



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:10 PM GMT

PDB ID : 1EEP
Title : 2.4 Å RESOLUTION CRYSTAL STRUCTURE OF BORRELIA BURGDORFERI INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE IN COMPLEX WITH A SULFATE ION
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Deposited on : 2000-02-01
Resolution : 2.40 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

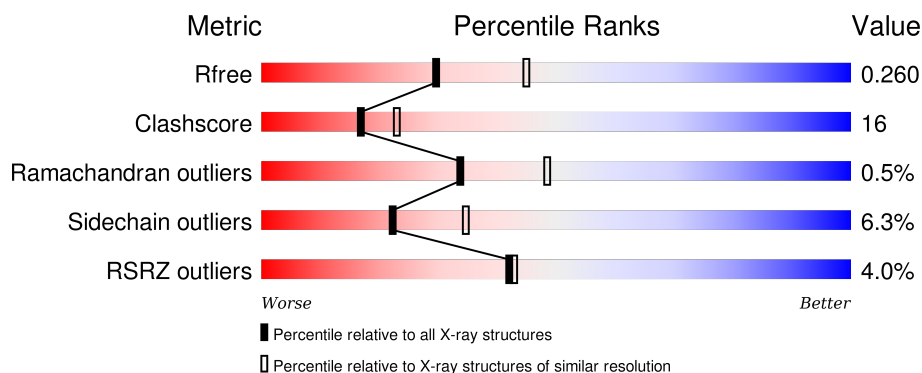
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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))
R_{free}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (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 ≥ 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	404	<div> <div>3%</div> <div>54%</div> <div>20%</div> <div>•</div> <div>22%</div> </div>
1	B	404	<div> <div>3%</div> <div>53%</div> <div>22%</div> <div>•</div> <div>22%</div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4681 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 INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	0	0
			2282	1447	389	434	12			
1	B	314	Total	C	N	O	S	0	0	0
			2282	1447	384	438	13			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

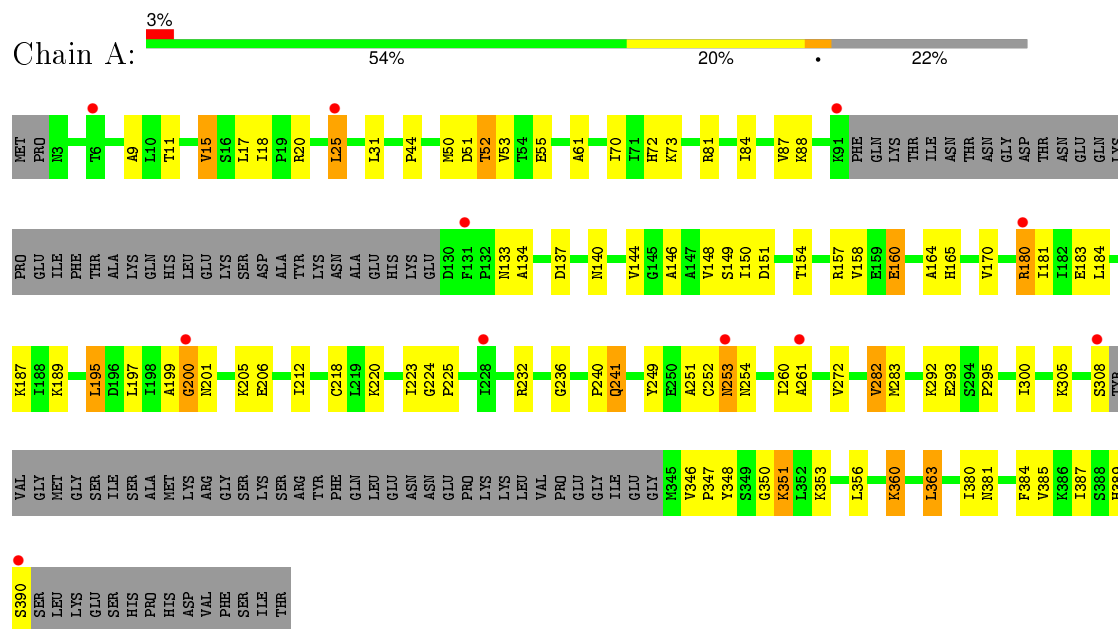
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	57	Total 57	O 57	0	0
3	B	50	Total 50	O 50	0	0

