	A	366	ILE	2.1

## 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 oligosaccharides 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. 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	SO4	A	472	5/5	0.96	0.13	40,42,43,45	0
2	SO4	A	471	5/5	0.97	0.13	35,38,39,40	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.