Full wwPDB X-ray Structure Validation Report (i)

Mar 6, 2026 – 06:18 AM UTC

PDB ID	:	1J2G / pdb_00001j2g
Title	:	Crystal structure of Urate oxidase from Bacillus SP. TB-90 co-crystallized with 8-Azaxanthine
Authors	:	Hibi, T.; Nago, T.; Nishiya, Y.; Oda, J.
Deposited on	:	2003-01-05
Resolution	:	2.20 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

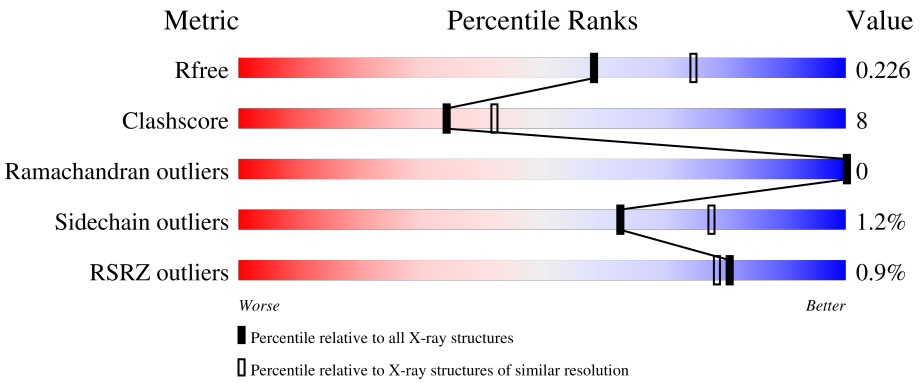
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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 >=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 <=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	319	% 85% 11% •
1	B	319	% 86% 9% • •
1	C	319	% 80% 16% •
1	D	319	% 83% 12% • •

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
3	AZA	A	4320	-	X	-	-

2 Entry composition (i)

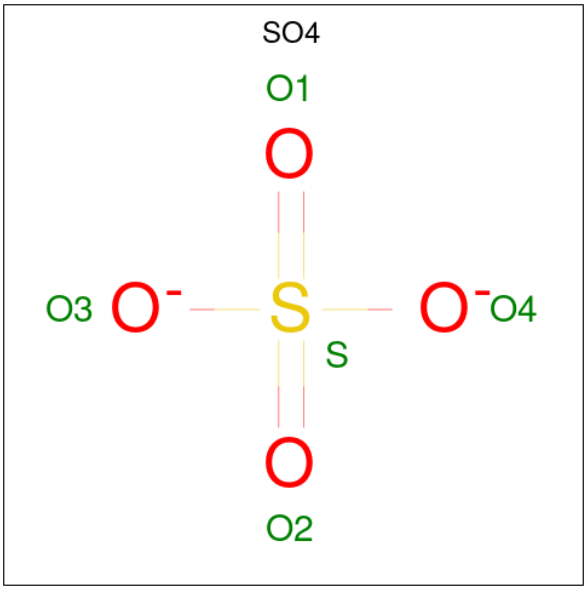
There are 4 unique types of molecules in this entry. The entry contains 10365 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Uricase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	306	2473	1585	409	475	4	0	0	0
1	B	306	2473	1585	409	475	4	0	0	0
1	C	306	2473	1585	409	475	4	0	0	0
1	D	306	2473	1585	409	475	4	0	0	0

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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

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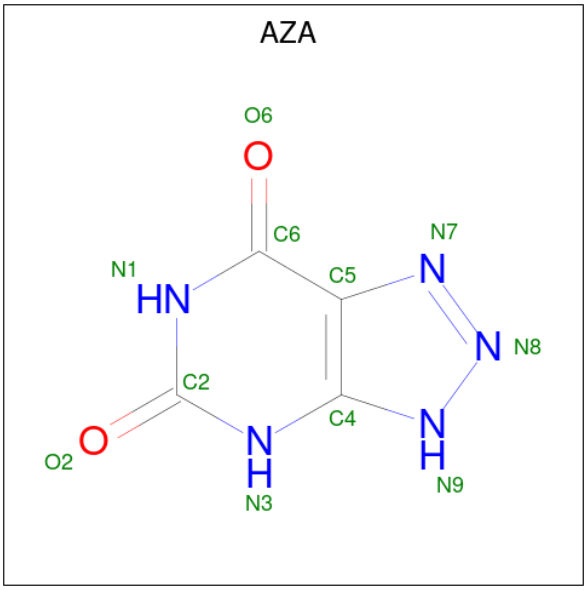
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0