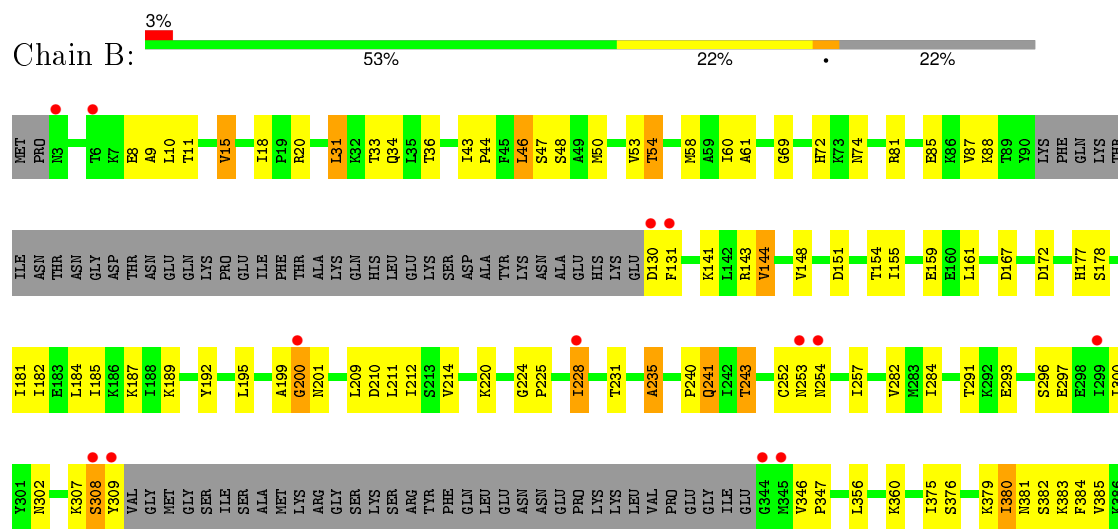
3 Residue-property plots

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: INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE



• Molecule 1: INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE



I387	SER
S388	SER
H389	LEU
	LYS
	GLU
	SER
	HIS
	PRO
	HIS
	ASP
	VAL
	PHE
	SER
	ILE
	THR

4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	123.28Å 123.28Å 130.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.40 29.83 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (8.00-2.40) 99.8 (29.83-2.40)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 2.39Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.214 , 0.262 0.214 , 0.260	Depositor DCC
R_{free} test set	3732 reflections (10.14%)	DCC
Wilson B-factor (Å ²)	29.3	Xtriage
Anisotropy	0.670	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 56.9	EDS
Estimated twinning fraction	0.028 for -h,k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 37863 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4681	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.89% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: 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	0.36	0/2304	0.67	1/3110 (0.0%)
1	B	0.33	0/2305	0.66	2/3116 (0.1%)
All	All	0.34	0/4609	0.66	3/6226 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	180	ARG	NE-CZ-NH2	7.32	123.96	120.30
1	B	46	LEU	CA-CB-CG	6.86	131.07	115.30
1	B	235	ALA	N-CA-C	-5.23	96.88	111.00

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	2282	0	2361	71	9
1	B	2282	0	2344	81	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	57	0	0	2	1
3	B	50	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4681	0	4705	152	9

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 16.

All (152) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:296:SER:HB2	1:B:307:LYS:HG3	1.40	1.02
1:B:241:GLN:HA	1:B:241:GLN:HE21	1.34	0.90
1:A:70:ILE:HD13	1:A:170:VAL:HG21	1.56	0.88
1:A:180:ARG:HG3	3:A:783:HOH:O	1.74	0.85
1:A:241:GLN:HE21	1:A:241:GLN:HA	1.42	0.84
1:B:9:ALA:HB1	1:B:243:THR:HG21	1.63	0.81
1:A:31:LEU:HD22	1:A:363:LEU:HD13	1.64	0.79
1:A:300:ILE:HD13	1:A:305:LYS:HG3	1.65	0.77
1:A:224:GLY:N	1:A:225:PRO:HD3	2.03	0.73
1:B:296:SER:CB	1:B:307:LYS:HG3	2.19	0.73
1:A:148:VAL:HG23	1:A:157:ARG:HD2	1.72	0.72
1:B:291:THR:O	1:B:307:LYS:HE3	1.88	0.72
1:A:81:ARG:HD2	1:A:160:GLU:HG3	1.70	0.72
1:B:15:VAL:HG22	1:B:384:PHE:HB3	1.69	0.72
1:A:387:ILE:HG22	1:A:389:HIS:H	1.55	0.70
1:B:48:SER:O	1:B:54:THR:HG22	1.93	0.68
1:A:50:MET:HB2	1:A:53:VAL:HG13	1.76	0.68
1:B:143:ARG:HG2	1:B:167:ASP:OD2	1.94	0.68
1:A:73:LYS:HE2	1:A:149:SER:HB3	1.76	0.67
1:B:20:ARG:CZ	1:B:381:ASN:HB3	2.25	0.66
1:B:241:GLN:HE21	1:B:241:GLN:CA	2.09	0.66
1:A:199:ALA:O	1:A:200:GLY:O	2.14	0.66
1:B:376:SER:O	1:B:380:ILE:HG12	1.96	0.65
1:B:199:ALA:O	1:B:200:GLY:O	2.15	0.65
1:B:9:ALA:CB	1:B:243:THR:HG21	2.27	0.64
1:B:48:SER:O	1:B:54:THR:CG2	2.45	0.64
1:B:231:THR:HG22	3:B:795:HOH:O	1.96	0.64
1:A:300:ILE:CD1	1:A:305:LYS:HG3	2.28	0.63
1:A:224:GLY:N	1:A:225:PRO:CD	2.61	0.63
1:A:356:LEU:O	1:A:360:LYS:HG2	1.99	0.63
1:A:51:ASP:HA	1:A:72:HIS:CD2	2.36	0.61
1:A:189:LYS:HE3	1:A:197:LEU:HG	1.82	0.61
1:A:261:ALA:HB3	1:A:282:VAL:HG23	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:11:THR:HG22	1:B:240:PRO:HB3	1.84	0.59
1:B:130:ASP:CG	1:B:131:PHE:H	2.06	0.59
1:B:382:SER:O	1:B:383:LYS:HD2	2.03	0.59
1:A:70:ILE:HD12	1:A:283:MET:CE	2.33	0.59
1:B:356:LEU:O	1:B:360:LYS:HG3	2.03	0.59
1:B:10:LEU:H	1:B:243:THR:CG2	2.17	0.58
1:B:53:VAL:HG22	1:B:54:THR:HG22	1.85	0.58
1:B:297:GLU:H	1:B:308:SER:HB3	1.68	0.58
1:B:346:VAL:HG23	1:B:347:PRO:HD2	1.85	0.58
1:B:224:GLY:N	1:B:225:PRO:HD3	2.18	0.57
1:A:205:LYS:HG3	1:A:251:ALA:HB2	1.85	0.57
1:B:155:ILE:HG13	1:B:187:LYS:HE3	1.85	0.57
1:A:380:ILE:HG13	1:A:381:ASN:N	2.20	0.56
1:B:225:PRO:HG3	3:B:796:HOH:O	2.06	0.56
1:A:189:LYS:HE2	1:A:195:LEU:O	2.06	0.56
1:A:18:ILE:HD11	1:A:385:VAL:HG13	1.86	0.56
1:B:154:THR:HG23	1:B:155:ILE:H	1.71	0.55