- Molecule 3 is 8-AZAXANTHINE (CCD ID: AZA) (formula: $C_4H_3N_5O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 11 4 5 2	0	0
3	B	1	Total C N O 11 4 5 2	0	0
3	C	1	Total C N O 11 4 5 2	0	0
3	D	1	Total C N O 11 4 5 2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	81	Total O 81 81	0	0
4	B	115	Total O 115 115	0	0
4	C	131	Total O 131 131	0	0

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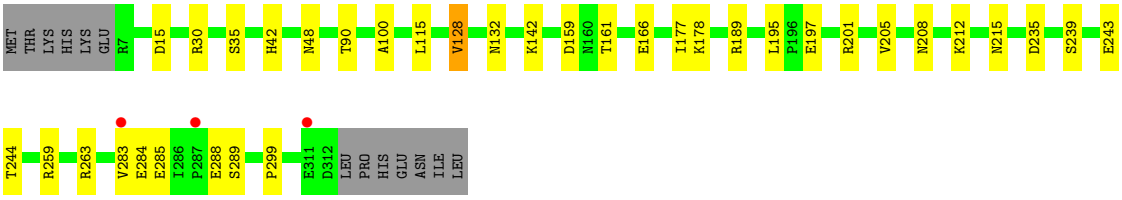
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	D	82	82	82	0	0

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.

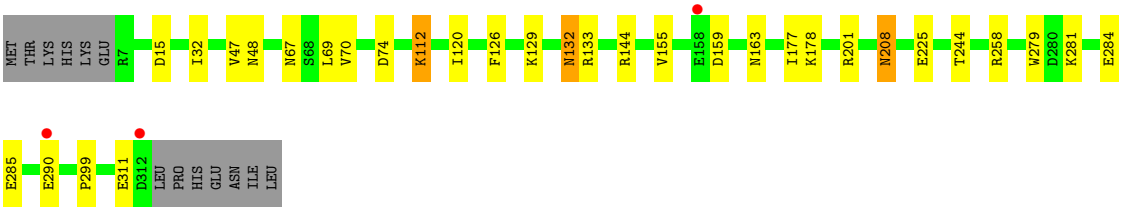
- Molecule 1: Uricase

Chain A:



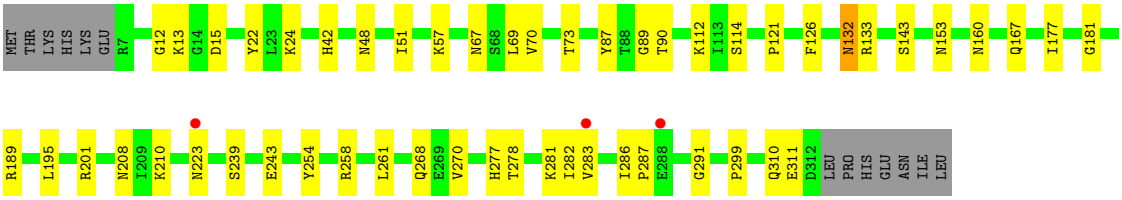
- Molecule 1: Uricase

Chain B:



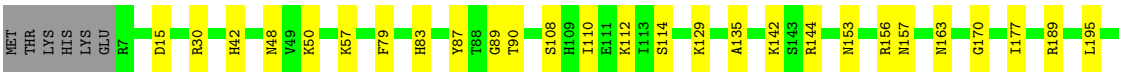
- Molecule 1: Uricase

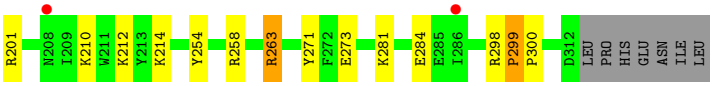
Chain C:



- Molecule 1: Uricase

Chain D:




R201
N208
I209
K210
W211
K212
Y213
K214
Y254
R258
R263
Y271
F272
E273
K281
E284
E285
I286
R298
P299
P300
D312
LEU
PRO
HIS
GLU
ASN
ILE
LEU

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	133.39Å 144.41Å 78.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.01 – 2.20 48.01 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.2 (48.01-2.20) 97.1 (48.01-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.06 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.180 , 0.218 0.191 , 0.226	Depositor DCC
R_{free} test set	3800 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	27.4	Xtriage
Anisotropy	0.194	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 32.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.43$, $< L^2 > = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	10365	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.80% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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, AZA

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	1.12	1/2530 (0.0%)	0.98	2/3428 (0.1%)
1	B	1.14	1/2530 (0.0%)	0.94	1/3428 (0.0%)
1	C	1.12	0/2530	0.96	2/3428 (0.1%)
1	D	1.15	0/2530	1.01	2/3428 (0.1%)
All	All	1.13	2/10120 (0.0%)	0.97	7/13712 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	283	VAL	CA-CB	5.33	1.60	1.54
1	B	32	ILE	C-O	-5.08	1.20	1.24

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	299	PRO	N-CA-C	6.16	118.22	110.70
1	C	299	PRO	N-CA-C	5.89	117.88	110.70
1	D	299	PRO	N-CA-C	5.70	117.66	110.70
1	A	299	PRO	N-CA-C	5.52	117.43	110.70
1	D	170	GLY	N-CA-C	5.13	119.08	110.56
1	C	278	THR	N-CA-C	5.07	117.45	110.35
1	A	132	ASN	N-CA-C	5.02	117.58	109.40

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	2473	0	2429	36	0
1	B	2473	0	2429	33	0
1	C	2473	0	2429	44	0
1	D	2473	0	2429	36	0
2	A	10	0	0	0	0
2	B	5	0	0	0	0
2	D	5	0	0	0	0
3	A	11	0	3	2	0
3	B	11	0	3	1	0
3	C	11	0	3	1	0
3	D	11	0	3	1	0
4	A	81	0	0	26	0
4	B	115	0	0	20	0
4	C	131	0	0	26	0
4	D	82	0	0	15	0
All	All	10365	0	9728	150	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 8.