1:B:154:THR:HG23	1:B:155:ILE:N	2.22	0.55
1:B:88:LYS:O	1:B:141:LYS:HD2	2.08	0.55
1:A:73:LYS:HG2	3:A:786:HOH:O	2.07	0.54
1:B:53:VAL:CG2	1:B:54:THR:HG22	2.36	0.54
1:B:54:THR:HB	1:B:58:MET:HG2	1.89	0.54
1:A:150:ILE:HD11	1:A:181:ILE:HD12	1.90	0.54
1:B:293:GLU:N	1:B:293:GLU:OE1	2.36	0.54
1:A:150:ILE:CD1	1:A:181:ILE:HD12	2.38	0.53
1:B:60:ILE:HG13	1:B:87:VAL:HG22	1.91	0.53
1:A:346:VAL:HG23	1:A:347:PRO:HD2	1.89	0.53
1:B:182:ILE:HG23	1:B:214:VAL:HG11	1.91	0.53
1:A:241:GLN:CA	1:A:241:GLN:HE21	2.18	0.53
1:B:9:ALA:CB	1:B:240:PRO:HD2	2.39	0.53
1:A:387:ILE:C	1:A:389:HIS:H	2.12	0.53
1:A:81:ARG:HG3	1:A:164:ALA:HB2	1.91	0.52
1:B:212:ILE:HD13	1:B:257:ILE:HG13	1.91	0.52
1:A:15:VAL:HG13	1:A:384:PHE:CD2	2.44	0.52
1:A:55:GLU:HB2	1:A:295:PRO:HG3	1.92	0.52
1:B:253:ASN:O	1:B:254:ASN:HB2	2.10	0.51
1:B:382:SER:C	1:B:383:LYS:HD2	2.30	0.51
1:A:212:ILE:HD11	1:A:252:CYS:SG	2.50	0.51
1:B:228:ILE:H	1:B:228:ILE:HD13	1.73	0.51
1:B:240:PRO:O	1:B:243:THR:HG23	2.11	0.51
1:A:305:LYS:HD3	1:A:348:TYR:CG	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:387:ILE:HG22	1:A:389:HIS:N	2.25	0.51
1:B:10:LEU:H	1:B:243:THR:HG22	1.74	0.51
1:B:50:MET:HB2	1:B:53:VAL:HG13	1.91	0.51
1:B:241:GLN:HA	1:B:241:GLN:NE2	2.15	0.49
1:B:81:ARG:O	1:B:85:GLU:HG3	2.13	0.49
1:B:297:GLU:O	1:B:308:SER:N	2.41	0.48
1:A:17:LEU:CD1	1:A:272:VAL:HG12	2.42	0.48
1:B:9:ALA:HB1	1:B:240:PRO:HD2	1.95	0.48
1:A:9:ALA:CB	1:A:240:PRO:HD2	2.43	0.48
1:A:253:ASN:HD22	1:A:254:ASN:H	1.60	0.48
1:B:87:VAL:HB	1:B:144:VAL:HG21	1.95	0.48
1:B:282:VAL:HG12	1:B:284:ILE:HG13	1.96	0.48
1:A:292:LYS:HB2	1:A:348:TYR:OH	2.13	0.48
1:B:61:ALA:HB2	1:B:293:GLU:HG2	1.96	0.47
1:A:218:CYS:SG	1:A:260:ILE:HG13	2.54	0.47
1:B:387:ILE:HG22	1:B:388:SER:N	2.29	0.47
1:B:81:ARG:NH2	1:B:85:GLU:OE2	2.47	0.47
1:A:249:TYR:C	1:A:251:ALA:H	2.19	0.46
1:A:52:THR:CG2	1:A:53:VAL:HG12	2.45	0.46
1:B:151:ASP:O	1:B:154:THR:HG22	2.15	0.46
1:B:31:LEU:O	1:B:44:PRO:HD3	2.16	0.46
1:A:206:GLU:H	1:A:206:GLU:CD	2.19	0.46
1:A:31:LEU:CD2	1:A:363:LEU:HD13	2.41	0.46
1:A:223:ILE:C	1:A:225:PRO:HD3	2.36	0.46
1:B:199:ALA:HB1	1:B:211:LEU:HD13	1.97	0.46
1:A:189:LYS:HD3	1:A:189:LYS:HA	1.82	0.46
1:B:375:ILE:O	1:B:379:LYS:HG3	2.15	0.45