All (150) 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:163:ASN:HB3	4:B:1411:HOH:O	1.38	1.24
1:B:69:LEU:HD23	4:B:1428:HOH:O	1.50	1.11
1:C:310:GLN:HB2	4:C:2438:HOH:O	1.53	1.06
1:B:112:LYS:HB2	4:B:1422:HOH:O	1.55	1.06
1:B:129:LYS:HD3	4:C:2437:HOH:O	1.60	1.00
1:B:208:ASN:HB2	4:B:1430:HOH:O	1.61	0.99
1:A:128:VAL:HG21	4:D:3385:HOH:O	1.60	0.99
1:A:142:LYS:HD2	4:A:4381:HOH:O	1.60	0.99
1:A:212:LYS:HE2	4:A:4391:HOH:O	1.63	0.99
1:B:281:LYS:HE3	4:B:1424:HOH:O	1.68	0.93
1:A:289:SER:HB2	4:D:3399:HOH:O	1.72	0.87
1:B:311:GLU:HB3	4:B:1419:HOH:O	1.76	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:ARG:HD3	4:A:4392:HOH:O	1.75	0.85
1:D:112:LYS:HD3	4:D:3395:HOH:O	1.79	0.82
1:C:208:ASN:CG	4:C:2433:HOH:O	2.23	0.82
4:A:4388:HOH:O	1:B:74:ASP:HB2	1.80	0.81
4:A:4371:HOH:O	1:D:144:ARG:HD2	1.80	0.81
1:A:30:ARG:HG3	4:A:4401:HOH:O	1.83	0.77
1:D:57:LYS:HD3	4:D:3400:HOH:O	1.86	0.75
1:B:144:ARG:HD2	4:C:2398:HOH:O	1.85	0.75
1:A:289:SER:CB	4:D:3399:HOH:O	2.33	0.74
1:B:285:GLU:CB	4:B:1431:HOH:O	2.34	0.73
1:D:212:LYS:HE2	4:D:3384:HOH:O	1.87	0.73
1:D:281:LYS:HD3	1:D:284:GLU:HG2	1.71	0.73
1:B:285:GLU:HB2	4:B:1431:HOH:O	1.88	0.72
1:A:288:GLU:HG3	4:A:4385:HOH:O	1.90	0.72
1:C:24:LYS:HE3	4:C:2444:HOH:O	1.89	0.71
1:C:15:ASP:HA	1:C:48:ASN:HD21	1.56	0.71
1:C:69:LEU:CD1	4:C:2448:HOH:O	2.39	0.70
1:D:110:ILE:O	1:D:156:ARG:NH1	2.24	0.70
1:B:15:ASP:HA	1:B:48:ASN:HD21	1.55	0.70
1:C:57:LYS:HB3	4:C:2448:HOH:O	1.90	0.70
1:A:15:ASP:HA	1:A:48:ASN:HD21	1.58	0.69
1:D:189:ARG:NH2	1:D:195:LEU:O	2.23	0.68
1:A:288:GLU:HG2	4:A:4395:HOH:O	1.95	0.66
1:A:166:GLU:CG	4:A:4391:HOH:O	2.43	0.66
1:A:161:THR:HG23	4:A:4396:HOH:O	1.95	0.65
1:C:223:ASN:HB2	4:C:2380:HOH:O	1.97	0.64
1:A:166:GLU:HG2	4:A:4391:HOH:O	1.98	0.63
1:D:214:LYS:HE2	4:D:3386:HOH:O	1.97	0.63
1:B:225:GLU:HG2	4:B:1410:HOH:O	1.99	0.63
1:C:210:LYS:HE2	4:C:2445:HOH:O	1.98	0.62
1:A:288:GLU:CG	4:A:4395:HOH:O	2.47	0.62
1:A:239:SER:O	1:A:243:GLU:HG3	1.99	0.62
1:C:277:HIS:HE1	4:C:2443:HOH:O	1.82	0.62
1:D:15:ASP:HA	1:D:48:ASN:HD21	1.65	0.61
1:A:30:ARG:NH1	4:A:4392:HOH:O	2.33	0.61
1:B:285:GLU:HB3	4:B:1431:HOH:O	2.00	0.60
1:B:201:ARG:HH12	3:B:1320:AZA:HN3	1.49	0.60
1:C:87:TYR:CZ	1:C:89:GLY:HA3	2.37	0.60
1:A:30:ARG:HG2	4:A:4380:HOH:O	2.01	0.60
1:A:201:ARG:HH12	3:A:4320:AZA:HN3	1.50	0.60
1:A:159:ASP:CG	4:A:4396:HOH:O	2.45	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:215:ASN:HB3	4:A:4387:HOH:O	2.00	0.60