1:B:231:THR:O	1:B:235:ALA:O	2.35	0.45
1:A:73:LYS:HE2	1:A:149:SER:CB	2.44	0.45
1:B:182:ILE:CG2	1:B:214:VAL:HG11	2.46	0.45
1:A:348:TYR:CE2	1:A:350:GLY:HA2	2.51	0.45
1:B:228:ILE:H	1:B:228:ILE:CD1	2.29	0.44
1:A:61:ALA:HB2	1:A:293:GLU:HG2	1.98	0.44
1:A:88:LYS:NZ	1:A:137:ASP:OD2	2.46	0.44
1:A:11:THR:HG22	1:A:240:PRO:HB3	2.00	0.44
1:A:292:LYS:HD2	1:A:351:LYS:HD2	2.00	0.44
1:B:11:THR:CG2	1:B:240:PRO:HB3	2.47	0.44
1:B:43:ILE:HG21	1:B:360:LYS:HD3	1.99	0.44
1:A:183:GLU:O	1:A:187:LYS:HG3	2.18	0.44
1:B:48:SER:O	1:B:53:VAL:HG22	2.17	0.44
1:A:205:LYS:HB3	1:A:205:LYS:HE2	1.78	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:72:HIS:HD2	1:B:74:ASN:HB2	1.83	0.44
1:A:87:VAL:HG11	1:A:144:VAL:HB	2.00	0.44
1:B:18:ILE:HD11	1:B:385:VAL:HG13	1.99	0.43
1:A:70:ILE:HD12	1:A:283:MET:HE3	2.00	0.43
1:A:148:VAL:HG22	1:A:154:THR:HG23	1.99	0.43
1:B:387:ILE:C	1:B:389:HIS:H	2.21	0.43
1:B:72:HIS:CD2	1:B:74:ASN:HB2	2.53	0.43
1:B:308:SER:O	1:B:309:TYR:CD2	2.71	0.43
1:A:154:THR:O	1:A:158:VAL:HG23	2.18	0.43
1:A:52:THR:HG23	1:A:53:VAL:HG12	2.01	0.43
1:A:232:ARG:O	1:A:236:GLY:HA2	2.19	0.43
1:B:189:LYS:HD2	1:B:189:LYS:HA	1.84	0.43
1:B:308:SER:OG	1:B:309:TYR:N	2.51	0.43
1:B:34:GLN:HG3	1:B:36:THR:O	2.19	0.42
1:B:33:THR:HB	1:B:375:ILE:HD12	2.01	0.42
1:A:81:ARG:NH2	1:A:160:GLU:OE2	2.52	0.42
1:B:177:HIS:HE1	1:B:210:ASP:OD2	2.02	0.42
1:A:88:LYS:HE3	1:A:165:HIS:O	2.20	0.42
1:B:201:ASN:HA	1:B:220:LYS:O	2.19	0.42
1:B:9:ALA:CA	1:B:243:THR:HG21	2.49	0.41
1:A:70:ILE:HD13	1:A:170:VAL:CG2	2.37	0.41
1:A:20:ARG:CZ	1:A:381:ASN:HB3	2.51	0.41
1:A:201:ASN:HA	1:A:220:LYS:O	2.20	0.41
1:A:84:ILE:HD11	1:A:146:ALA:HB2	2.03	0.41
1:A:253:ASN:HD22	1:A:254:ASN:N	2.19	0.41
1:A:31:LEU:O	1:A:44:PRO:HD3	2.19	0.41
1:A:25:LEU:HD22	1:A:25:LEU:N	2.36	0.41
1:B:178:SER:HB3	3:B:774:HOH:O	2.20	0.41
1:B:181:ILE:O	1:B:185:ILE:HG13	2.20	0.41
1:B:307:LYS:HD2	1:B:307:LYS:HA	1.84	0.41
1:B:252:CYS:HA	3:B:704:HOH:O	2.21	0.41
1:B:300:ILE:N	1:B:300:ILE:HD12	2.36	0.41
1:A:353:LYS:HB3	1:A:353:LYS:HE2	1.89	0.40
1:B:159:GLU:HA	1:B:192:TYR:OH	2.20	0.40
1:B:47:SER:OG	1:B:69:GLY:HA2	2.21	0.40
1:B:8:GLU:O	1:B:8:GLU:HG3	2.20	0.40
1:A:133:ASN:O	1:A:134:ALA:C	2.60	0.40