1:D:210:LYS:HE2	4:D:3398:HOH:O	2.02	0.60
1:A:288:GLU:CD	4:A:4395:HOH:O	2.45	0.59
1:A:212:LYS:CE	4:A:4391:HOH:O	2.32	0.59
1:A:285:GLU:HG2	4:A:4397:HOH:O	2.01	0.59
1:A:35:SER:HB2	1:A:235:ASP:HB2	1.85	0.59
1:C:277:HIS:CE1	4:C:2443:HOH:O	2.55	0.59
1:D:210:LYS:HD3	4:D:3398:HOH:O	2.03	0.59
1:D:299:PRO:HD2	1:D:300:PRO:HD3	1.85	0.58
1:D:57:LYS:CD	4:D:3400:HOH:O	2.45	0.58
1:C:282:ILE:HG22	1:C:283:VAL:HG23	1.87	0.57
1:C:268:GLN:NE2	4:C:2438:HOH:O	2.37	0.56
1:A:189:ARG:NH2	1:A:195:LEU:O	2.37	0.56
1:C:114:SER:HB2	1:C:153:ASN:HD22	1.69	0.56
1:D:254:TYR:CE2	1:D:258:ARG:HD2	2.41	0.56
1:C:310:GLN:CB	4:C:2438:HOH:O	2.27	0.56
4:B:1435:HOH:O	1:C:22:TYR:CE2	2.53	0.55
1:C:223:ASN:CB	4:C:2380:HOH:O	2.54	0.55
1:C:201:ARG:HH12	3:C:2320:AZA:HN3	1.54	0.55
1:D:201:ARG:HH12	3:D:3320:AZA:HN3	1.54	0.55
1:B:284:GLU:HG3	4:B:1431:HOH:O	2.05	0.55
1:C:311:GLU:CD	4:C:2439:HOH:O	2.50	0.54
1:A:166:GLU:HG3	4:A:4391:HOH:O	2.06	0.53
1:A:178:LYS:NZ	1:A:244:THR:O	2.42	0.53
1:C:24:LYS:CE	4:C:2444:HOH:O	2.54	0.52
1:D:157:ASN:ND2	1:D:163:ASN:OD1	2.42	0.52
1:A:197:GLU:CD	4:A:4382:HOH:O	2.53	0.52
1:C:261:LEU:HD21	1:C:270:VAL:HG23	1.92	0.52
1:A:42:HIS:HE1	1:A:90:THR:O	1.93	0.52
1:B:112:LYS:HB3	1:B:155:VAL:HG12	1.91	0.51
1:B:258:ARG:HD3	4:B:1434:HOH:O	2.09	0.51
1:C:286:ILE:HD12	1:C:291:GLY:C	2.36	0.51
1:C:239:SER:O	1:C:243:GLU:HG3	2.10	0.51
1:C:208:ASN:CB	4:C:2433:HOH:O	2.59	0.51
1:C:208:ASN:HB3	4:C:2433:HOH:O	2.10	0.51
1:D:50:LYS:HE3	4:D:3392:HOH:O	2.11	0.51
1:B:284:GLU:HG2	4:B:1413:HOH:O	2.10	0.50
1:D:50:LYS:CE	4:D:3392:HOH:O	2.59	0.50
1:A:30:ARG:CG	4:A:4401:HOH:O	2.53	0.49
1:A:284:GLU:CG	4:A:4400:HOH:O	2.60	0.49
3:A:4320:AZA:N8	4:A:4388:HOH:O	2.32	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:167:GLN:NE2	4:C:2369:HOH:O	2.31	0.49
4:B:1433:HOH:O	1:C:282:ILE:HD11	2.13	0.48
1:C:126:PHE:HB2	1:C:133:ARG:NH2	2.29	0.48
1:D:30:ARG:NH2	1:D:263:ARG:O	2.46	0.48
1:C:121:PRO:HB2	1:C:143:SER:HB3	1.95	0.47
1:B:126:PHE:HB2	1:B:133:ARG:NH2	2.29	0.47
4:B:1433:HOH:O	1:C:282:ILE:CD1	2.62	0.47
1:D:87:TYR:CZ	1:D:89:GLY:HA3	2.49	0.47
1:D:108:SER:HA	1:D:156:ARG:NH2	2.30	0.47
1:D:299:PRO:CD	1:D:300:PRO:HD3	2.44	0.47
1:B:208:ASN:C	1:B:208:ASN:HD22	2.22	0.47
1:C:133:ARG:HD3	4:C:2426:HOH:O	2.15	0.46
1:C:189:ARG:NH2	1:C:195:LEU:O	2.47	0.46
1:B:177:ILE:CD1	1:B:279:TRP:CZ3	2.98	0.46
1:A:285:GLU:CG	4:A:4397:HOH:O	2.63	0.46
1:C:281:LYS:HB2	4:C:2436:HOH:O	2.16	0.45
1:B:177:ILE:HD13	1:B:279:TRP:CH2	2.52	0.45
1:B:285:GLU:HG2	4:B:1420:HOH:O	2.16	0.45
1:C:160:ASN:ND2	4:C:2450:HOH:O	2.49	0.45
4:A:4371:HOH:O	1:D:144:ARG:CD	2.53	0.45
1:C:12:GLY:HA3	1:C:51:ILE:O	2.17	0.45
1:D:48:ASN:C	1:D:48:ASN:HD22	2.25	0.45
1:C:42:HIS:HE1	1:C:90:THR:O	2.00	0.44
1:D:42:HIS:HE1	1:D:90:THR:O	2.00	0.44
1:C:69:LEU:HD12	4:C:2448:HOH:O	2.09	0.44
1:B:178:LYS:NZ	1:B:244:THR:O	2.50	0.44
1:D:271:TYR:CE2	1:D:273:GLU:HG3	2.52	0.44
1:C:132:ASN:H	1:C:132:ASN:HD22	1.65	0.44
1:C:181:GLY:HA2	4:C:2446:HOH:O	2.17	0.43
1:D:156:ARG:HH11	1:D:156:ARG:HD2	1.62	0.43
1:D:298:ARG:HB3	1:D:299:PRO:CD	2.48	0.43
1:B:290:GLU:HB2	4:B:1435:HOH:O	2.18	0.43
1:C:287:PRO:HG3	4:C:2451:HOH:O	2.17	0.43
1:B:67:ASN:HD22	1:B:70:VAL:HG21	1.84	0.43
1:B:126:PHE:HB2	1:B:133:ARG:CZ	2.49	0.43
1:D:48:ASN:C	1:D:48:ASN:ND2	2.77	0.43
1:B:177:ILE:CD1	1:B:279:TRP:CH2	3.02	0.42
1:A:205:VAL:O	1:A:205:VAL:HG23	2.19	0.42
1:D:142:LYS:HG2	4:D:3387:HOH:O	2.19	0.42
1:B:159:ASP:HB3	4:B:1432:HOH:O	2.20	0.42
1:C:13:LYS:HD3	1:C:73:THR:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:129:LYS:HE2	1:D:135:ALA:O	2.20	0.42
1:B:132:ASN:HD22	1:B:132:ASN:H	1.67	0.42
1:B:284:GLU:CG	4:B:1431:HOH:O	2.65	0.42
1:D:57:LYS:HD2	4:D:3389:HOH:O	2.18	0.41
1:D:79:PHE:CE1	1:D:83:HIS:CE1	3.08	0.41
1:A:48:ASN:C	1:A:48:ASN:HD22	2.28	0.41
1:B:47:VAL:N	1:B:120:ILE:HD12	2.36	0.41
1:D:114:SER:HB2	1:D:153:ASN:ND2	2.36	0.41
1:C:287:PRO:HD3	4:C:2451:HOH:O	2.19	0.41
1:C:67:ASN:HD22	1:C:70:VAL:HG21	1.87	0.40
1:A:189:ARG:HH21	1:A:197:GLU:HG3	1.85	0.40
1:D:210:LYS:CD	4:D:3398:HOH:O	2.67	0.40
1:C:254:TYR:CZ	1:C:258:ARG:HD2	2.56	0.40
1:A:100:ALA:HB2	1:A:115:LEU:HD12	2.03	0.40
1:D:114:SER:HB2	1:D:153:ASN:HD22	1.87	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	304/319 (95%)	297 (98%)	7 (2%)	0	100	100
1	B	304/319 (95%)	296 (97%)	8 (3%)	0	100	100
1	C	304/319 (95%)	296 (97%)	8 (3%)	0	100	100
1	D	304/319 (95%)	297 (98%)	7 (2%)	0	100	100
All	All	1216/1276 (95%)	1186 (98%)	30 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	273/286 (96%)	268 (98%)	5 (2%)	51	68
1	B	273/286 (96%)	270 (99%)	3 (1%)	65	79
1	C	273/286 (96%)	270 (99%)	3 (1%)	65	79
1	D	273/286 (96%)	271 (99%)	2 (1%)	76	87
All	All	1092/1144 (96%)	1079 (99%)	13 (1%)	63	78