All (9) 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	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:LEU:CD2	1:A:180:ARG:NH2[3_655]	1.07	1.13
1:A:25:LEU:CD1	1:A:180:ARG:NH1[3_655]	1.20	1.00
1:A:25:LEU:CD2	1:A:180:ARG:CZ[3_655]	1.38	0.82
1:A:25:LEU:CG	1:A:180:ARG:NH1[3_655]	1.61	0.59
1:A:25:LEU:CG	1:A:180:ARG:NH2[3_655]	1.65	0.55
1:A:25:LEU:CG	1:A:180:ARG:CZ[3_655]	1.72	0.48
1:A:25:LEU:CD1	1:A:180:ARG:CZ[3_655]	2.10	0.10
1:A:390:SER:O	3:A:711:HOH:O[3_655]	2.12	0.08
1:A:25:LEU:CD2	1:A:180:ARG:NE[3_655]	2.14	0.06

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	308/404 (76%)	289 (94%)	18 (6%)	1 (0%)	46	63
1	B	308/404 (76%)	288 (94%)	18 (6%)	2 (1%)	30	43
All	All	616/808 (76%)	577 (94%)	36 (6%)	3 (0%)	34	48

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	200	GLY
1	B	200	GLY
1	B	308	SER

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	244/343 (71%)	229 (94%)	15 (6%)	23	36
1	B	245/343 (71%)	229 (94%)	16 (6%)	21	33
All	All	489/686 (71%)	458 (94%)	31 (6%)	22	35

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	VAL
1	A	25	LEU
1	A	52	THR
1	A	140	ASN
1	A	151	ASP
1	A	160	GLU
1	A	184	LEU
1	A	195	LEU
1	A	241	GLN
1	A	253	ASN
1	A	282	VAL
1	A	308	SER
1	A	351	LYS
1	A	360	LYS
1	A	363	LEU
1	B	15	VAL
1	B	31	LEU
1	B	46	LEU
1	B	54	THR
1	B	144	VAL
1	B	148	VAL
1	B	161	LEU
1	B	172	ASP
1	B	184	LEU
1	B	195	LEU
1	B	209	LEU
1	B	228	ILE
1	B	241	GLN
1	B	243	THR
1	B	302	ASN
1	B	380	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	140	ASN
1	A	194	ASN
1	A	241	GLN
1	A	253	ASN
1	B	72	HIS
1	B	74	ASN
1	B	177	HIS
1	B	241	GLN
1	B	302	ASN
1	B	358	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	A	600	-	4,4,4	2.70	1 (25%)	6,6,6	0.68	0
2	SO4	B	601	-	4,4,4	2.66	1 (25%)	6,6,6	0.71	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
2	SO4	A	600	-	-	0/0/0/0	0/0/0/0
2	SO4	B	601	-	-	0/0/0/0	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	SO4	O4-S	5.04	1.65	1.47
2	A	600	SO4	O4-S	5.16	1.65	1.47

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, 95th 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 ²)	Q<0.9
1	A	314/404 (77%)	-0.14	11 (3%) 48 48	12, 30, 75, 100	0
1	B	314/404 (77%)	0.00	14 (4%) 37 38	14, 31, 72, 97	0
All	All	628/808 (77%)	-0.07	25 (3%) 42 43	12, 30, 74, 100	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	344	GLY	7.0
1	B	309	TYR	5.9
1	B	308	SER	5.6
1	A	390	SER	5.4
1	A	25	LEU	4.2
1	A	91	LYS	4.1
1	B	6	THR	4.0
1	B	200	GLY	3.8
1	B	254	ASN	3.7
1	A	180	ARG	3.7
1	B	345	MET	3.6
1	A	308	SER	3.4
1	A	6	THR	3.3
1	B	130	ASP	3.2
1	B	389	HIS	3.2
1	A	200	GLY	2.8
1	B	228	ILE	2.6
1	B	3	ASN	2.5
1	B	131	PHE	2.5
1	A	228	ILE	2.4
1	A	131	PHE	2.3
1	A	253	ASN	2.2
1	A	261	ALA	2.2
1	B	299	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	253	ASN	2.2

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, 95th 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 ²)	Q<0.9
2	SO4	A	600	5/5	0.97	0.18	1.18	16,33,47,57	0
2	SO4	B	601	5/5	0.96	0.19	1.11	31,31,53,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.