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	128	VAL
1	A	177	ILE
1	A	208	ASN
1	A	259	ARG
1	A	263	ARG
1	B	112	LYS
1	B	132	ASN
1	B	208	ASN
1	C	112	LYS
1	C	132	ASN
1	C	177	ILE
1	D	177	ILE
1	D	263	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	HIS
1	A	48	ASN
1	A	67	ASN
1	A	157	ASN
1	A	167	GLN
1	A	175	GLN

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Mol	Chain	Res	Type
1	A	304	GLN
1	B	48	ASN
1	B	67	ASN
1	B	132	ASN
1	B	157	ASN
1	B	163	ASN
1	B	208	ASN
1	B	226	ASN
1	C	48	ASN
1	C	67	ASN
1	C	132	ASN
1	C	153	ASN
1	C	160	ASN
1	C	163	ASN
1	C	175	GLN
1	C	232	GLN
1	D	48	ASN
1	D	153	ASN
1	D	157	ASN
1	D	208	ASN
1	D	223	ASN

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)

8 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	D	503	-	4,4,4	0.30	0	6,6,6	0.38	0
3	AZA	C	2320	-	12,12,12	3.65	6 (50%)	12,17,17	2.24	6 (50%)
3	AZA	B	1320	-	12,12,12	2.89	6 (50%)	12,17,17	1.89	4 (33%)
2	SO4	A	504	-	4,4,4	0.32	0	6,6,6	0.53	0
3	AZA	A	4320	-	12,12,12	3.80	9 (75%)	12,17,17	2.54	6 (50%)
3	AZA	D	3320	-	12,12,12	2.50	6 (50%)	12,17,17	2.28	5 (41%)
2	SO4	B	501	-	4,4,4	0.27	0	6,6,6	0.47	0
2	SO4	A	502	-	4,4,4	0.26	0	6,6,6	0.11	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	AZA	C	2320	-	-	-	0/2/2/2
3	AZA	B	1320	-	-	-	0/2/2/2
3	AZA	D	3320	-	-	-	0/2/2/2
3	AZA	A	4320	-	-	-	0/2/2/2

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2320	AZA	N9-N8	8.71	1.45	1.35
3	A	4320	AZA	N7-N8	8.07	1.47	1.32
3	A	4320	AZA	C4-N9	5.84	1.39	1.34
3	B	1320	AZA	N9-N8	5.76	1.42	1.35
3	C	2320	AZA	N7-N8	5.71	1.42	1.32
3	B	1320	AZA	N7-N8	5.24	1.41	1.32
3	D	3320	AZA	N7-N8	4.87	1.41	1.32
3	D	3320	AZA	N9-N8	4.67	1.40	1.35
3	A	4320	AZA	N9-N8	4.44	1.40	1.35
3	C	2320	AZA	C5-C4	3.94	1.45	1.38
3	A	4320	AZA	C2-N3	-3.75	1.31	1.37
3	C	2320	AZA	C2-N3	-3.48	1.31	1.37
3	A	4320	AZA	C5-C4	3.43	1.44	1.38
3	C	2320	AZA	C5-N7	3.32	1.40	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1320	AZA	C4-N3	-3.26	1.32	1.37
3	B	1320	AZA	C2-N3	-3.09	1.32	1.37
3	A	4320	AZA	C5-N7	2.81	1.40	1.36
3	B	1320	AZA	C5-C4	2.69	1.43	1.38
3	A	4320	AZA	C4-N3	-2.67	1.32	1.37
3	D	3320	AZA	C5-C4	2.55	1.43	1.38
3	B	1320	AZA	C6-N1	-2.44	1.34	1.38
3	D	3320	AZA	C4-N3	-2.33	1.33	1.37
3	A	4320	AZA	C2-N1	-2.33	1.33	1.37
3	D	3320	AZA	C6-N1	-2.21	1.34	1.38
3	C	2320	AZA	C4-N9	2.08	1.35	1.34
3	A	4320	AZA	C6-N1	-2.07	1.35	1.38
3	D	3320	AZA	C2-N3	-2.06	1.34	1.37

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	4320	AZA	N3-C2-N1	4.54	122.88	115.74
3	A	4320	AZA	C6-C5-N7	4.26	137.45	130.26
3	D	3320	AZA	N3-C2-N1	4.10	122.19	115.74
3	C	2320	AZA	N3-C2-N1	3.77	121.66	115.74
3	C	2320	AZA	C6-C5-N7	3.61	136.35	130.26
3	B	1320	AZA	N3-C2-N1	3.59	121.38	115.74
3	D	3320	AZA	C6-C5-N7	3.57	136.28	130.26
3	B	1320	AZA	C6-C5-N7	3.42	136.04	130.26
3	A	4320	AZA	O2-C2-N3	-3.20	116.17	121.86
3	C	2320	AZA	O2-C2-N3	-3.01	116.51	121.86
3	D	3320	AZA	N3-C4-N9	2.90	129.31	124.57
3	A	4320	AZA	C6-N1-C2	-2.64	122.73	126.37
3	A	4320	AZA	N3-C4-N9	2.59	128.79	124.57
3	D	3320	AZA	C6-N1-C2	-2.57	122.84	126.37
3	A	4320	AZA	C5-N7-N8	-2.56	105.67	108.60
3	C	2320	AZA	C5-N7-N8	-2.35	105.91	108.60
3	D	3320	AZA	C5-N7-N8	-2.30	105.97	108.60
3	C	2320	AZA	C6-N1-C2	-2.28	123.23	126.37
3	B	1320	AZA	O2-C2-N3	-2.28	117.81	121.86
3	C	2320	AZA	O6-C6-C5	-2.25	120.60	126.53
3	B	1320	AZA	N3-C4-N9	2.08	127.97	124.57

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2320	AZA	1	0
3	B	1320	AZA	1	0
3	A	4320	AZA	2	0
3	D	3320	AZA	1	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 (i)

6.1 Protein, DNA and RNA chains (i)

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	306/319 (95%)	-0.11	3 (0%)	79	77	11, 22, 44, 57	0
1	B	306/319 (95%)	-0.32	3 (0%)	79	77	8, 17, 40, 55	0
1	C	306/319 (95%)	-0.36	3 (0%)	79	77	6, 15, 40, 61	0
1	D	306/319 (95%)	-0.16	2 (0%)	84	82	10, 20, 38, 52	0
All	All	1224/1276 (95%)	-0.24	11 (0%)	81	79	6, 19, 41, 61	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	312	ASP	3.2
1	C	283	VAL	3.1
1	A	311	GLU	2.9
1	A	287	PRO	2.7
1	D	286	ILE	2.4
1	C	288	GLU	2.3
1	C	223	ASN	2.2
1	D	208	ASN	2.1
1	B	290	GLU	2.1
1	B	158	GLU	2.1
1	A	283	VAL	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, 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	B-factors(Å^2)	Q<0.9
2	SO4	B	501	5/5	0.87	0.15	64,65,66,66	0
2	SO4	A	504	5/5	0.90	0.10	68,68,70,72	0
3	AZA	D	3320	11/11	0.91	0.12	26,27,30,34	0
3	AZA	C	2320	11/11	0.92	0.13	25,28,31,31	0
3	AZA	A	4320	11/11	0.94	0.13	32,34,36,37	0
2	SO4	A	502	5/5	0.94	0.11	52,52,53,53	0
2	SO4	D	503	5/5	0.94	0.12	50,51,52,52	5
3	AZA	B	1320	11/11	0.95	0.12	27,31,33,34	0

6.5 Other polymers (i)

There are no such residues in this entry.